Project_Report

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1 Identification of Xylanase Genes from the Rumen Metagenome

Content creators:

Mahdi Anvari 610700002
Sadegh Rizi 610700007
Amirhossein Norouzi 610700014

University of Tehran, Department of Biotechnology

1.1 Introduction

Xylanases are a group of enzymes that play a crucial role in the breakdown of hemicellulose, a major component of plant cell walls. Their ability to degrade xylan, a complex polysaccharide, into simple sugars makes them essential in various industrial applications, including the production of biofuels, paper, and food products. The rumen, a complex digestive compartment in ruminant animals, contains a diverse microbial community that produces a range of enzymes, including xylanases, to break down dietary fibers. Identifying xylanase genes from the rumen metagenome can provide valuable insights into the genetic potential of these microorganisms and enhance our understanding of their role in fiber digestion. This project aims to find and characterize xylanase genes in the rumen metagenome, investigating their diversity and potential applications in industry.

1.2 Methods

1.2.1 Step 1: Identification of Potential Xylanase Sequences

```
[1]: %use bash
     cd Queries/
```

```
[2]: %use bash
     ls -1 | wc -l
```

We have downloaded 1,005 known xylanase queries from the CAZy database to use in a BLAST task for comparing with our contigs.

```
[3]: %use bash
     ls
```

Let's open one of them

```
[4]: %use bash
     cat A44594⎕.fasta
```

```
[5]: %use bash
     cd ..
     cat Queries/* > Queries.fasta
```

```
[6]: %use bash
     head -n 20 Queries.fasta
```

Since these are all protein sequences, we will use the tblastn tool for the BLAST task.

```
[7]: %use bash
     cd y5.final.contigs/
```

Now it's time to use tblastn and create a database from our contig file.

```
[ ]: %use bash
     makeblastdb -in y5.final.contigs.fa -dbtype nucl -out xylanase_db
```

Since this step is time-consuming and has already been completed, we will not execute this cell.

Next, we need to use this database to perform the BLAST task with our queries.

```
[ ]: %use bash
     tblastn -query ../Queries.fasta -db xylanase_db -out ../tblastn_result.out␣
      ↪-evalue 1e-5 -num_threads 7
```

Since this step is time-consuming and has already been completed, we will not execute this cell.

```
[9]: %use bash
     cd ..
```

```
[9]: %use bash
     head -n 20 tblastn_result.out
```

```
pir||A44594      k141_107880     48.691  191     85      5       6       187
586     26      8.89e-50        166
pir||A44594      k141_3922551    47.120  191     88      5       6       187
177     737     3.02e-47        161
pir||A44594      k141_3299547    46.316  190     89      5       7       187
779     222     1.43e-46        160
pir||A44594      k141_7053183    45.789  190     90      5       7       187
632     75      9.29e-46        158
pir||A44594      k141_3016448    47.027  185     89      4       11      188
142     690     2.06e-45        155
pir||A44594      k141_2003823    46.073  191     88      5       11      187
149     718     3.04e-45        157
pir||A44594      k141_3866072    45.026  191     92      5       6       187
```

```
121      681     1.38e-44          154
pir||A44594     k141_6831025    44.737  190     92      5       7       187
215     772     1.72e-43          152
pir||A44594     k141_6865374    47.340  188     90      4       7       187
3572    3015    1.85e-43          160
pir||A44594     k141_8364398    44.385  187     95      3       8       187
325     879     3.82e-43          152
pir||A44594     k141_405434     44.211  190     93      5       7       187
711     154     7.42e-43          150
pir||A44594     k141_2912295    44.385  187     95      4       7       186
555     1       7.55e-43          147
pir||A44594     k141_1421443    44.737  190     94      6       6       187
278     838     1.18e-42          150
pir||A44594     k141_6422758    46.524  187     91      4       8       187
472     1026    3.65e-42          155
pir||A44594     k141_8403825    49.375  160     69      4       37      187
3       473     5.49e-42          144
pir||A44594     k141_8341534    46.196  184     90      4       11      187
756     211     6.09e-42          153
pir||A44594     k141_8341534    43.316  187     97      4       8       187
1491    937     3.12e-39          145
pir||A44594     k141_8702412    43.590  195     95      5       7       187
1084    1665    1.51e-41          152
pir||A44594     k141_2737913    43.077  195     96      5       7       187
2120    2701    3.14e-41          153
pir||A44594     k141_1982495    43.850  187     96      3       8       187
1397    843     3.41e-41          150
```

[10]:
```bash
%use bash
sed -n '$=' tblastn_result.out
```

381439

We obtained fewer than 400,000 results from our BLAST search. These are potential sequences coding for xylanase, but they need to be filtered first. We will perform this filtration using Python in this section. After that, we also convert the nucleotide sequences to amino acides.

1.2.2 Run Filtering&Translation.ipynb

[11]:
```bash
%use bash
grep -c '^>' filtered_output.fasta
```

1844

The Python notebook has filtered and translated the contigs into amino acid sequences. Now, it's time to cluster these sequences and select representatives.

1.2.3 Step 2: Clustering and Selection of Representatives

```
[12]: %use bash
      cd-hit -i filtered_output.fasta -o clustered_sequences.fasta -c 0.97 -n 5
```

```
================================================================
Program: CD-HIT, V4.8.1 (+OpenMP), Aug 20 2021, 08:39:56
Command: cd-hit -i filtered_output.fasta -o
         clustered_sequences.fasta -c 0.97 -n 5

Started: Fri Aug 16 18:53:08 2024
================================================================
                          Output
----------------------------------------------------------------
total seq: 1844
longest and shortest : 642 and 100
Total letters: 340001
Sequences have been sorted

Approximated minimal memory consumption:
Sequence        : 0M
Buffer          : 1 X 10M = 10M
Table           : 1 X 65M = 65M
Miscellaneous   : 0M
Total           : 76M

Table limit with the given memory limit:
Max number of representatives: 2488903
Max number of word counting entries: 90422496

comparing sequences from          0  to        1844
.
    1844  finished        583  clusters

Approximated maximum memory consumption: 77M
writing new database
writing clustering information
program completed !

Total CPU time 0.17
```

```
[13]: %use bash
      grep -c '^>' clustered_sequences.fasta
```

```
583
```

We used CD-HIT to cluster the sequences, reducing our 1,844 amino acid sequences to 583 representative sequences.

1.2.4 Step 3: Modeling the Conserved Region and Filtering Sequences

Our group decided to model two subfamilies of xylanase, GH10 and GH11, and search for them within our filtered data. We downloaded 30 known protein sequences for each of these subfamilies from UniProt and began the modeling process using these sequences. We used MSA and HMM for modeling these subfamilies.

```
[15]: %use bash
      cd Modeling/
      ls
```

GH10   GH11

Let's start the modeling with GH10 subfamily.

```
[16]: %use bash
      cd GH10/
```

```
[17]: %use bash
      cd Sequences/
```

```
[18]: %use bash
      ls
```

```
C5J411.fasta.txt  O94163.fasta.txt
P40943.fasta.txt  Q5S7A8.fasta.txt
G4MLU0.fasta.txt  P07528.fasta.txt
P56588.fasta.txt  Q6PRW6.fasta.txt
I1RQU5.fasta.txt  P07529.fasta.txt
Q00177.fasta.txt  Q8J1Y4.fasta.txt
I1S3T9.fasta.txt  P23360.fasta.txt
Q01176.fasta.txt  Q96VB6.fasta.txt
O59859.fasta.txt  P23551.fasta.txt
Q0H904.fasta.txt  Q9P8J1.fasta.txt
O60206.fasta.txt  P23556.fasta.txt
Q12603.fasta.txt  W0HFK8.fasta.txt
O69231.fasta.txt  P29417.fasta.txt
Q2PGV8.fasta.txt
O74717.fasta.txt  P33559.fasta.txt
Q4JHP5.fasta.txt
```

These are the 30 sequences for modeling GH10 subfamily. Let's open one of them.

```
[19]: %use bash
      cat C5J411.fasta.txt
```

```
>sp|C5J411|XYNC_ASPNG Probable endo-1,4-beta-xylanase C OS=Aspergillus niger
OX=5061 GN=xlnC PE=2 SV=2
MVQIKVAALAMLFASQVLSEPIDPRQASVSIDTKFKAHGKKYLGNIGDQYTLTKNSKTPA
IIKADFGALTPENSMKWDATEPSRGQFSFSGSDYLVNFAQSNNKLIRGHTLVWHSQLPSW
```

```
VQSITDKNTLIEVMKNHITTVMQHYKGKIYAWDVVNEIFNEDGSLRDSVFYKVIGEDYVR
IAFETARAADPNAKLYINDYNLDSASYSKLTGMVSHVKKWIAAGIPIDGIGSQTHLSAGG
GAGISGALNALAGAGTKEIAVTELDIAGASSTDYVEVVEACLNQPKCIGITVWGVADPDS
WRSSSTPLLFDSNYNPKPAYDAIANAL
```

[20]:
```
%use bash
cd ../
```

[21]:
```
%use bash
cat Sequences/* > GH10_sequences.fasta
```

[22]:
```
%use bash
head -n 20 GH10_sequences.fasta
```

```
>sp|C5J411|XYNC_ASPNG Probable endo-1,4-beta-xylanase C OS=Aspergillus niger
OX=5061 GN=xlnC PE=2 SV=2
MVQIKVAALAMLFASQVLSEPIDPRQASVSIDTKFKAHGKKYLGNIGDQYTLTKNSKTPA
IIKADFGALTPENSMKWDATEPSRGQFSFSGSDYLVNFAQSNNKLIRGHTLVWHSQLPSW
VQSITDKNTLIEVMKNHITTVMQHYKGKIYAWDVVNEIFNEDGSLRDSVFYKVIGEDYVR
IAFETARAADPNAKLYINDYNLDSASYSKLTGMVSHVKKWIAAGIPIDGIGSQTHLSAGG
GAGISGALNALAGAGTKEIAVTELDIAGASSTDYVEVVEACLNQPKCIGITVWGVADPDS
WRSSSTPLLFDSNYNPKPAYDAIANAL
>sp|G4MLU0|XYN5_PYRO7 Endo-1,4-beta-xylanase 5 OS=Pyricularia oryzae (strain
70-15 / ATCC MYA-4617 / FGSC 8958) OX=242507 GN=XYL5 PE=3 SV=1
MTRLATLITLAGLLAVSPGAYAQRNRNDTGGSTGAEGLNSLAVKAGLLYFGTASDTRNFA
DEPYMSVVNNTNEFGMIVPENSMKWEATEKEPGRFSFANADRVRALTKANGQMLRCHALT
WHSQLPNFVKTTAWTRDTLTAAIESHISNEVGHFAGDCYAWDVVNEAVNENGSFRDSPFH
RTLGTDFLAISFRAAAAADPNAKLYYNDFNIETPGPKANAAMGIVRLLKEQGVRIDGVGF
QGHLTVGSTPSRAQLASQLQRFADLGVEVTYTELDIRHKSLPVSSRAAQDQARDYVSVIG
SCLDVTACVGVMVWQPTDKYSWIPETFPGTGDACLFDANMNPKPAYTSVSSLLAAAAATA
PASVVPPASVTTSKTPIQAGAGRETVSIAGLTLALSSLAFGMFML
>sp|I1RQU5|XYN1_GIBZE Endo-1,4-beta-xylanase 1 OS=Gibberella zeae (strain ATCC
MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) OX=229533 GN=XYL1 PE=1
SV=1
MAWLQPTLCRKELESRQTSGLDAAMKAAGKKYFGTALTVRNDAGETNVLNTKGEFGSITP
ENAMKWEAIQPNRGQFNWGPADQHANAATQRGMELRCHTLVWHSQLPSWVANGNWNNQTL
QQVMKDHINAVMGRYKGKCTHWDVVNEALNEDGTYRDSVFYRVIGEAFIPIAFRMVLAAD
PTTKLYYNDYNLEYGGAKTAGAIRITKLIQSYGLRIDGVGLQAHMTSESTPTQSTVTPSR
```

[24]:
```
%use bash
# MSA
mafft --auto GH10_sequences.fasta > MSA_GH10_xylanases.fasta
```

```
outputhat23=16
treein = 0
compacttree = 0
stacksize: 8192 kb
rescale = 1
```

```
All-to-all alignment.
tbfast-pair (aa) Version 7.490
alg=L, model=BLOSUM62, 2.00, -0.10, +0.10, noshift, amax=0.0
0 thread(s)

outputhat23=16
Loading 'hat3.seed' …
done.
Writing hat3 for iterative refinement
rescale = 1
Gap Penalty = -1.53, +0.00, +0.00
tbutree = 1, compacttree = 0
Constructing a UPGMA tree …
    20 / 30
done.

Progressive alignment …
STEP    26 /29
Reallocating..done. *alloclen = 1876
STEP    29 /29
done.
tbfast (aa) Version 7.490
alg=A, model=BLOSUM62, 1.53, -0.00, -0.00, noshift, amax=0.0
1 thread(s)

minimumweight = 0.000010
autosubalignment = 0.000000
nthread = 0
randomseed = 0
blosum 62 / kimura 200
poffset = 0
niter = 16
sueff_global = 0.100000
nadd = 16
Loading 'hat3' … done.
rescale = 1

    20 / 30
Segment    1/  1    1- 605
STEP 006-017-1  identical.
Oscillating.

done
dvtditr (aa) Version 7.490
alg=A, model=BLOSUM62, 1.53, -0.00, -0.00, noshift, amax=0.0
0 thread(s)
```

Strategy:
 L-INS-i (Probably most accurate, very slow)
 Iterative refinement method (<16) with LOCAL pairwise alignment information

If unsure which option to use, try 'mafft --auto input > output'.
For more information, see 'mafft --help', 'mafft --man' and the mafft page.

The default gap scoring scheme has been changed in version 7.110 (2013 Oct).
It tends to insert more gaps into gap-rich regions than previous versions.
To disable this change, add the --leavegappyregion option.

[26]:
```bash
%use bash
head -n 20 MSA_GH10_xylanases.fasta
```

```
>sp|C5J411|XYNC_ASPNG Probable endo-1,4-beta-xylanase C OS=Aspergillus niger
OX=5061 GN=xlnC PE=2 SV=2
----M-------VQIKVAALAMLFASQVLSEP------------------IDPRQASV
SIDTKFKAHGKKYL--GNIGDQYTLTKNSKTPAII--KADFGALTPENSMKWDATEPSRG
------------------------QFSFSGSDYLVNFAQSNNKLIRGHTLVWHSQLPS
WVQSIT---------------DKNTLIEVMKNHITTVM-----QHYKGKIYAWDVVNEI
FNEDGS--LR-DSVF-YKVIGEDYVRIAFETARA------ADPNAKLYINDYNLDSASYS
KLT-GMVSHVKKWIAAGIPIDGIGS------------------QTHLSAGG-------
----GAGISGALNALAGAGTKEIAVTELDIA-----------------------GASS
TDYVEVVEACLNQPKCI-GITVWGVADPDSWRS------------------------
--SSTP---------------------LLFDSNYNPKPAYDA--------------
----IANAL-------------------------------------------------
-
>sp|G4MLU0|XYN5_PYRO7 Endo-1,4-beta-xylanase 5 OS=Pyricularia oryzae (strain
70-15 / ATCC MYA-4617 / FGSC 8958) OX=242507 GN=XYL5 PE=3 SV=1
----M----------TRLATLITLAGLLAVSPGAYAQ---------RNRNDTGGSTGAE
GLNSLAVKAGLLYF--GTASDTRNFAD-EPYMSVVNNTNEFGMIVPENSMKWEATEKEPG
------------------------RFSFANADRVRALTKANGQMLRCHALTWHSQLPN
FVKTTA--------------WTRDTLTAAIESHISNEV-----GHFAGDCYAWDVVNEA
VNENGS--FR-DSPF-HRTLGTDFLAISFRAAAA------ADPNAKLYYNDFNIETPG-P
KAN-AAMGIVRLLKEQGVRIDGVGF------------------QGHLTVGST------
--PSRAQLASQLQRFADLGV-EVTYTELDIRH----KSLP---------VSSRAAQDQA
```

[28]:
```bash
%use bash
# Modeling with HMM
hmmbuild GH10_xylanase.hmm MSA_GH10_xylanases.fasta
hmmsearch --tblout GH10_results.txt GH10_xylanase.hmm ../../clustered_sequences.
  ↪fasta
```

```
# hmmbuild :: profile HMM construction from multiple sequence alignments
# HMMER 3.3.2 (Nov 2020); http://hmmer.org/
# Copyright (C) 2020 Howard Hughes Medical Institute.
# Freely distributed under the BSD open source license.
```

```
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# input alignment file:            MSA_GH10_xylanases.fasta
# output HMM file:                 GH10_xylanase.hmm
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

# idx name                    nseq  alen  mlen eff_nseq re/pos description
#---- -------------------- ----- ----- ----- -------- ------ -----------
1      MSA_GH10_xylanases      30   601   340     1.31  0.590

# CPU time: 0.11u 0.00s 00:00:00.11 Elapsed: 00:00:00.13
# hmmsearch :: search profile(s) against a sequence database
# HMMER 3.3.2 (Nov 2020); http://hmmer.org/
# Copyright (C) 2020 Howard Hughes Medical Institute.
# Freely distributed under the BSD open source license.
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# query HMM file:                  GH10_xylanase.hmm
# target sequence database:        ../../clustered_sequences.fasta
# per-seq hits tabular output:     GH10_results.txt
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

Query:        MSA_GH10_xylanases  [M=340]
Scores for complete sequences (score includes all domains):
   --- full sequence ---   --- best 1 domain ---    -#dom-
    E-value  score  bias    E-value  score  bias    exp  N  Sequence
Description
    -------  ------ -----    ------- ------ -----    ---- --  --------
-----------
   1.9e-105  347.8   0.1   2.4e-105  347.5   0.1    1.0  1  k141_4174516
   6.4e-104  342.8   0.1      9e-104  342.3   0.1    1.1  1  k141_8751303
   5.1e-100  329.9   3.0   5.7e-100  329.8   3.0    1.0  1  k141_2596728
   6.2e-100  329.7   2.8   7.8e-100  329.3   2.8    1.1  1  k141_8352380
    1.5e-99  328.4   1.2    2.7e-99  327.6   1.2    1.3  1  k141_7876638
    1.9e-98  324.8   0.5    2.2e-98  324.6   0.5    1.0  1  k141_7518864
    2.2e-98  324.6   0.3    2.4e-98  324.4   0.3    1.0  1  k141_3207327
    3.9e-98  323.8   3.5    4.7e-98  323.5   3.5    1.0  1  k141_8446463
    2.5e-96  317.8   2.9    2.8e-96  317.7   2.9    1.0  1  k141_3648730
    7.2e-96  316.3   0.0    1.1e-95  315.7   0.0    1.2  1  k141_382248
    1.3e-94  312.2   3.2    1.5e-94  312.0   3.2    1.0  1  k141_7690424
    5.1e-91  300.4   2.1    5.7e-91  300.2   2.1    1.0  1  k141_2078416
    1.1e-89  296.0   0.4    1.3e-89  295.7   0.4    1.0  1  k141_5777399
    1.4e-89  295.6   1.2    1.8e-89  295.3   1.2    1.0  1  k141_6414633
    1.2e-87  289.3   1.8    1.5e-87  289.0   1.8    1.0  1  k141_1984896
    3.2e-87  287.9   1.6    3.6e-87  287.7   1.6    1.0  1  k141_3321694
    2.4e-85  281.7   1.6    2.7e-85  281.6   1.6    1.0  1  k141_1057675
    2.9e-85  281.4   1.7    4.4e-85  280.8   1.7    1.2  1  k141_4163169
    4.8e-85  280.7   1.7    5.3e-85  280.6   1.7    1.0  1  k141_2349245
    5.5e-85  280.5   2.6    6.9e-85  280.2   2.6    1.0  1  k141_3537260
    1.2e-84  279.4   0.9    1.4e-84  279.2   0.9    1.0  1  k141_169673
```

9

2.2e-84	278.5	1.2	2.7e-84	278.3	1.2	1.0	1	k141_8427476
3.1e-84	278.0	0.0	4e-84	277.7	0.0	1.0	1	k141_4868594
3.6e-83	274.6	2.0	4.4e-83	274.3	2.0	1.1	1	k141_5492129
8.1e-82	270.1	0.4	1.1e-81	269.7	0.4	1.2	1	k141_5537034
1.4e-81	269.3	0.2	1.7e-81	269.0	0.2	1.0	1	k141_4843626
1e-79	263.2	0.5	1.1e-79	263.0	0.5	1.0	1	k141_3972401
2.2e-79	262.1	0.1	3.6e-79	261.4	0.1	1.2	1	k141_3363962
5e-78	257.6	0.3	8.5e-78	256.9	0.3	1.3	1	k141_2686647
2.8e-77	255.2	0.1	4.1e-77	254.6	0.1	1.2	1	k141_967616
3.8e-77	254.8	0.6	4.2e-77	254.6	0.6	1.0	1	k141_2682329
8.1e-77	253.7	0.8	9.2e-77	253.5	0.8	1.0	1	k141_2078378
1e-76	253.3	1.0	6.4e-46	152.1	0.2	2.0	2	k141_3977683
1.9e-76	252.5	2.4	1.5e-75	249.5	2.4	1.9	1	k141_3525868
2.4e-75	248.9	0.0	3.1e-75	248.5	0.0	1.1	1	k141_8086075
1.3e-71	236.6	0.3	1.4e-71	236.4	0.3	1.0	1	k141_8350670
1.1e-70	233.5	0.1	1.3e-70	233.3	0.1	1.0	1	k141_9450604
1.6e-68	226.4	2.1	1.7e-68	226.3	2.1	1.0	1	k141_8466112
1.5e-67	223.2	0.1	1.8e-67	222.9	0.1	1.0	1	k141_1693700
2.1e-67	222.7	2.2	2.6e-67	222.4	2.2	1.1	1	k141_764324
9.2e-67	220.6	0.1	2.5e-66	219.2	0.1	1.6	1	k141_3957828
1e-66	220.4	3.1	1.3e-66	220.1	3.1	1.1	1	k141_3597594
3.2e-66	218.8	1.2	1.2e-65	217.0	1.2	1.7	1	k141_6262298
3.4e-66	218.7	0.4	4.1e-66	218.5	0.4	1.0	1	k141_5897125
5.1e-66	218.2	0.0	5.8e-66	218.0	0.0	1.0	1	k141_6147756
5.6e-66	218.0	1.0	7.1e-66	217.7	1.0	1.1	1	k141_8518009
2.2e-65	216.1	0.0	2.5e-65	215.9	0.0	1.0	1	k141_6541486
1e-64	213.9	0.1	1.3e-64	213.6	0.1	1.0	1	k141_2110739
1.1e-64	213.8	0.3	1.4e-64	213.4	0.3	1.1	1	k141_2681456
1.7e-64	213.2	0.0	1.8e-64	213.1	0.0	1.0	1	k141_3275240
2.6e-64	212.5	1.5	3.4e-64	212.2	1.5	1.1	1	k141_5782979
1.7e-62	206.6	4.1	1.8e-62	206.5	4.1	1.0	1	k141_9166542
1.1e-61	203.9	0.0	1.3e-61	203.7	0.0	1.0	1	k141_7127811
5.3e-61	201.7	0.1	6.2e-61	201.4	0.1	1.1	1	k141_3919179
1.1e-60	200.6	0.3	1.3e-60	200.4	0.3	1.0	1	k141_4551951
4.6e-60	198.6	0.3	5.6e-60	198.3	0.3	1.0	1	k141_2382513
1.1e-59	197.3	0.0	2.1e-59	196.4	0.0	1.4	1	k141_3934167
1.1e-59	197.3	0.0	1.5e-59	196.9	0.0	1.0	1	k141_8098396
1.4e-59	197.0	0.0	1.6e-59	196.8	0.0	1.0	1	k141_9008962
1.5e-59	196.9	1.9	1.6e-59	196.8	1.9	1.0	1	k141_6886796
2e-59	196.5	0.4	2.2e-59	196.3	0.4	1.0	1	k141_5776680
2.1e-59	196.4	1.2	2.2e-59	196.3	1.2	1.0	1	k141_363992
2.4e-59	196.3	0.2	2.6e-59	196.1	0.2	1.0	1	k141_8769892
3.7e-59	195.6	1.5	4e-59	195.5	1.5	1.0	1	k141_4984645
3.9e-59	195.5	0.0	4.5e-59	195.3	0.0	1.0	1	k141_5834011
1.7e-58	193.4	0.2	1.9e-58	193.3	0.2	1.0	1	k141_345001
6.4e-58	191.5	0.9	7.2e-58	191.4	0.9	1.0	1	k141_2725076
6.8e-58	191.5	0.1	7.7e-58	191.3	0.1	1.0	1	k141_8362774
8.6e-58	191.1	0.7	9.8e-58	190.9	0.7	1.0	1	k141_2943029

9.1e-58	191.0	0.0	1.3e-57	190.6	0.0	1.2	1	k141_6418135
1.7e-57	190.1	0.0	1.9e-57	190.0	0.0	1.0	1	k141_9437986
2.3e-57	189.7	0.1	2.6e-57	189.6	0.1	1.0	1	k141_2976020
6.1e-57	188.3	0.1	7.5e-57	188.0	0.1	1.0	1	k141_7696858
1.4e-55	183.8	0.8	1.6e-55	183.7	0.8	1.0	1	k141_3033986
2.9e-55	182.8	0.0	3.6e-55	182.5	0.0	1.1	1	k141_2060042
9e-55	181.2	1.0	1e-54	181.0	1.0	1.0	1	k141_8989385
1.2e-53	177.5	0.7	1.4e-53	177.3	0.7	1.0	1	k141_2722401
1.3e-53	177.4	0.7	1.4e-53	177.2	0.7	1.0	1	k141_8400597
2e-53	176.8	0.1	2.3e-53	176.6	0.1	1.0	1	k141_1740359
2.8e-52	173.0	0.1	3.5e-52	172.7	0.1	1.1	1	k141_6095884
3.6e-52	172.6	0.3	3.9e-52	172.5	0.3	1.0	1	k141_2071297
7.8e-52	171.5	0.0	1e-51	171.2	0.0	1.0	1	k141_85666
2.2e-51	170.0	0.0	2.6e-51	169.8	0.0	1.0	1	k141_3223482
2.4e-51	169.9	0.2	1.1e-50	167.7	0.2	1.8	1	k141_8814130
1.8e-50	167.1	0.0	2.5e-50	166.6	0.0	1.1	1	k141_3254317
3.6e-50	166.1	0.0	4e-50	165.9	0.0	1.0	1	k141_5481546
6.4e-50	165.2	0.2	7e-50	165.1	0.2	1.0	1	k141_5245547
7.6e-50	165.0	0.0	9e-50	164.7	0.0	1.1	1	k141_1676112
1.4e-49	164.1	0.2	1.6e-49	163.9	0.2	1.0	1	k141_770369
1.6e-49	163.9	0.5	6.8e-49	161.8	0.5	1.7	1	k141_9388058
2.2e-49	163.5	0.0	3e-49	163.0	0.0	1.1	1	k141_1004518
5.6e-49	162.1	0.0	6.2e-49	162.0	0.0	1.0	1	k141_1687580
6e-49	162.0	0.0	6.6e-49	161.9	0.0	1.0	1	k141_2899687
1e-48	161.3	0.2	5.1e-48	159.0	0.2	1.8	1	k141_8453879
1.9e-48	160.4	1.5	2.2e-48	160.2	1.5	1.0	1	k141_6119917
2.4e-48	160.0	0.0	3e-48	159.7	0.0	1.1	1	k141_9355598
1.9e-47	157.1	0.0	2.1e-47	157.0	0.0	1.0	1	k141_8034862
3.8e-47	156.1	0.0	4.1e-47	156.0	0.0	1.0	1	k141_5145849
4.7e-47	155.8	1.7	5.5e-47	155.6	1.7	1.0	1	k141_6755562
5.9e-47	155.5	0.4	6.5e-47	155.3	0.4	1.0	1	k141_3918953
7e-47	155.2	0.8	8.5e-47	155.0	0.8	1.0	1	k141_381421
9.6e-47	154.8	0.9	1.1e-46	154.6	0.9	1.0	1	k141_5473247
1e-46	154.7	0.1	2e-46	153.7	0.1	1.4	1	k141_5899885
1.9e-46	153.8	0.1	2.2e-46	153.6	0.1	1.0	1	k141_6547853
4e-46	152.8	0.9	4.9e-46	152.5	0.9	1.0	1	k141_3957880
4.4e-46	152.6	0.0	4.9e-46	152.5	0.0	1.0	1	k141_5915145
6e-46	152.2	0.3	6.5e-46	152.1	0.3	1.0	1	k141_729729
6.8e-46	152.0	0.0	7.8e-46	151.8	0.0	1.0	1	k141_6539735
7.7e-46	151.8	0.0	8.8e-46	151.6	0.0	1.0	1	k141_4184415
1.3e-45	151.0	0.2	1.4e-45	150.9	0.2	1.0	1	k141_7073722
2e-45	150.5	0.1	3.4e-45	149.7	0.1	1.3	1	k141_99796
2.4e-45	150.2	0.0	2.9e-45	149.9	0.0	1.0	1	k141_7842613
2.7e-45	150.0	0.0	2.8e-45	150.0	0.0	1.0	1	k141_2698953
7.2e-45	148.6	0.0	8.4e-45	148.4	0.0	1.0	1	k141_2362932
4.2e-44	146.1	2.5	4.8e-44	145.9	2.5	1.0	1	k141_3542624
6e-44	145.6	0.2	7.1e-44	145.4	0.2	1.0	1	k141_8990501
6.2e-44	145.5	0.0	7.6e-44	145.3	0.0	1.1	1	k141_81645

9.5e-44	144.9	0.0	1.2e-43	144.6	0.0	1.1	1	k141_6568681
1.3e-43	144.5	0.0	1.5e-43	144.3	0.0	1.0	1	k141_8720743
1.6e-43	144.2	0.0	1.8e-43	144.0	0.0	1.0	1	k141_1664273
2.6e-43	143.5	0.1	8.6e-43	141.8	0.1	1.7	1	k141_3339881
4.9e-43	142.6	0.2	5.4e-43	142.5	0.2	1.0	1	k141_8387005
8.7e-43	141.8	0.1	9.9e-43	141.6	0.1	1.0	1	k141_2242540
1.3e-42	141.2	0.0	1.4e-42	141.1	0.0	1.0	1	k141_5128900
2e-42	140.6	0.4	2.2e-42	140.5	0.4	1.0	1	k141_2744974
2.8e-42	140.1	0.1	4.5e-42	139.4	0.1	1.3	1	k141_6768541
3.3e-42	139.9	0.0	3.7e-42	139.7	0.0	1.0	1	k141_4566406
1.2e-41	138.1	0.0	1.3e-41	137.9	0.0	1.0	1	k141_7705448
1.2e-41	138.0	0.0	1.4e-41	137.9	0.0	1.0	1	k141_1668845
1.4e-41	137.8	0.0	1.7e-41	137.5	0.0	1.0	1	k141_3876761
1.7e-41	137.5	0.0	2e-41	137.3	0.0	1.0	1	k141_8781579
3.8e-41	136.4	0.9	8.3e-41	135.3	0.9	1.5	1	k141_1675803
4.2e-41	136.2	0.0	5e-41	136.0	0.0	1.1	1	k141_3232248
4.4e-41	136.2	0.1	5.3e-41	135.9	0.1	1.0	1	k141_2280578
1.3e-40	134.7	0.2	1.5e-40	134.4	0.2	1.1	1	k141_3959547
1.8e-40	134.1	0.3	2e-40	134.0	0.3	1.0	1	k141_1937314
1.9e-40	134.1	0.0	2.4e-40	133.8	0.0	1.0	1	k141_2407103
1.4e-39	131.3	0.1	1.7e-39	130.9	0.1	1.0	1	k141_9388540
1.6e-39	131.0	0.0	2e-39	130.8	0.0	1.1	1	k141_4594216
2.7e-39	130.3	0.0	3.4e-39	130.0	0.0	1.1	1	k141_8695735
3.8e-39	129.8	0.1	4.2e-39	129.7	0.1	1.0	1	k141_5883362
6.8e-39	129.0	5.4	3.9e-31	103.5	1.1	2.0	2	k141_1997068
7.7e-39	128.8	0.2	9.3e-39	128.5	0.2	1.1	1	k141_7383052
1.5e-38	127.8	0.0	1.7e-38	127.7	0.0	1.0	1	k141_1948421
3e-38	126.9	0.3	3.5e-38	126.6	0.3	1.0	1	k141_4670308
4.6e-38	126.2	0.0	5e-38	126.1	0.0	1.0	1	k141_4225899
4.8e-38	126.2	0.1	5.4e-38	126.0	0.1	1.0	1	k141_2291693
5.2e-38	126.1	5.7	3.5e-19	64.2	1.8	2.0	2	k141_2694739
5.4e-38	126.0	0.0	6.8e-38	125.7	0.0	1.0	1	k141_2979614
8.2e-38	125.4	3.0	1e-37	125.1	3.0	1.1	1	k141_1386000
2.2e-37	124.0	0.0	2.4e-37	123.9	0.0	1.0	1	k141_4259347
2.4e-37	123.9	0.0	3.1e-37	123.5	0.0	1.1	1	k141_1742464
7.3e-37	122.3	0.1	8e-37	122.2	0.1	1.0	1	k141_4241265
7.8e-37	122.2	0.0	8.8e-37	122.0	0.0	1.0	1	k141_4869652
9.6e-37	121.9	0.1	1e-36	121.8	0.1	1.0	1	k141_4819625
1.7e-36	121.1	0.1	1.8e-36	121.0	0.1	1.0	1	k141_343
2.2e-36	120.7	0.0	2.5e-36	120.6	0.0	1.0	1	k141_2323150
2.5e-36	120.6	0.8	6.1e-36	119.3	0.8	1.5	1	k141_3884748
3.1e-36	120.2	0.0	4.8e-36	119.6	0.0	1.3	1	k141_7435489
4.2e-36	119.8	0.9	1.1e-35	118.4	0.9	1.6	1	k141_1664014
1.1e-35	118.4	0.6	2.6e-35	117.2	0.6	1.5	1	k141_9322642
1.9e-35	117.7	0.1	2.3e-35	117.4	0.1	1.0	1	k141_4998935
2.2e-35	117.4	0.0	3.9e-35	116.6	0.0	1.4	1	k141_4558183
2.8e-35	117.1	1.1	3.1e-35	116.9	1.1	1.0	1	k141_184032
4.8e-35	116.3	0.1	1e-34	115.2	0.1	1.5	1	k141_361768

5.7e-35	116.1	0.0	6.4e-35	115.9	0.0	1.0	1	k141_2288917
6.5e-35	115.9	3.4	6.6e-20	66.6	0.8	2.0	2	k141_4261451
8.8e-35	115.5	0.0	9.8e-35	115.3	0.0	1.0	1	k141_5870918
3.6e-34	113.5	0.1	3.9e-34	113.3	0.1	1.0	1	k141_4499349
4e-34	113.3	0.0	4.4e-34	113.2	0.0	1.0	1	k141_3870991
4.6e-34	113.1	0.1	5e-34	113.0	0.1	1.0	1	k141_1429605
6.3e-34	112.6	0.2	6.8e-34	112.5	0.2	1.0	1	k141_8660148
1.4e-33	111.5	0.1	1.7e-33	111.3	0.1	1.0	1	k141_1782222
1.5e-33	111.4	0.1	1.7e-33	111.3	0.1	1.0	1	k141_5844076
2.5e-33	110.7	0.0	3e-33	110.4	0.0	1.0	1	k141_481571
6.2e-33	109.4	0.0	7.2e-33	109.2	0.0	1.0	1	k141_2284669
6.5e-33	109.3	0.0	7.7e-33	109.1	0.0	1.0	1	k141_7048725
1.4e-32	108.2	0.0	1.8e-32	107.9	0.0	1.0	1	k141_776577
4.1e-32	106.7	0.1	5e-32	106.4	0.1	1.0	1	k141_9159224
5.7e-32	106.2	0.0	6.2e-32	106.1	0.0	1.0	1	k141_7799275
7e-32	105.9	0.0	8.5e-32	105.6	0.0	1.0	1	k141_3706617
7.3e-32	105.9	0.1	8.2e-32	105.7	0.1	1.0	1	k141_3643877
9.2e-32	105.5	0.0	1.1e-31	105.2	0.0	1.0	1	k141_2354029
9.6e-32	105.5	0.0	1.1e-31	105.3	0.0	1.0	1	k141_5298442
1e-31	105.4	2.2	1.1e-22	75.7	0.0	2.0	2	k141_2355823
1.3e-31	105.1	0.0	1.8e-31	104.6	0.0	1.1	1	k141_722619
1.8e-31	104.6	0.0	2.3e-31	104.2	0.0	1.1	1	k141_4320936
2e-31	104.4	0.0	2.2e-31	104.3	0.0	1.0	1	k141_739152
3.3e-31	103.7	0.1	3.8e-31	103.5	0.1	1.0	1	k141_4902322
3.7e-31	103.5	0.1	4.5e-31	103.3	0.1	1.1	1	k141_4902342
3.8e-31	103.5	0.0	4.6e-31	103.2	0.0	1.0	1	k141_133522
4.4e-31	103.3	0.0	5e-31	103.1	0.0	1.0	1	k141_1715345
4.7e-31	103.2	0.1	5.4e-31	103.0	0.1	1.0	1	k141_1456835
4.8e-31	103.2	0.0	7e-31	102.6	0.0	1.1	1	k141_7508629
5.9e-31	102.9	0.0	6.6e-31	102.7	0.0	1.0	1	k141_9101925
7e-31	102.6	0.1	7.6e-31	102.5	0.1	1.0	1	k141_1451767
9.3e-31	102.2	0.0	1e-30	102.1	0.0	1.0	1	k141_8505961
1.2e-30	101.9	0.0	1.3e-30	101.8	0.0	1.0	1	k141_4656282
1.2e-30	101.8	4.9	2.7e-30	100.7	4.9	1.5	1	k141_8805185
1.2e-30	101.8	0.0	1.4e-30	101.7	0.0	1.0	1	k141_4835079
1.5e-30	101.6	0.0	1.5e-30	101.5	0.0	1.0	1	k141_8371797
1.5e-30	101.6	0.0	2e-30	101.1	0.0	1.1	1	k141_143768
1.8e-30	101.3	0.0	1.9e-30	101.2	0.0	1.0	1	k141_9041310
2.8e-30	100.6	0.3	6.2e-30	99.5	0.3	1.5	1	k141_7833819
3.2e-30	100.5	0.0	7.8e-30	99.2	0.0	1.5	1	k141_981745
3.7e-30	100.2	0.0	3.9e-30	100.2	0.0	1.0	1	k141_7501167
4.4e-30	100.0	0.1	5e-30	99.8	0.1	1.0	1	k141_2015286
4.4e-30	100.0	0.0	6.2e-30	99.5	0.0	1.1	1	k141_3368813
4.6e-30	99.9	0.0	5.2e-30	99.8	0.0	1.0	1	k141_3970024
5.2e-30	99.8	0.1	5.9e-30	99.6	0.1	1.0	1	k141_3873057
5.6e-30	99.7	0.0	6.2e-30	99.5	0.0	1.0	1	k141_7764613
6.1e-30	99.5	0.0	7.9e-30	99.2	0.0	1.1	1	k141_504816
6.3e-30	99.5	5.2	8.2e-19	63.0	0.2	2.0	2	k141_5204268

6.7e-30	99.4	0.0	7.7e-30	99.2	0.0	1.0	1	k141_6467628
7.8e-30	99.2	0.0	8.6e-30	99.1	0.0	1.0	1	k141_7820046
1.1e-29	98.6	0.1	1.3e-29	98.4	0.1	1.0	1	k141_386242
1.2e-29	98.6	0.0	1.6e-29	98.1	0.0	1.1	1	k141_6162000
1.8e-29	98.0	0.0	1.9e-29	97.9	0.0	1.1	1	k141_116719
2.2e-29	97.7	0.0	2.6e-29	97.5	0.0	1.0	1	k141_6477998
3.5e-29	97.1	0.0	3.9e-29	96.9	0.0	1.0	1	k141_4320792
4.6e-29	96.7	0.7	5.2e-29	96.5	0.7	1.0	1	k141_7233680
4.9e-29	96.6	0.0	6.8e-29	96.1	0.0	1.1	1	k141_3381700
5e-29	96.5	0.0	5.6e-29	96.4	0.0	1.0	1	k141_6742680
6.9e-29	96.1	0.0	7.7e-29	95.9	0.0	1.0	1	k141_5789127
1.2e-28	95.3	0.1	1.5e-28	95.0	0.1	1.0	1	k141_6835332
2.6e-28	94.2	1.2	7e-28	92.8	1.2	1.5	1	k141_1980774
3e-28	94.0	0.0	4.1e-28	93.5	0.0	1.1	1	k141_1734958
3.4e-28	93.8	0.3	3.9e-28	93.6	0.3	1.0	1	k141_3346314
3.8e-28	93.7	0.0	5.4e-28	93.1	0.0	1.1	1	k141_4200987
4.5e-28	93.4	0.0	6.3e-28	92.9	0.0	1.1	1	k141_793644
6.3e-28	92.9	0.0	6.7e-28	92.8	0.0	1.0	1	k141_107045
1.2e-27	92.0	0.0	1.4e-27	91.8	0.0	1.1	1	k141_4537008
1.5e-27	91.7	0.0	1.9e-27	91.4	0.0	1.1	1	k141_417097
2.3e-27	91.1	0.0	3e-27	90.7	0.0	1.1	1	k141_164929
2.7e-27	90.9	0.7	3.3e-27	90.6	0.7	1.1	1	k141_1399820
4.4e-27	90.1	0.9	4.7e-27	90.1	0.9	1.0	1	k141_6478272
5.1e-27	89.9	0.1	6.2e-27	89.6	0.1	1.1	1	k141_7803464
6.7e-27	89.5	6.7	8.8e-17	56.3	0.5	2.0	2	k141_6822803
9.1e-27	89.1	0.0	1.2e-26	88.7	0.0	1.1	1	k141_1962144
1.5e-26	88.4	2.2	1.9e-26	88.1	2.2	1.1	1	k141_8337506
3.3e-26	87.3	0.0	3.6e-26	87.1	0.0	1.0	1	k141_2401341
4.1e-26	87.0	0.1	1.1e-25	85.5	0.1	1.6	1	k141_1105734
6.1e-26	86.4	0.0	7.2e-26	86.2	0.0	1.0	1	k141_8164561
8.7e-26	85.9	0.0	1e-25	85.6	0.0	1.1	1	k141_6868187
8.9e-26	85.9	0.1	9.8e-26	85.7	0.1	1.0	1	k141_5933602
1e-25	85.7	1.3	1.2e-25	85.4	1.3	1.0	1	k141_4348153
1.1e-25	85.6	0.0	1.2e-25	85.4	0.0	1.0	1	k141_7416581
1.3e-25	85.3	0.1	1.4e-25	85.2	0.1	1.0	1	k141_328913
1.3e-25	85.3	0.6	1.4e-25	85.2	0.6	1.1	1	k141_5146991
1.4e-25	85.2	0.3	1.5e-25	85.1	0.3	1.0	1	k141_8183010
1.6e-25	85.0	0.0	1.8e-25	84.8	0.0	1.0	1	k141_8660669
1.8e-25	84.8	0.1	2.1e-25	84.6	0.1	1.0	1	k141_4173172
2.1e-25	84.6	0.2	2.5e-25	84.4	0.2	1.0	1	k141_7444673
2.2e-25	84.6	0.1	2.3e-25	84.5	0.1	1.0	1	k141_8366699
2.2e-25	84.6	0.0	2.7e-25	84.3	0.0	1.1	1	k141_2038176
2.2e-25	84.5	0.0	2.6e-25	84.3	0.0	1.1	1	k141_475762
3.6e-25	83.8	0.1	9.2e-25	82.5	0.1	1.5	1	k141_4916380
4.2e-25	83.6	0.2	4.8e-25	83.5	0.2	1.0	1	k141_4333985
4.6e-25	83.5	0.0	5.2e-25	83.3	0.0	1.0	1	k141_4570102
5e-25	83.4	0.0	5.6e-25	83.2	0.0	1.0	1	k141_3272949
8.8e-25	82.6	0.0	9.6e-25	82.5	0.0	1.0	1	k141_1292909

2.2e-24	81.2	0.0	2.9e-24	80.9	0.0	1.1	1	k141_4512856
2.8e-24	81.0	0.0	3e-24	80.8	0.0	1.0	1	k141_1100704
3.1e-24	80.8	0.0	3.9e-24	80.5	0.0	1.1	1	k141_9117506
8.8e-24	79.3	0.0	1.1e-23	79.0	0.0	1.1	1	k141_4280798
9.8e-24	79.1	0.0	1.2e-23	78.9	0.0	1.0	1	k141_9056285
1e-23	79.1	0.2	1.8e-23	78.2	0.2	1.4	1	k141_4506069
1e-23	79.0	1.8	1.9e-23	78.2	1.8	1.3	1	k141_3574528
1.1e-23	79.0	0.0	1.3e-23	78.7	0.0	1.1	1	k141_8168242
1.9e-23	78.2	0.1	2e-23	78.1	0.1	1.0	1	k141_6221619
2.7e-23	77.7	0.0	3.6e-23	77.3	0.0	1.1	1	k141_7772334
4.5e-23	77.0	0.1	4.9e-23	76.8	0.1	1.0	1	k141_7492124
1.3e-22	75.5	0.2	1.3e-22	75.4	0.2	1.0	1	k141_2386947
1.3e-22	75.4	0.1	1.8e-22	75.0	0.1	1.1	1	k141_4192004
1.5e-22	75.3	0.0	1.9e-22	74.9	0.0	1.1	1	k141_7067511
1.9e-22	74.9	2.3	2.1e-22	74.8	2.3	1.0	1	k141_6489240
2.3e-22	74.6	0.1	2.7e-22	74.4	0.1	1.0	1	k141_6896667
2.8e-22	74.4	0.0	3e-22	74.3	0.0	1.0	1	k141_4196785
3.1e-22	74.2	0.0	3.7e-22	73.9	0.0	1.1	1	k141_2612004
3.2e-22	74.2	0.0	4.2e-22	73.8	0.0	1.2	1	k141_3018142
3.9e-22	73.9	0.0	4.4e-22	73.7	0.0	1.0	1	k141_5942936
7.7e-22	72.9	0.0	9.9e-22	72.5	0.0	1.0	1	k141_4920788
8.6e-22	72.7	0.0	1e-21	72.5	0.0	1.0	1	k141_5276643
8.9e-22	72.7	0.0	1.2e-21	72.3	0.0	1.2	1	k141_106785
1.9e-21	71.6	0.0	2.2e-21	71.4	0.0	1.0	1	k141_3963985
2e-21	71.5	0.0	2.2e-21	71.4	0.0	1.0	1	k141_6895992
2.3e-21	71.4	0.0	2.6e-21	71.2	0.0	1.0	1	k141_6566158
2.3e-21	71.3	0.2	2.9e-21	71.0	0.2	1.0	1	k141_5813762
2.6e-21	71.2	0.2	3e-21	71.0	0.2	1.0	1	k141_4289006
3.3e-21	70.8	0.0	4.1e-21	70.5	0.0	1.1	1	k141_8764640
5.8e-21	70.0	0.0	7.3e-21	69.7	0.0	1.1	1	k141_5216115
6.2e-21	69.9	0.1	2e-20	68.3	0.1	1.7	1	k141_2255399
6.5e-21	69.9	0.0	7e-21	69.8	0.0	1.0	1	k141_2593531
8.1e-21	69.6	0.0	9.3e-21	69.4	0.0	1.0	1	k141_1956985
2.6e-20	67.9	0.5	3.5e-20	67.5	0.5	1.2	1	k141_7099078
3.2e-20	67.6	0.3	3.7e-20	67.4	0.3	1.0	1	k141_8196762
3.8e-20	67.3	0.0	5.1e-20	66.9	0.0	1.1	1	k141_7521840
4.6e-20	67.1	0.2	5.6e-20	66.8	0.2	1.0	1	k141_2114742
5.1e-20	66.9	0.0	6e-20	66.7	0.0	1.1	1	k141_7473579
1e-19	66.0	0.2	1.1e-19	65.8	0.2	1.0	1	k141_722048
1.1e-19	65.9	0.1	1.2e-19	65.7	0.1	1.0	1	k141_381101
1.6e-19	65.3	0.0	1.8e-19	65.1	0.0	1.0	1	k141_1792251
1.7e-19	65.2	0.6	1.8e-19	65.1	0.6	1.0	1	k141_6451618
2.1e-19	64.9	0.1	2.2e-19	64.8	0.1	1.0	1	k141_1055552
2.1e-19	64.9	0.0	2.7e-19	64.6	0.0	1.1	1	k141_5292368
2.1e-19	64.9	0.2	2.4e-19	64.7	0.2	1.0	1	k141_6278524
2.3e-19	64.8	0.8	2.5e-19	64.7	0.8	1.0	1	k141_7545186
2.5e-19	64.7	0.0	2.7e-19	64.5	0.0	1.0	1	k141_6791180
2.6e-19	64.6	0.0	3e-19	64.4	0.0	1.1	1	k141_715426

3.7e-19	64.1	0.0	4.6e-19	63.8	0.0	1.1	1	k141_7712328
4e-19	64.0	0.0	5e-19	63.7	0.0	1.1	1	k141_6844872
4.3e-19	63.9	0.0	4.7e-19	63.8	0.0	1.0	1	k141_1144944
4.7e-19	63.8	0.1	5.3e-19	63.6	0.1	1.0	1	k141_3956792
5.1e-19	63.6	0.0	5.4e-19	63.5	0.0	1.0	1	k141_9442212
5.2e-19	63.6	1.7	2.8e-18	61.2	1.7	1.8	1	k141_3380878
5.3e-19	63.6	0.1	6.5e-19	63.3	0.1	1.0	1	k141_5451066
6e-19	63.4	0.2	7.1e-19	63.2	0.2	1.0	1	k141_8646947
6.5e-19	63.3	0.0	8e-19	63.0	0.0	1.1	1	k141_5523933
8.3e-19	62.9	0.0	1e-18	62.7	0.0	1.1	1	k141_2683772
1.1e-18	62.6	0.0	1.4e-18	62.2	0.0	1.1	1	k141_8386520
1.3e-18	62.3	0.7	1.5e-18	62.1	0.7	1.0	1	k141_6460686
1.6e-18	62.0	0.8	1.8e-18	61.9	0.8	1.0	1	k141_5470296
1.8e-18	61.8	0.0	2e-18	61.7	0.0	1.0	1	k141_2343559
2.4e-18	61.5	0.0	3.5e-18	60.9	0.0	1.2	1	k141_2370290
3.7e-18	60.8	0.0	4.2e-18	60.6	0.0	1.0	1	k141_1425005
4.5e-18	60.5	0.0	5.6e-18	60.2	0.0	1.1	1	k141_4636443
5.7e-18	60.2	0.0	6.6e-18	60.0	0.0	1.0	1	k141_8841745
7.2e-18	59.8	0.0	7.9e-18	59.7	0.0	1.0	1	k141_8150841
7.2e-18	59.8	0.0	8.8e-18	59.6	0.0	1.1	1	k141_4955497
8.2e-18	59.7	0.0	9.2e-18	59.5	0.0	1.1	1	k141_83729
1.1e-17	59.3	0.0	1.3e-17	59.0	0.0	1.0	1	k141_7140457
1.1e-17	59.2	0.3	1.5e-17	58.8	0.3	1.1	1	k141_3315131
2.7e-17	58.0	0.0	3.3e-17	57.7	0.0	1.1	1	k141_2330025
3.2e-17	57.7	0.0	3.8e-17	57.5	0.0	1.1	1	k141_7170802
3.6e-17	57.5	0.0	4.3e-17	57.3	0.0	1.1	1	k141_4678575
3.7e-17	57.5	0.0	4.9e-17	57.1	0.0	1.1	1	k141_446825
4.2e-17	57.3	0.0	4.4e-17	57.3	0.0	1.0	1	k141_5811690
4.8e-17	57.2	0.2	5.8e-17	56.9	0.2	1.0	1	k141_3933205
4.9e-17	57.1	0.6	1.3e-16	55.7	0.6	1.6	1	k141_3884755
5.9e-17	56.8	0.2	6.7e-17	56.7	0.2	1.1	1	k141_173967
5.9e-17	56.8	0.2	7.3e-17	56.6	0.2	1.1	1	k141_4004474
6.5e-17	56.7	0.4	7.7e-17	56.5	0.4	1.0	1	k141_1992987
7.7e-17	56.5	0.0	9.7e-17	56.1	0.0	1.1	1	k141_3542429
8.8e-17	56.3	0.1	9.8e-17	56.1	0.1	1.0	1	k141_961282
1.4e-16	55.6	0.0	1.6e-16	55.4	0.0	1.1	1	k141_1952417
1.5e-16	55.5	0.0	2e-16	55.1	0.0	1.1	1	k141_3526777
1.6e-16	55.5	0.1	1.7e-16	55.3	0.1	1.0	1	k141_3369516
1.6e-16	55.4	0.0	2.2e-16	55.0	0.0	1.1	1	k141_1939943
1.7e-16	55.4	0.0	2.3e-16	54.9	0.0	1.1	1	k141_2689211
1.7e-16	55.3	0.0	2.3e-16	54.9	0.0	1.1	1	k141_6113822
2.9e-16	54.6	0.3	3.3e-16	54.4	0.3	1.0	1	k141_7536866
3.7e-16	54.2	0.0	4.6e-16	53.9	0.0	1.1	1	k141_971700
3.8e-16	54.2	0.0	4.2e-16	54.0	0.0	1.0	1	k141_6202951
3.9e-16	54.2	0.0	5e-16	53.8	0.0	1.1	1	k141_3569566
4.2e-16	54.1	0.0	5.2e-16	53.7	0.0	1.1	1	k141_6860267
5.8e-16	53.6	0.0	6.3e-16	53.5	0.0	1.1	1	k141_8414726
7.4e-16	53.2	0.0	8.3e-16	53.1	0.0	1.0	1	k141_5586099

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7.5e-16   53.2   0.0   9.7e-16   52.9   0.0   1.1   1   k141_2372622
1.8e-15   51.9   0.1   2.3e-15   51.6   0.1   1.1   1   k141_5259053
2.3e-15   51.6   0.0   3.2e-15   51.2   0.0   1.1   1   k141_3370902
2.5e-15   51.5   0.0   2.9e-15   51.3   0.0   1.1   1   k141_322990
2.9e-15   51.3   0.0   3.8e-15   50.9   0.0   1.1   1   k141_2025155
4.7e-15   50.6   0.2   5.1e-15   50.5   0.2   1.0   1   k141_8794455
5.6e-15   50.4   0.0   7.9e-15   49.9   0.0   1.2   1   k141_8083224
6.1e-15   50.2   0.1   7.9e-15   49.9   0.1   1.1   1   k141_3361406
6.6e-15   50.1   0.0   9.7e-15   49.6   0.0   1.2   1   k141_3206100
8.1e-15   49.8   0.2   8.9e-15   49.7   0.2   1.0   1   k141_4598294
  1e-14   49.5   1.3   7.6e-13   43.3   1.3   2.0   1   k141_8171587
1.6e-14   48.8   0.3   2.1e-14   48.5   0.3   1.1   1   k141_8363470
  2e-14   48.5   0.0   2.2e-14   48.4   0.0   1.0   1   k141_3005971
2.1e-14   48.4   0.2   2.7e-14   48.1   0.2   1.1   1   k141_5950360
  3e-14   47.9   0.0   3.8e-14   47.6   0.0   1.1   1   k141_677431
4.8e-14   47.3   0.1   6.9e-14   46.8   0.1   1.1   1   k141_5494989
6.8e-14   46.8   0.0   7.3e-14   46.7   0.0   1.0   1   k141_6758321
  7e-14   46.7   0.1   9.4e-14   46.3   0.1   1.1   1   k141_2001968
7.5e-14   46.6   0.0   8.2e-14   46.5   0.0   1.1   1   k141_7179537
8.3e-14   46.5   0.1     1e-13   46.2   0.1   1.1   1   k141_9339147
9.9e-14   46.2   0.1   1.1e-13   46.1   0.1   1.1   1   k141_4818106
1.1e-13   46.1   0.0   1.3e-13   45.8   0.0   1.1   1   k141_8171708
1.6e-13   45.6   0.1   1.9e-13   45.3   0.1   1.1   1   k141_9141803
1.7e-13   45.5   0.0   2.3e-13   45.0   0.0   1.1   1   k141_8971703
2.4e-13   45.0   0.0   5.7e-13   43.7   0.0   1.4   1   k141_6494427
3.1e-13   44.6   0.0   3.7e-13   44.4   0.0   1.1   1   k141_5928501
3.3e-13   44.5   0.0   3.6e-13   44.4   0.0   1.1   1   k141_1962241
5.2e-13   43.9   0.1   6.1e-13   43.6   0.1   1.1   1   k141_3029768
5.8e-13   43.7   0.0   7.3e-13   43.4   0.0   1.1   1   k141_3877129
6.9e-13   43.5   0.0     8e-13   43.3   0.0   1.1   1   k141_4517395
7.5e-13   43.4   0.0   9.1e-13   43.1   0.0   1.1   1   k141_1043855
  8e-13   43.3   0.0   9.7e-13   43.0   0.0   1.0   1   k141_1958016
  1e-12   42.9   0.0   1.3e-12   42.6   0.0   1.1   1   k141_8028958
1.1e-12   42.8   0.1   1.3e-12   42.5   0.1   1.1   1   k141_2084643
1.7e-12   42.2   0.0   2.3e-12   41.8   0.0   1.1   1   k141_740240
2.3e-12   41.8   0.1     3e-12   41.4   0.1   1.1   1   k141_9468170
2.6e-12   41.6   0.1   3.1e-12   41.3   0.1   1.1   1   k141_4903408
2.8e-12   41.5   0.0   3.1e-12   41.3   0.0   1.0   1   k141_5131461
3.4e-12   41.2   0.0   4.6e-12   40.8   0.0   1.1   1   k141_5153724
8.5e-12   39.9   0.2   1.1e-11   39.5   0.2   1.1   1   k141_1750054
9.9e-12   39.7   0.0   1.4e-11   39.2   0.0   1.1   1   k141_2589822
3.3e-11   38.0   0.0   3.3e-11   38.0   0.0   1.1   1   k141_7756742
8.1e-11   36.7   0.0   9.8e-11   36.4   0.0   1.1   1   k141_9128397
9.8e-11   36.4   0.0   1.1e-10   36.2   0.0   1.1   1   k141_7094414
1.9e-10   35.5   0.0   2.2e-10   35.3   0.0   1.1   1   k141_5469463
2.5e-10   35.1   0.1   3.3e-10   34.7   0.1   1.1   1   k141_8982903
3.7e-10   34.5   0.0   4.5e-10   34.2   0.0   1.1   1   k141_8992782
  4e-10   34.4   0.1   5.3e-10   34.0   0.1   1.1   1   k141_4516513
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    4.5e-10   34.2   0.0    5.6e-10   33.9   0.0    1.1   1  k141_2612768
    6.1e-10   33.8   0.1      8e-10   33.4   0.1    1.1   1  k141_1708990
    6.8e-10   33.6   0.1      9e-10   33.2   0.1    1.1   1  k141_1112321
    9.5e-10   33.2   0.1      1e-09   33.0   0.1    1.1   1  k141_2597435
      1e-09   33.0   0.0    1.1e-09   32.9   0.0    1.0   1  k141_7688599
    1.3e-09   32.7   0.1    1.7e-09   32.3   0.1    1.1   1  k141_367108
    1.3e-09   32.7   0.0    1.4e-09   32.6   0.0    1.0   1  k141_748038
    1.9e-09   32.2   0.0    2.3e-09   31.9   0.0    1.1   1  k141_1465015
    2.5e-09   31.8   0.0    3.2e-09   31.4   0.0    1.2   1  k141_9484671
    3.8e-09   31.2   0.0    4.8e-09   30.8   0.0    1.1   1  k141_3608109
    4.6e-09   30.9   0.0      6e-09   30.5   0.0    1.1   1  k141_8781529
    1.2e-08   29.5   0.0    1.2e-08   29.5   0.0    1.1   1  k141_6150587
    1.6e-08   29.1   0.0    1.8e-08   28.9   0.0    1.1   1  k141_8997217
    2.2e-08   28.7   0.0    2.2e-08   28.7   0.0    1.0   1  k141_3860753
    2.8e-08   28.3   0.1    3.4e-08   28.0   0.1    1.1   1  k141_6504065
    5.6e-08   27.3   0.1    7.3e-08   27.0   0.1    1.2   1  k141_5528618
    6.1e-08   27.2   0.0    6.6e-08   27.1   0.0    1.1   1  k141_8048993
    1.5e-07   26.0   0.0    1.8e-07   25.7   0.0    1.1   1  k141_3253199
    3.9e-06   21.3   0.3    5.3e-06   20.8   0.3    1.2   1  k141_3015703
      6e-06   20.7   0.1    7.5e-06   20.3   0.1    1.1   1  k141_9286174
    8.1e-05   16.9   0.0    0.00012   16.4   0.0    1.2   1  k141_5934387
    0.00014   16.2   0.1    0.00018   15.8   0.1    1.2   1  k141_8733759


Domain annotation for each sequence (and alignments):
>> k141_4174516
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  347.5   0.1  1.8e-105  2.4e-105      34     335 ..      55     381 ..
21     385 .. 0.91


  Alignments for each domain:
  == domain 1  score: 347.5 bits;  conditional E-value: 1.8e-105
  MSA_GH10_xylanases  34 dallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg
kfsFegadelvnfakkngkklRgHtlvWhsQlPswv 122
                        d  lk a+k+yf  G av++++++++ +   +ik++f+s+t+eN+MK++
+ep++g+f++e+ad++++f+++ng k+RgHtl+WhsQ+ +w+
       k141_4174516  55 D-
GLKDAYKDYFkiGVAVNNRNVTDADQITLIKREFNSITAENAMKPQPTEPRKGEFNWEDADRIADFCRANGIKMRGHTLM
WHSQIGAWM 144
                        3.7899*****************************************
********************************* PP


  MSA_GH10_xylanases 123 ssik…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…l
resvfyrvlgedyvkiafeaareadpnakLyiNDYn 203
                        +++       ke++ + +k+hi+ +v+rYk+ vy WDVvNE++ +
```

18

```
lr+s+ y++ ge+++ +afe+a+eadpna L++NDYn
        k141_4174516 145 YQDEkgnlLPKEEFYANMKHHIQAIVNRYKDVVYCWDVVNEAVADSPVypgrpeL
RNSPMYQIAGEEFIYKAFEYAHEADPNALLFYNDYN 235
                        **998999999***************************************99864444456*
******************************* PP


  MSA_GH10_xylanases 204 lesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslg
vevaitELDialele…ateeklea 281
                         ++ ak++ +++lvk++++agvp+dGiG+q+H+++  ps++e+ +a+n ++
+++tELDi+++ +           +++ +
        k141_4174516 236 DAEP-AKSQRIYNLVKRMKDAGVPVDGIGMQAHYNVYGPSMKEVDDAINLYSTVV
KHIHLTELDIRINEDmggglrfnqgqatVSDWERTL 325
                        *999.***************************************************9
9**********666679******9998877778889 PP


  MSA_GH10_xylanases 282
qakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynai 335
                        q+++yv+++k++++ k+++ +vt+W+v+D+dsWl  +++pllfdenynpK+ay
a+
        k141_4174516 326
QQDQYVNLFKVLRKHKDVIdCVTFWNVSDRDSWLGaRNYPLLFDENYNPKQAYLAV 381
9*******************************964789**************988 PP


>> k141_8751303
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  342.3   0.1  6.6e-104    9e-104      22     334 ..      36      375 ..
16     379 .. 0.92


  Alignments for each domain:
  == domain 1  score: 342.3 bits;  conditional E-value: 6.6e-104
  MSA_GH10_xylanases  22 aklesrqaaesldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeN
sMKweaiepsrgkfsFegadelvnfakkngkklRgH 110
                        a+++ ++a+  l + lk a+k+yf  G av+++++++
++a+ik++f+s+tpeN+MK++ +ep++g f++e+ad+++nfa++ng klRgH
        k141_8751303  36 ASAQRNNAPVVLTDGLKDAYKDYFmiGVAVNNRNVTDPDQMALIKREFNSITPEN
AMKPQPTEPEKGVFNWEEADRIANFARQNGIKLRGH 126
                        1256678899999*********************************************
******************************* PP


  MSA_GH10_xylanases 111 tlvWhsQlPswvssik…adketllevlknhiktvvgrYkgkvyaWDVvNEil
nedgs…lresvfyrvlgedyvkiafeaarea 191
                        tl+WhsQ+  w+  +        ke++ + +k+hi+ vv+rYk+
vyaWDVvNE++++           +r+s+ +++ ge+++ +afe+a+ea
        k141_8751303 127 TLMWHSQVGRWMYMDDkgnlLPKEEFYANMKHHIDAVVNRYKDVVYAWDVVNEAV
QDSPVregqspMRQSPMFQIAGEEFIYKAFEYAHEA 217
```

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                        **************9988888899*********************************
98543334478********************* PP

  MSA_GH10_xylanases 192 dpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvae
lkkalnalaslgvevaitELDialele… 273
                         dpna L++NDYn  ++  k++ + +lv+++++agvpidGiG+q+H+++  p+
+e+ +a++++ s    ++itELDi++++e
        k141_8751303 218 DPNALLFYNDYNDADP-
GKSQRIFELVQRMKAAGVPIDGIGMQGHYNIYGPTPEEVDAAITKYKSIVKHIHITELDIRVNTErggqlnfnr 307
                        **************99.9*******************************
*********************888889******* PP


  MSA_GH10_xylanases 274
…ateekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpayna 334
                         +++ +   q+++y++++k++++ k++v +vt+W+v D+dsWl
++spllfd++y+pK +y
        k141_8751303 308
gqatpIEAWQTALQNDQYASLFKVLRKHKDVVdCVTFWNVGDRDSWLGaNNSPLLFDTEYQPKRSYFL 375
**9886777788899****************************964899**************965 PP


>> k141_2596728
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  329.8   3.0  4.2e-100  5.7e-100      40     330 ..      1     317 [.
1     318 [] 0.95


  Alignments for each domain:
  == domain 1  score: 329.8 bits;  conditional E-value: 4.2e-100
  MSA_GH10_xylanases  40 agkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFeg
adelvnfakkngkklRgHtlvWhsQlPswvssik.. 126
                         a+k+yf  G av++++++  + +++ ++f+s+t+eN+MK++
+ep++g+f++e+ad+++nf++++g k+RgHtl+WhsQ+ +w+ +++
        k141_2596728   1 AYKDYFkiGVAVNNRNVAEPDQIKVVLREFNSITAENAMKPQPTEPRKGEFNWED
ADKIANFCREHGIKMRGHTLMWHSQIGTWMYQDEkg 91
                        599**************************************************
****************************9989 PP


  MSA_GH10_xylanases 127 ..adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfy
rvlgedyvkiafeaareadpnakLyiNDYnlesasa 209
                          ke++ + +k+hi+ +v+rYk+ vy WDVvNE++ +        lr+s+
y++ ge+++ +afe+a+eadpna L++NDYn  ++ a
        k141_2596728  92 nlLPKEEFYANMKHHIQAIVNRYKDVVYCWDVVNEAVADSPVypgrpeLRNSPMY
QIAGEEFIYKAFEYAHEADPNALLFYNDYNDAEP-A 181
                         99999****************************9986444456*******
****************************999.* PP


                                  20
```

```
  MSA_GH10_xylanases 210 klegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevait
ELDialele…ateekleaqakdyv 287
                        k++ +++lvk++++agvp+dGiG+q+H+++  p+++e+ +a++ ++
+++tELDi+++ +           +++ +   q+++yv
        k141_2596728 182 KSQRIYNLVKRMKDAGVPVDGIGMQAHYNVYGPTMEEVDNAIKLYSTVVKHIHLT
ELDIRVNEDmggglrfrqgasqVADWERTLQQDQYV 272
                        ****************************************************99*****
*****666679*******9987666777889***** PP


  MSA_GH10_xylanases 288 evvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKp 330
                        +++k++++ k+++ +vt+W+v+DkdsWl  +++pllfdeny+pK+
        k141_2596728 273 NLFKVLRKHKDVIdCVTFWNVSDKDSWLGaNNYPLLFDENYKPKQ 317
                        **************************964889**********8 PP


>> k141_8352380
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  329.3   2.8  5.7e-100  7.8e-100      48     337 ..       2     316 ..
1      318 [. 0.95


  Alignments for each domain:
  == domain 1  score: 329.3 bits;  conditional E-value: 5.7e-100
  MSA_GH10_xylanases  48 avdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakk
ngkklRgHtlvWhsQlPswvssik…adketllle 134
                        av+++++++   ++a+ik++f+s+t+eN+MK++ +ep++g
f++e+ad+++nfa++ng klRgHtl+WhsQ+  w+  +       ke++ +
        k141_8352380   2 AVNNRNVTDPDQMALIKREFNSITAENAMKPQPTEPEKGVFNWEEADRIANFARQ
NGIKLRGHTLMWHSQVGRWMYMDDkgnlLPKEEFYA 92
                        789999****************************************************
*********************9988888899***** PP


  MSA_GH10_xylanases 135 vlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvki
afeaareadpnakLyiNDYnlesasaklegmvklvk 219
                        +k+hi+ vv+rYk+ vyaWDVvNE++++          +r+s+ +++ ge+++
+afe+a+eadpna L++NDYn  ++  k++ + +lv+
        k141_8352380  93
NMKHHIDAVVNRYKDVVYAWDVVNEAVQDSPVrngqspMRQSPMFQIAGEEFIYKAFEYAHEADPNALLFYNDYNDAEP-
GKSQRIFELVQ 182
                        ***************************98543333478******************
*******************999.9********** PP


  MSA_GH10_xylanases 220 klleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele.
…ateekleaqakdyvevvkaclev 296
                        ++++agvpidGiG+q+H+++ +p+ +e+ +a++++ s    ++itELDi++++e
+++ +   qa++y++++k++++
        k141_8352380 183 RMKAAGVPIDGIGMQGHYNIYSPTAEEIDAAITKYKSIVKHIHITELDIRVNTEq
```

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ggqlnfsrgqgapVASWQNTLQADQYANLFKVLRKH 273
                   ****************************************************88878
9**********98777778899************** PP


  MSA_GH10_xylanases 297 kkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                         +++v +vt+W+++D+dsWl   +spllfd+ny+pK+ayn + +
         k141_8352380 274 ADVVdCVTFWNLSDRDSWLGaANSPLLFDSNYRPKQAYNIVKN 316
                         ******************964789**************98865 PP


>> k141_7876638
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  327.6   1.2     2e-99   2.7e-99      36     337 ..       6     343 ..
3     346 .. 0.95


  Alignments for each domain:
  == domain 1  score: 327.6 bits;  conditional E-value: 2e-99
  MSA_GH10_xylanases  36 llkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkf
sFegadelvnfakkngkklRgHtlvWhsQlPswvss 124
                         +lk a+k+yf  G a +q+++++  + +++k++f+s+t+eN MK+ +++p++g
+++e+ad+++nf+++ng klRgH l+WhsQ  +w+++
        k141_7876638   6 KLKDAYKNYFmiGVALNQRNVSTPDQINLVKAEFNSITAENDMKPGELHPKEGVW
NWEKADKIANFCRQNGIKLRGHCLCWHSQFADWMFT 96
                         6899*****************************************************
********************************** PP


  MSA_GH10_xylanases 125 ik…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…
…lresvfyrvlgedyvkiafeaareadpnak 196
                         +k     ++ke + e+l++hi+tvv+rYk+ vyaWDVvNE++ +d+
+r+s ++r++g++++++af++areadpna
        k141_7876638  97 DKkgkeVKKEVFYERLRDHIHTVVNRYKDVVYAWDVVNEAMADDNGggprwgrfg
gqepspYRQSRHFRLCGDEFIAKAFQFAREADPNAL 187
                         99999999***************************************99975567777777
7888899************************ PP


  MSA_GH10_xylanases 197 LyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkal
nalaslgvevaitELDialele… 273
                         L++NDY+  ++  k+e ++++vkk+++agvpidGiG+q+H+++  ps+++l+ka+
++ +l   ++itELDi++++e
        k141_7876638 188 LFYNDYSCVDE-
GKRERIYNMVKKMKDAGVPIDGIGMQGHYNIYFPSEEQLEKAIVRFKELVKHIHITELDIRMNQEmggqlqfsrgenkp
277
                         *******9988.9*********************************************
*****************888899********9886 PP


  MSA_GH10_xylanases 274
```

```
ateekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                        ++  +    +++y +++k++++ k+++ +vt+W++ D+dsWl  ++ pl
fdeny+pK+ay+ai +
        k141_7876638 278
VAGYMNTMLTDQYSRIFKIFRKHKDVIdCVTFWNLGDRDSWLGvNNHPLPFDENYKPKQAYYAIKN 343
555666677899*********************986899***************987 PP


>> k141_7518864
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  324.6   0.5   1.6e-98   2.2e-98      24     328 ..      18     352 .]
2     352 .] 0.93


  Alignments for each domain:
  == domain 1  score: 324.6 bits;  conditional E-value: 1.6e-98
  MSA_GH10_xylanases  24 lesrqaaesldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsM
KweaiepsrgkfsFegadelvnfakkngkklRgHtl 112
                         r+  ++ d+  k +++ yf  G av+ ++++++ +++iikk+++s+t+eN
MK+ +++p++g++++ +ad+++nf+++ng k+RgH l
        k141_7518864  18 QFRRNPDANPDKGYKDTYQGYFtvGVAVNMRNIQDAATVEIIKKNYNSVTAENDM
KPISVHPKEGEWTWGNADAIANFCRQNGIKMRGHCL 108
                         23455556679999*******************************************
****************************** PP


  MSA_GH10_xylanases 113 vWhsQlPswvssik…adketllevlknhiktvvgrYkgkvyaWDVvNEilne
dgs…lresvfyrvlgedyvkiafeaare 190
                         +WhsQ +w++++k   ++ke + ++l++hi+ vv+rYk+ vyaWDVvNE++++
g        +res  y+++g++++++afe+a+e
        k141_7518864 109 CWHSQFCDWMFTDKngkpVTKEVFYQRLREHIHAVVNRYKDVVYAWDVVNEAMSD
AGRgwggrepnpYRESRAYQLCGDEFIAKAFEFAHE 199
                         *************999999***************************************
9988888888899******************* PP


  MSA_GH10_xylanases 191 adpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsva
elkkalnalaslgvevaitELDialele… 273
                         adpna L +NDYn  ++ ak++ ++++vkk+++agvpi GiG+q+H++a
ps++e+++a++++++l   +++tELDi+l+ e
        k141_7518864 200 ADPNAILVYNDYNAFQP-
AKRDRIYNMVKKMQQAGVPITGIGMQGHYNAYGPSEEEVEEAIKKYSELVKHIQVTELDIRLNEEmggqlqfs 289
                         *************99.***********************************
***********************6666799***** PP


  MSA_GH10_xylanases 274
…ateekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynp 328
                          a+ + +  q+++y ++++++++k+++ +vt+W+v+D+dsW+  ++ pl
fden++p
```

```
          k141_7518864 290
rgnagaAPGHLVTMQTDRYIKLFRLYRKYKDVIdNVTFWNVSDRDSWVGvNNHPLPFDENLRP 352
*****989999***********************************986899*******876 PP


>> k141_3207327
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  324.4   0.3   1.8e-98   2.4e-98      59      338 ..       4     305 ..
1     306 [] 0.96


  Alignments for each domain:
  == domain 1  score: 324.4 bits;  conditional E-value: 1.8e-98
  MSA_GH10_xylanases  59 eeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlv
WhsQlPswvssik…adketllevlknhiktvvg 145
                         ++++i+++++s+t+eN MK++ +ep++g++++e ad++++f+++ng  lRgH
lvWh+Q+ +w+ +++    ++k+ ll+++++hi+ +v+
        k141_3207327   4 QMSLIRREYNSITAENDMKPQLTEPREGEYTWERADRIADFCRQNGIRLRGHCLV
WHNQIGQWIYTDSegreVTKDVLLQRIRKHIQAIVS 94
                         6789***************************************************
**********9999999******************* PP


  MSA_GH10_xylanases 146 rYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaareadpnak
LyiNDYnlesasaklegmvklvkkllleagvpidGiG 232
                         rYk+ +y WDVvNE++ +d +    +r+s  y++ g+d+++ af+aareadpna
L++NDYn  ++ +k++ ++++vk++++ gvpidGiG
        k141_3207327  95
RYKDVIYCWDVVNEAITDDKNaenpYRQSRLYKIAGDDFIREAFRAAREADPNALLFYNDYNECDP-
VKRKRIYEMVKEMKADGVPIDGIG 184
                         ****************9998878889**************************
*********99.*********************** PP


  MSA_GH10_xylanases 233 sqsHlsagapsvaelkkalnalaslgvevaitELDialele…a
teekleaqakdyvevvkaclevkkcv.gvtvWgvaD 309
                         +q+H+++ +ps +e+ ++++ + s    +++tELD++++ e
++ee+ + q+++y+ ++++++  ++ + +vt+W+++D
        k141_3207327 185 MQGHYNIYSPSADEVDESIRLYKSVVNHIHVTELDVRVNREmggqlqfsrdavdI
SEEVKQMQERQYEALFRTFRRHADAIeCVTFWNLSD 275
                         *********************************777789**********99
99999************************ PP


  MSA_GH10_xylanases 310 kdsWls.eespllfdenynpKpaynaivka 338
                         +dsWl  +++pl fd ny pKp y++i +a
        k141_3207327 276 RDSWLGaNNYPLPFDVNYDPKPVYQRIKDA 305
                         ****964889**************9875 PP


>> k141_8446463
```

```
     #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
  ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  323.5   3.5   3.4e-98   4.7e-98      57     337 ..       3     301 ..
1     303 [. 0.97


  Alignments for each domain:
  == domain 1  score: 323.5 bits;  conditional E-value: 3.4e-98
  MSA_GH10_xylanases  57 skeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngkklRgHt
lvWhsQlPswvssikadketllevlknhiktvvgrY 147
                          +++a+ikk+f+s+t+eN MK++ +ep++g+f++e+ad+++nfa++ng klRgH
l+WhsQ+ +w+  ++ +ke + +++knhi+ vv+rY
        k141_8446463   3 PEQQALIKKEFNSMTAENDMKPQPTEPKEGEFNWENADKIANFARQNGIKLRGHC
LMWHSQIGEWMLGDNPTKEVFYQRMKNHIQAVVSRY 93
                         578999**************************************************
******************************** PP


  MSA_GH10_xylanases 148 kgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaareadpnakLy
iNDYnlesasaklegmvklvkkllleagvpidGiGsq 234
                          k+ vy WDVvNE++ +d +     +r+s  y+++g++++++af++areadp++
L++NDYn   ++ +k++ ++++vk +++agvpidGiG+q
        k141_8446463  94
KDVVYCWDVVNEAMTDDKNavdpYRQSAMYKLCGDEFIAKAFQFAREADPKVLLFYNDYNECDP-
VKSQRIYNMVKAMKQAGVPIDGIGMQ 183
                         ***************99989999**********************************
*******99.*********************** PP


  MSA_GH10_xylanases 235 sHlsagapsvaelkkalnalaslgvevaitELDialele…ate
ekleaqakdyvevvkaclevkkcv.gvtvWgvaDkd 311
                          +H+++  p+++e+ +al+ + +    +++tELD +++ e
+t+++ ++ a++y++v+k++++ k+++ +vt+W++ D+d
        k141_8446463 184 GHYNIYGPTEQEVDNALTLYKKIVKHIHVTELDNRVTEEmggqlrfsregvnVTD
SVKQHLADQYARVFKVFRKHKDVIdCVTFWNLGDRD 274
                         ****************************************996666889*********9999
99999*************************** PP


  MSA_GH10_xylanases 312 sWls.eespllfdenynpKpaynaivk 337
                          sWl   ++pl fd++y+pK ay+ i +
        k141_8446463 275 SWLGaANYPLPFDSEYKPKLAYEYIKD 301
                         **964789*************99865 PP


>> k141_3648730
     #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
  ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  317.7   2.9      2e-96   2.8e-96      73     337 ..       1     283 [.
```

```
1       286 [. 0.97

  Alignments for each domain:
  == domain 1  score: 317.7 bits;  conditional E-value: 2e-96
  MSA_GH10_xylanases  73 eNsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssika
dketllevlknhiktvvgrYkgkvyaWDVvNEilne 163
                         eN MK+e +ep++g+f++egad+++nfa++ng klRgH l+WhsQ+ +w+++++
+ke + +++knhi+ vv+rYk+ vyaWDVvNE++ +
         k141_3648730    1 ENDMKPEPTEPRQGQFNWEGADRIANFARQNGIKLRGHCLMWHSQIGHWMTEDNP
TKEVFYARMKNHIEAVVSRYKDVVYAWDVVNEAMTD 91
                         8*****************************************************
*******************************9 PP


  MSA_GH10_xylanases 164 dgs…lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegm
vklvkklleagvpidGiGsqsHlsagapsvaelkka 250
                         d++    +r+sv y+++g++++++afe+a++adpna L++NDYn  ++ +k++ +
++vkk+++agvpi+GiG+q+H+++  ps++++ ka
         k141_3648730   92 DANaqdpYRQSVMYKLCGDEFIAKAFEYAHAADPNALLFYNDYNECDP-
VKSQRIFNMVKKMKDAGVPIHGIGMQGHYNIYGPSEEDVDKA 181
                         99888899*********************************99.******
********************************* PP


  MSA_GH10_xylanases 251 lnalaslgvevaitELDialele…ateekleaqakdyvevvka
clevkkcv.gvtvWgvaDkdsWls.eespllfdeny 326
                         l+ + +    +++tELDi+ ++e             +t++  ++
a++y++v++++++ k+++ +vt+W+++D+dsWl  +++pl fd +y
         k141_3648730  182 LTLYKQVVDHIHVTELDIRANQEmggqlafsrdganVTDSLKQHLADQYARVFRV
FRKHKDVIdCVTFWNLSDRDSWLGqNNYPLPFDVDY 272
                         *******99**********766689*********98888899999**********
*********************963789******** PP


  MSA_GH10_xylanases 327 npKpaynaivk 337
                         +pK ay+ i +
         k141_3648730 273 KPKMAYEYIRD 283
                         ******99876 PP


>> k141_382248
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  315.7   0.0   8.1e-96   1.1e-95       3     337 ..      20     388 ..
18     390 .. 0.94


  Alignments for each domain:
  == domain 1  score: 315.7 bits;  conditional E-value: 8.1e-96
  MSA_GH10_xylanases   3 slkvlallllllaalaavsaaklesrqaaesldallkaagkkyf..Gtavdqkele
kskeeaiikkdfgsltpeNsMKweaiepsrgkfsFe 91
```

```
                                ++k l l+ l+++l+++sa + + +q      d  lk a+k+yf  G a
+q++++++   ++++ k+f+s+t+eN  K+ +i+p++g ++Fe
          k141_382248   20 KIKNLSLTFLVSTLFISSAWA-
QWQQRDPRADVGLKDAYKDYFtiGVALNQRNVSDDARKELVLKQFNSVTAENDWKPGEIHPKEGVWNFE 109
                           56777777788888877754.345555689999*********************
******************************* PP


  MSA_GH10_xylanases   92 gadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllevlknhikt
vvgrYkgkvyaWDVvNEilnedgs… 166
                           +ad++++f+++ng k+RgH l+WhsQ  +w++++k    ++ke +
e+l++hi+tvv+rYk+ vyaWDVvNE++ +dg
          k141_382248 110 KADKIADFCRQNGIKMRGHCLCWHSQFADWMFTDKkgkdVTKEVFYERLREHIHT
VVNRYKDVVYAWDVVNEAMADDGGgprwgrrpgeep 200
                           ***********************************9999999**************
*********************97777778888889 PP


  MSA_GH10_xylanases  167 ..lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvk
klleagvpidGiGsqsHlsagapsvaelkkalnala 255
                             +r+s ++r++g++++++af++areadp+  L +NDY+  ++  k+e
++++vkk+++agvpidGiG+q+H+++  ps+++l+ka+ ++
          k141_382248 201 spYRQSRHFRLCGDEFIAKAFQFAREADPTGILIYNDYSCVDE-
GKRERIYNMVKKMKDAGVPIDGIGMQGHYNIYFPSEEQLEKAIVRFK 290
                           999**************************************9988.9**********
******************************* PP


  MSA_GH10_xylanases  256 slgvevaitELDialele…ateekleaqakdyvevvkaclev
kkcv.gvtvWgvaDkdsWls.eespllfdenynpKp 330
                           +    ++itELD++++ e             +++ +   q+++y++++k++++
++++ +vt+W++ D+dsWl  ++ pl fdeny+pK+
          k141_382248 291 EIVNHIHITELDLRMNNEsggqlmfsrgearpQPAYMSTLQTDQYARLFKIFRKH
ADVIdNVTFWNLGDRDSWLGvNNHPLPFDENYRPKQ 381
                           **************88879***********998899999****************
******************986899*********** PP


  MSA_GH10_xylanases  331 aynaivk 337
                           + ai +
          k141_382248 382 CFRAIRD 388
                           ***9975 PP


>> k141_7690424
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  312.0   3.2   1.1e-94   1.5e-94      51     314 ..      2     282 ..
1     286 [] 0.97


  Alignments for each domain:
```

```
   == domain 1  score: 312.0 bits;  conditional E-value: 1.1e-94
  MSA_GH10_xylanases  51 qkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngk
klRgHtlvWhsQlPswvssikadketllevlknhik 141
                         q+++++++++a+ik++f+s+t eN MK+e +ep++g+f++e+ad+++nf+++ng
klRgH l+WhsQ+  w++  + +ke + +++knhi+
        k141_7690424   2 QRNVTNAEQQALIKREFNSMTCENDMKPEPTEPNEGQFNWENADRIANFCRANGI
KLRGHCLMWHSQIGRWMTDGNPTKEVFYQRMKNHIQ 92
                        78899999*************************************************
***************************** PP


  MSA_GH10_xylanases 142 tvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaaread
pnakLyiNDYnlesasaklegmvklvkklleagvpi 228
                         vv+rYk+ vy WDVvNE++ +d +    +r+sv
y+++g++++++af++areadpna L++NDYn  ++ +k++ ++++vkk+++agvpi
        k141_7690424  93
AVVTRYKDIVYCWDVVNEAMTDDKNaedpYRQSVMYKLCGDEFIAKAFQFAREADPNALLFYNDYNECDP-
VKSKRIYNMVKKMKDAGVPI 182
                        *******************9998888899*************************
*************99.****************** PP


  MSA_GH10_xylanases 229 dGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele…
…ateekleaqakdyvevvkaclevkkcv.gvtvW 305
                         dGiG+q+H+++  p+++e+ +a++ +     +++tELDi+++ e
+t+++ ++ a++y++v++a+++ k+++ +vt+W
        k141_7690424 183 DGIGMQGHYNIYGPTEKEVDDAISLYKTVVKHIHVTELDIRVNEEmggqlrfsre
gvnVTDSVKQHLADQYARVFRAFRKHKDVIdCVTFW 273
                        ****************************999**********776689********
**999999999********************* PP


  MSA_GH10_xylanases 306 gvaDkdsWl 314
                         ++ D+dsWl
        k141_7690424 274 NLGDRDSWL 282
                        *******8 PP


>> k141_2078416
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  300.2   2.1   4.2e-91   5.7e-91      74      326 ..       1     271 []
1      271 [] 0.97


  Alignments for each domain:
  == domain 1  score: 300.2 bits;  conditional E-value: 4.2e-91
  MSA_GH10_xylanases  74 NsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikad
ketllevlknhiktvvgrYkgkvyaWDVvNEilned 164
                         N MK+e +ep++g+f++egad+++nfa++ng klRgH l+WhsQ+  w++ ++
+ke + +++knhi+ vv+rYk+ vyaWDVvNE++ +d
```

```
          k141_2078416    1 NDMKPEPTEPRQGQFNWEGADRIANFARQNGIKLRGHCLMWHSQIGRWMTDDNPT
KEVFYQRMKNHIEAVVNRYKDVVYAWDVVNEAMTDD 91
                              99*****************************************************
*******************************9 PP


  MSA_GH10_xylanases 165 gs…lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmv
klvkklleagvpidGiGsqsHlsagapsvaelkkal 251
                              ++     +r+s  y+++g++++++afe+a++adpna L++NDYn  ++ +k++
++++vkk+++agvpi+GiG+q+H+++  p+++++ kal
          k141_2078416   92 ANaedpYRQSAMYKLCGDEFIAKAFEYAHAADPNALLFYNDYNECDP-
VKSQRIYNMVKKMKDAGVPIHGIGMQGHYNIYGPKEEDIDKAL 181
                              9888999**************************************99.*******
******************** PP


  MSA_GH10_xylanases 252 nalaslgvevaitELDialele…ateekleaqakdyvevvkac
levkkcv.gvtvWgvaDkdsWls.eespllfdeny 326
                              + + +     +++tELDi+ ++e            ++++  ++
a++y++v+++++  k+++ +vt+W+++D+dsWl  +++pl fd +y
          k141_2078416 182 ELYKQVVSHIHVTELDIRANQEmggqlafrrdgaaVNDSLKQHLADQYARVFRVF
RTHKDVIdCVTFWNLSDRDSWLGqNNYPLPFDVDY 271
                              ******************766689*********987888888899**********
********************963789*****876 PP


>> k141_5777399
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  295.7   0.4   9.6e-90   1.3e-89      13     273 ..      19     283 ..
7     309 .. 0.90


  Alignments for each domain:
  == domain 1  score: 295.7 bits;  conditional E-value: 9.6e-90
  MSA_GH10_xylanases  13 laalaavsaaklesrqaaesldallkaagkkyf..Gtavdqkelekskeeaiikk
dfgsltpeNsMKweaiepsrgkfsFegadelvnfak 101
                              ++ ++++  ++++s +a+++l  +lk+a+k+yf  G av+q++++++
++a++k++f+s+t+eN MK+e +ep++g++++e+ad++++f++
          k141_5777399   19 TFFFTIALVTSVTSCSAQNTLS-
SLKEAYKDYFliGVAVNQRNISNADQAAMVKREFNSITAENDMKPERTEPREGEYTWEAADRIADFCR 108
                              3333334444577788877777.99***************************
********************************* PP


  MSA_GH10_xylanases 102 kngkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvyaWDV
vNEilnedgs…lresvfyrvlgedyvkiafeaa 188
                              kng klRgH l+Wh+Q+  w+ +++ +ke + +++++hi+ +v+rYk+ vy
WDVvNE++ +d+     +r+s+ y++ g++++++afe+a
          k141_5777399 109 KNGIKLRGHCLMWHNQIGRWMYEDNPSKEVFFQRMRSHIHAIVNRYKDVVYCWDV
VNEAITDDARaedpYRQSPLYKIAGDEFIAKAFEYA 199
```

```
                         **************************************************
********9888899******************** PP

  MSA_GH10_xylanases 189 readpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagaps
vaelkkalnalaslgvevaitELDialele 273
                         readpna L++NDYn  ++ +k++ ++++vkk+++agvpidGiG+q+H ++
p+++e+ +a++ +       +++tELDi+++ e
        k141_5777399 200 READPNALLFYNDYNECDS-
VKSRRIYEMVKKMKAAGVPIDGIGMQGHSNIYGPKEEEIDRAISLYKTVVSHIHVTELDIRVNNE 283
                         **************9877.*******************************
**************99**********6555 PP


>> k141_6414633
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------   ------- -------
------- -------    ----
   1 !  295.3   1.2   1.3e-89   1.8e-89      31     272 ..      13     259 ..
3     265 .. 0.96


  Alignments for each domain:
  == domain 1  score: 295.3 bits;  conditional E-value: 1.3e-89
  MSA_GH10_xylanases  31 esldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiep
srgkfsFegadelvnfakkngkklRgHtlvWhsQlP 119
                         +   + lk a+k+yf  G av+q+++++++++a+ik++f+s+t eN MK+e
+ep++g+f++++ad+++nf+++ng klRgH l+WhsQ+
        k141_6414633  13 AVWAQGLKDAYKDYFmiGVAVNQRNVTNAEQKALIKREFNSMTCENDMKPEPTEP
NEGQFNWDNADRIANFCRANGIKLRGHCLMWHSQIG 103
                         45667899***********************************************
******************************** PP


  MSA_GH10_xylanases 120 swvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lres
vfyrvlgedyvkiafeaareadpnakLyiNDYnles 206
                         w++  + +ke + +++knhi+ vv+rYk+ vy WDVvNE++ +d +
+r+sv y+++g++++++af++areadpna L++NDYn +
        k141_6414633 104 RWMTDGNPTKEVFYQRMKNHIQAVVSRYKDIVYCWDVVNEAMTDDKNaedpYRQS
VMYKLCGDEFIAKAFQFAREADPNALLFYNDYNECD 194
                         *****************************************9998888899***
******************************9 PP


  MSA_GH10_xylanases 207
asaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialel 272
                         + +k++ ++++vkk+++agvpidGiG+q+H+++  p+++e+ +a++ +
+++tELDi+++
        k141_6414633 195
P-VKSKRIYNMVKKMKDAGVPIDGIGMQGHYNIYGPTEKEVDDAISLYKTVVKHIHVTELDIRVNE 259
9.******************************************999**********544 PP
```

```
>> k141_1984896
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  289.0   1.8   1.1e-87   1.5e-87      46     273 ..       1     231 [.
1     241 [. 0.97


  Alignments for each domain:
  == domain 1  score: 289.0 bits;  conditional E-value: 1.1e-87
  MSA_GH10_xylanases   46 GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfa
kkngkklRgHtlvWhsQlPswvssikadketllevl 136
                            G av+q+++++++++a+ik++f s+t+eN MK+e
+ep++g+f++egad+++nfa++ng klRgH l+WhsQ+  w+++++ +ke + +++
        k141_1984896    1 GVAVNQRNVTNAEQQALIKREFSSMTAENDMKPEPTEPRQGQFNWEGADRIANFA
RQNGIKLRGHCLMWHSQIGRWMTNDNPTKEVFYQRM 91
                            889*************************************************
****************************** PP


  MSA_GH10_xylanases  137 knhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafea
areadpnakLyiNDYnlesasaklegmvklvkklle 223
                            k+hi+ vv+rYk+ vyaWDVvNE++ +d++    +r+sv
y+++g++++++afe+a++adpna L++NDYn  ++ +k++ ++++vkk+++
        k141_1984896   92
KSHIEAVVSRYKDVVYAWDVVNEAMTDDANaqdpYRQSVMYKLCGDEFIAKAFEYAHAADPNALLFYNDYNECDP-
VKSQRIYNMVKKMKD 181
                            ************************999888899********************
*******************99.*************** PP


  MSA_GH10_xylanases  224 agvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele 273
                            agvpi+GiG+q+H+++  p+++++ kal+ + +    +++tELDi+ ++e
        k141_1984896  182 AGVPIHGIGMQGHYNIYGPNEEDVDKALSLYKQVVSHIHVTELDIRANQE 231
                            *****************************************5444 PP


>> k141_3321694
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  287.7   1.6   2.6e-87   3.6e-87      82     337 ..       1     274 [.
1     277 [. 0.97


  Alignments for each domain:
  == domain 1  score: 287.7 bits;  conditional E-value: 2.6e-87
  MSA_GH10_xylanases   82 epsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketllevl
knhiktvvgrYkgkvyaWDVvNEilnedgs…lr 168
                            ep++g+f++e+ad+++nfa++ng klRgH l+WhsQ+  w+  ++ +ke +
e++++hi+ vv+rYk+ +y WDVvNE++++++   +r
```

```
        k141_3321694    1 EPQEGQFNWENADRIANFARQNGIKLRGHCLMWHSQIGRWMLGDNPTKEVFYERM
RKHIHAVVSRYKDVIYCWDVVNEAMEDNANatdpYR 91
                          79*********************************************************
************************99888899* PP


  MSA_GH10_xylanases 169 esvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklle
agvpidGiGsqsHlsagapsvaelkkalnalaslgv 259
                          +s   yr++g++++++af++areadp+a L++NDY++ ++   k++
++++vkk++++gvpidGiG+q+H+++  ps+a+l +a++ +
        k141_3321694   92 QSAMYRLCGDEFIEKAFQFAREADPKALLFYNDYSTVDP-
HKRDRIYNMVKKMKAKGVPIDGIGMQAHYNIYYPSEARLDSAITLFKTIVK 181
                          ********************************************99.9**************
********************************99 PP


  MSA_GH10_xylanases 260 evaitELDialele…ateekleaqakdyvevvkaclevkkcv.
gvtvWgvaDkdsWls.eespllfdenynpKpaynai 335
                          ++itE+Di+++ e                +t+++ ++ a++y++ ++++++ k+++
+vt+W++ D+dsWl  +++pl +d +y+pK ay+ i
        k141_3321694  182 HIHITEFDIRVNEEmggglqfsregatVTDSVKQHLADQYARCFRVFRKHKDVId
CVTFWNLGDRDSWLGqNNYPLPWDVDYKPKMAYDYI 272
                          **********777689**********9999999999********************
*************963789**************999 PP


  MSA_GH10_xylanases 336 vk 337
                          +
        k141_3321694 273 KD 274
                          76 PP


>> k141_1057675
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  281.6   1.6   1.9e-85   2.7e-85      72      306 ..       1      252 []
1     252 [] 0.97


  Alignments for each domain:
  == domain 1  score: 281.6 bits;  conditional E-value: 1.9e-85
  MSA_GH10_xylanases  72 peNsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssik
adketllevlknhiktvvgrYkgkvyaWDVvNEiln 162
                          +eN MK+e +ep++g+f++egad+++nfa++ng klRgH l+WhsQ+  w++ ++
+ke + +++k+hi+ vv+rYk+ vyaWDVvNE++
        k141_1057675    1 AENDMKPEPTEPRQGQFNWEGADRIANFARQNGIKLRGHCLMWHSQIGRWMTDDN
PTKEVFYQRMKSHIEAVVNRYKDVVYAWDVVNEAMT 91
                          69*********************************************************
****************************** PP


  MSA_GH10_xylanases 163 edgs…lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasakleg
```

32

```
mvklvkklleagvpidGiGsqsHlsagapsvaelkk 249
                        +d++     +r+sv y+++g++++++afe+a++adpna L++NDYn  ++ +k++
++++vkk+++agvpi+GiG+q+H+++   ps++++ k
        k141_1057675   92 DDANaedpYRQSVMYKLCGDEFIAKAFEYAHAADPNALLFYNDYNECDP-
VKSQRIYNMVKKMKDAGVPIHGIGMQGHYNIYGPSEEDVDK 181
                        *99888999************************************99.*****
******************************** PP


  MSA_GH10_xylanases 250
alnalaslgvevaitELDialele…ateekleaqakdyvevvkaclevkkcv.gvtvWg 306
                        al+ + +    +++tELDi+ ++e            +t++  +
a++y++v++++++ k+++ +vt+W+
        k141_1057675 182
ALSLYKQVVSHIHVTELDIRANHEmggqlafsrdgaaVTDSLKQFLADQYARVFRVFRKHKDVIdCVTFWN 252
*********************888789*********98788888889**********************5 PP


>> k141_4163169
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  280.8   1.7   3.2e-85   4.4e-85      37     306 ..      10     313 .]
5     313 .] 0.97


  Alignments for each domain:
  == domain 1  score: 280.8 bits;  conditional E-value: 3.2e-85
  MSA_GH10_xylanases  37 lkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfs
FegadelvnfakkngkklRgHtlvWhsQlPswvssi 125
                        lk a+k+yf  G av+q++++++ + +iikk+f+s+t+eN  K+ +i+p++g
++Fe+ad+++nf+++ng k+RgH l+WhsQ  +w++++
        k141_4163169   10 LKDAYKDYFtiGVAVNQNNVTDAAQIEIIKKQFNSVTAENDWKPGEIHPKEGVWN
FEKADKIANFCRENGIKMRGHCLCWHSQFADWMFTD 100
                        6899*************************************************
******************************** PP


  MSA_GH10_xylanases 126 k…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…
…lresvfyrvlgedyvkiafeaareadpnakLy 198
                        k     ++k+ + e+l++hi+tvv+rYk+ vyaWDVvNE++ +dg
+r+s +++++g++++++afe+areadp+  L
        k141_4163169 101 KkgkpVKKDVFYERLRDHIHTVVNRYKDVVYAWDVVNEAMADDGRpfefvdgkmv
kaspYRQSRHFKLCGDEFIAKAFEFAREADPDGVLI 191
                        999999*********************************988888888888
888899*************************** PP


  MSA_GH10_xylanases 199 iNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalna
laslgvevaitELDialele…at 275
                        +NDY+  ++  k+e ++++vkk++eagvpidGiG+q+H+++
p++++l+ka++++++    ++itELD+++++e               ++
```

```
        k141_4163169 192 YNDYSCVDN-GKRERIYEMVKKMKEAGVPIDGIGMQGHYNIYFPDEEQLEKAIER
FSEIVNIIHITELDLRTNTEsggqlmfargeakpQA 281
                        *****9977.9*********************************************
****************888799*********99878 PP

  MSA_GH10_xylanases 276 eekleaqakdyvevvkaclevkkcv.gvtvWg 306
                        ++ +   q+++y+++++++++ k+++ +vt+W+
        k141_4163169 282 AHIATLQEDQYNRLFRIFRKHKDVIkNVTFWN 313
                        889999***********************5 PP


>> k141_2349245
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  280.6   1.7   3.9e-85   5.3e-85      53     269 ..       2     221 ..
1      222 [] 0.98


  Alignments for each domain:
  == domain 1  score: 280.6 bits;  conditional E-value: 3.9e-85
  MSA_GH10_xylanases  53 elekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngkkl
RgHtlvWhsQlPswvssikadketllevlknhiktv 143
                        +++++++a+ik++f s+t+eN MK+e +ep++g+f++egad+++nfa++ng
klRgH l+WhsQ+  w+++++ +ke + +++knhi+ v
        k141_2349245   2 NVTNAEQQALIKREFSSMTAENDMKPEPTEPRQGQFNWEGADRIANFARQNGIKL
RGHCLMWHSQIGRWMTEDNPTKEVFYQRMKNHIEAV 92
                        56778999*********************************************
******************************** PP


  MSA_GH10_xylanases 144 vgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaareadpn
akLyiNDYnlesasaklegmvklvkklleagvpidG 230
                        v+rYk+ vyaWDVvNE++ +d++      +r+sv
y+++g++++++afe+a++adpna L++NDYn  ++ +k++ + ++vkk+++agvpi+G
        k141_2349245  93
VNRYKDVVYAWDVVNEAMTDDANaedpYRQSVMYKLCGDEFIAKAFEYAHAADPNALLFYNDYNECDP-
VKSQRIFNMVKKMKDAGVPIHG 182
                        *******************99888999***************************
***********99.******************** PP

  MSA_GH10_xylanases 231 iGsqsHlsagapsvaelkkalnalaslgvevaitELDia 269
                        iG+q+H+++  p+++++ kal+ + +     +++tELDi+
        k141_2349245 183 IGMQGHYNIYGPKEEDIDKALSLYKQVVSHIHVTELDIR 221
                        **********************************8 PP


>> k141_3537260
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
```

34

```
------- -------    ----
  1 !  280.2   2.6   5.1e-85   6.9e-85      31      255 ..       7      236 ..
  2       238 .. 0.97


   Alignments for each domain:
   == domain 1  score: 280.2 bits;  conditional E-value: 5.1e-85
   MSA_GH10_xylanases  31 esldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiep
srgkfsFegadelvnfakkngkklRgHtlvWhsQlP 119
                          +s + lk a+++yf  G av+q+++++++++++ikk+f+s+t+eN MK+e
+ep++g+f++e+ad+++nfa++ng klRgH l+WhsQ+
         k141_3537260   7 TSWAQGLKDAYQDYFmiGVAVNQRNVTNAEQMELIKKEFNSITAENDMKPEPTEP
REGEFNWEAADRIANFARQNGIKLRGHCLMWHSQIG 97
                          5777889**************************************************
***************************** PP


   MSA_GH10_xylanases 120 swvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lres
vfyrvlgedyvkiafeaareadpnakLyiNDYnles 206
                          w++++ ++ke++ +++knhi+ +v+rYk+ vyaWDVvNE++++d++    +r+s
yr++g++++++af++a+eadpna L++NDY++ +
         k141_3537260  98 RWMTAEGTTKEQFYARMKNHIQAIVTRYKDVVYAWDVVNEAISDDANatdpYRQS
AMYRLCGDEFIEKAFQYAHEADPNALLFYNDYSTVD 188
                          **************************************************9888999***
********************************9 PP


   MSA_GH10_xylanases 207 asaklegmvklvkkllleagvpidGiGsqsHlsagapsvaelkkalnala 255
                          + k++ ++++vkk++++gvpidGiG+q+H+++ ps+a+l +a++ +
         k141_3537260 189 P-HKRDRIYNMVKKMKAKGVPIDGIGMQAHYNIYYPSEARLDSAITLFK 236
                          9.9*****************************************99885 PP


>> k141_169673
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
  1 !  279.2   0.9     1e-84   1.4e-84      66      301 ..       1      253 [.
  1       254 [] 0.96


   Alignments for each domain:
   == domain 1  score: 279.2 bits;  conditional E-value: 1e-84
   MSA_GH10_xylanases  66 dfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPs
wvssikadketllevlknhiktvvgrYkgkvyaWDV 156
                          +f s+t+eN MK+e +ep++g+f++egad+++nfa++ng klRgH l+WhsQ+
w++s++ +ke + +++k+hi+ vv+rYk+ vyaWDV
         k141_169673   1 EFSSMTAENDMKPEPTEPRQGQFNWEGADRIANFARQNGIKLRGHCLMWHSQIGR
WMTSDNPTKEVFYQRMKSHIEAVVSRYKDVVYAWDV 91
                          699**************************************************
***************************** PP
```

```
  MSA_GH10_xylanases 157 vNEilnedgs…lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesa
saklegmvklvkklleagvpidGiGsqsHlsagaps 243
                          vNE++ +d++    +r+sv y+++g++++++afe+a++adp+a L++NDYn  ++
+k++ ++++vkk+++agvpi+GiG+q+H+++  p+
          k141_169673  92
VNEAMTDDANaqdpYRQSVMYKLCGDEFIAKAFEYAHAADPKALLFYNDYNECDP-
VKSQRIYNMVKKMKDAGVPIHGIGMQGHYNIYGPK 181
                          ******999888899*****************************************99
.***************************** PP


  MSA_GH10_xylanases 244
vaelkkalnalaslgvevaitELDialele…ateekleaqakdyvevvkaclevkkcv.g 301
                          ++++ kal+ + +    +++tELDi+ ++e            +t++  +
a++y++v++++++ k+++ +
          k141_169673 182
EEDIDKALTLYKQVVSHIHVTELDIRANQEmggqlafsrdgaaVTDSLKQFLADQYARVFRVFRKHKDVIdC 253
************************766689*********9877788888999**********99998855 PP


>> k141_8427476
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  278.3   1.2    2e-84   2.7e-84      92     337 ..      2     265 ..
1     267 [. 0.97


  Alignments for each domain:
  == domain 1  score: 278.3 bits;  conditional E-value: 2e-84
  MSA_GH10_xylanases  92 gadelvnfakkngkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgr
YkgkvyaWDVvNEilnedgs…lresvfyrvlge 178
                          +ad+++nf+++ng klRgH l+WhsQ+ +w+ +++ +ke l +++++hi+
vv+rYk+ vy WD vNE++ +d +    +r+s+fy++ g+
        k141_8427476   2 AADRIANFCRQNGIKLRGHCLMWHSQIGEWMYKDNPTKEVLFARMRKHIHAVVSR
YKDVVYCWDAVNEAMTDDKNavdpYRQSQFYKIAGD 92
                          79****************************************************
*****************99989999*********** PP


  MSA_GH10_xylanases 179 dyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGs
qsHlsagapsvaelkkalnalaslgvevaitELDia 269
                          +++++af++areadp+a L++NDYn  ++ +k++ ++++vk
+++agvpidGiG+q+H+++  p+++e+ +a++ + +    +++tELDi+
        k141_8427476  93 EFIAKAFQYAREADPKALLFYNDYNECDP-
VKSQRIYNMVKAMKQAGVPIDGIGMQGHYNIYGPTEKEVDDAITLYKKIVKHIHVTELDIR 182
                          *************************99.***********************
***************************** PP


  MSA_GH10_xylanases 270 lele…ateekleaqakdyvevvkaclevkkcv.gvtvWgvaDk
dsWls.eespllfdenynpKpaynaivk 337
```

36

```
                              +++e              ++++   ++ a++y++v+k++++ k+++ +vt+W++
D+dsWl    ++pl fd++y+pK ay+ i +
        k141_8427476 183 VNTEmggqlrfsrggvtVSDSIKQHLADQYARVFKVFRKHKDVIdCVTFWNLGDR
DSWLGaANYPLPFDSEYKPKLAYDFIKN 265
                             888889*********98888888999*****************************
***964789*************99876 PP


>> k141_4868594
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  277.7   0.0     3e-84     4e-84      22     271 ..      45     304 ..
24     311 .. 0.91


  Alignments for each domain:
  == domain 1  score: 277.7 bits;  conditional E-value: 3e-84
  MSA_GH10_xylanases  22 aklesrqaaesldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeN
sMKweaiepsrgkfsFegadelvnfakkngkklRgH 110
                        a+  +rq++e  d  lk a+k+yf  G av+++++ +  +  ++
++f+s+t+eN+MK+e +ep++g+f++e+ad++++f+++ng  +RgH
        k141_4868594  45 AQWGPRQIPEPTD-
GLKDAYKDYFkiGVAVNNRNVVDPDQIRVVLREFNSITAENAMKPEPTEPRKGEFNWEDADRIADFCRANGIRMRGH
134
                        3467788887777.899***************************************
******************************** PP


  MSA_GH10_xylanases 111 tlvWhsQlPswvssik…adketllevlknhiktvvgrYkgkvyaWDVvNEil
nedgs…lresvfyrvlgedyvkiafeaarea 191
                        tl+WhsQ+ sw+ +++      +ke++ + +k+hi+ +v+rYk+ vy WDVvNE++
+         lr+s+ y++ ge+++ +afe+a+ea
        k141_4868594 135 TLMWHSQIGSWMYQDEkgnlLSKEEFYANMKHHIQAIVNRYKDIVYCWDVVNEAV
ADSPVfpgrseLRNSPMYQIAGEEFIYKAFEYAHEA 225
                        *************9999999*****************************9
99754333445*********************** PP


  MSA_GH10_xylanases 192
dpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDiale
271
                        dp+a L++NDY   ++ ak++ +++lvk++++agvp+dGiG+q+H+++
ps++e+ +a++ +++     ++ tELD++++
        k141_4868594 226 DPDALLFYNDYHDAEP-
AKSQRIYNLVKRMKDAGVPVDGIGMQAHYNVYGPSMKEVDDAIQLYSKVVKHIHFTELDVRVN 304
*********99999.************************************************************943
PP


>> k141_5492129
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
```

37

```
envfrom   env to      acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  274.3   2.0   3.2e-83   4.4e-83      96      337 ..      1      260 [.
1      263 [. 0.96

  Alignments for each domain:
  == domain 1  score: 274.3 bits;  conditional E-value: 3.2e-83
  MSA_GH10_xylanases   96 lvnfakkngkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgk
vyaWDVvNEilnedgs…lresvfyrvlgedyvk 182
                            ++nfa++ng klRgH l+WhsQ+  w++ ++ +ke + +++knhi+ vv+rYk+
vyaWDVvNE++ +d++    +r+sv y+++g+++++
        k141_5492129    1 VANFARQNGIKLRGHCLMWHSQIGRWMTDDNPTKEVFYQRMKNHIEAVVSRYKDV
VYAWDVVNEAMTDDANaedpYRQSVMYKLCGDEFIA 91
                            579*****************************************************
*************99888999*************** PP


  MSA_GH10_xylanases  183 iafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHl
sagapsvaelkkalnalaslgvevaitELDialele 273
                            +afe+a++adp+a L++NDYn  ++ +k++
++++vkk+++agvpi+GiG+q+H+++  p+++++ kal+ + +    +++tELDi+ + e
        k141_5492129   92 KAFEYAHAADPDALLFYNDYNECDP-
VKSQRIYNMVKKMKDAGVPIHGIGMQGHYNIYGPKEEDIDKALTLYKQVVSHIHVTELDIRANAE 181
                            *********************99.****************************
******************************7777 PP


  MSA_GH10_xylanases  274
…ateekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk
337
                                                +t++   +  a++y++v++++++ k+++ +vt+W+++D+dsWl
+++pl fd +y+pK ay+ i +
        k141_5492129  182
mggqlafsrdgavVTDSLKQFLADQYARVFRVFRKHKDVIdCVTFWNLSDRDSWLGqNNYPLPFDVDYKPKMAYEYIRD
260
89**********8888888889***********************************963789***************99876
PP


>> k141_5537034
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  269.7   0.4   8.1e-82   1.1e-81      61      313 ..      3      287 .]
1      287 [] 0.96

  Alignments for each domain:
  == domain 1  score: 269.7 bits;  conditional E-value: 8.1e-82
  MSA_GH10_xylanases   61 aiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWh
```

```
sQlPswvssik…adketllevlknhiktvvgrY 147
                       +iikk+f+s+t+eN+ K+ +i+p++g ++F  ad+++nf+++ng k+RgH
l+WhsQ +w++++k    ++ke + e+l++hi+tvv+rY
      k141_5537034   3 EIIKKQFNSVTAENAWKPGEIHPKEGVWNFGLADSIANFCRENGIKMRGHCLCWH
SQFADWMFTDKkgkpVKKEVFYERLREHIHTVVNRY 93
                       79********************************************************
**********999999******************** PP


  MSA_GH10_xylanases 148 kgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaa
readpnakLyiNDYnlesasaklegmvklvkkllea 224
                       k+ vyaWDVvNE++ +dg                +r+s
+++++g++++++afe+areadp+  L +NDY+  ++  k+e ++ +vkk+++a
      k141_5537034  94
KDVVYAWDVVNEAMADDGRpfefvdgkmvpaspYRQSRHFKLCGDEFIAKAFEFAREADPTGVLIYNDYSCVDN-
GKRERIYTMVKKMKDA 183
                       ****************98888888888888899********************
***************9977.9************** PP


  MSA_GH10_xylanases 225 gvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele…
…ateekleaqakdyvevvkaclevkkcv. 300
                       gvpidGiG+q+H+++  p++++l+ka++++ +   ++itELD+++++e
++      q+++y++++k++++ k+++
      k141_5537034 184 GVPIDGIGMQGHYNIYFPEEEQLEKAITRFKEIVNIIHITELDLRTNTEtggqlm
fsrgeakpQAPYIGTLQEDQYARLFKIFRKHKDVIk 274
                       ****************************************9**********777789****
****9975444555779999*************** PP


  MSA_GH10_xylanases 301 gvtvWgvaDkdsW 313
                       +vt+W+++DkdsW
      k141_5537034 275 NVTFWNLSDKDSW 287
                       ************ PP


>> k141_4843626
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  269.0   0.2   1.2e-81   1.7e-81      94     335 ..      1     266 [.
1     270 [. 0.95


  Alignments for each domain:
  == domain 1  score: 269.0 bits;  conditional E-value: 1.2e-81
  MSA_GH10_xylanases  94 delvnfakkngkklRgHtlvWhsQlPswvssik…adketllevlknhiktvv
grYkgkvyaWDVvNEilnedgs…lresvfyr 174
                       d+++nf++++g k+RgHtl+WhsQ+ +w+ +++     ke++ + +k+hi+
+v+rYk+ vy WDVvNE++ +        lr+s+ y+
      k141_4843626   1 DKIANFCREHGIKMRGHTLMWHSQIGTWMYQDEkgnlLPKEEFYANMKHHIQAIV
NRYKDVVYCWDVVNEAVADSPVrpgapeLRNSPMYQ 91
```

39

```
                                89************************************998999999****************
*****************99754444566********* PP

  MSA_GH10_xylanases 175 vlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpid
GiGsqsHlsagapsvaelkkalnalaslgvevaitE 265
                            + ge+++ +afe+a+eadp+a L++NDYn  ++  k++ +
+lvk++++agvp+dGiG+q+H+++ +p+++++ +a++ +++    +++tE
        k141_4843626  92 IAGEEFIYKAFEYAHEADPDALLFYNDYNDAEP-
GKSQRIFNLVKRMKDAGVPVDGIGMQGHYNIYSPAMEDVDAAIRLYSQVVKHIHVTE 181
                            *****************************999.9******************
********************************** PP


  MSA_GH10_xylanases 266 LDialele…ateekleaqakdyvevvkaclevkkcv.gvtvWg
vaDkdsWls.eespllfdenynpKpaynai 335
                            LDi++++e              ++  +   q+++yv++++++++ k++v
+vt+W+v+D+dsWl   ++pllfdeny+pK+ay a+
        k141_4843626 182 LDIRVNTEmggglrfsqgagrVSGWEQTLQQDQYVNLFRVLRKHKDVVdCVTFWN
VSDRDSWLGaANAPLLFDENYRPKQAYLAV 266
                            ****888899*******99997777788999*************************
*******964789***************988 PP


>> k141_3972401
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  263.0   0.5   8.4e-80   1.1e-79      51     272 ..       2     232 ..
1     250 [. 0.93


  Alignments for each domain:
  == domain 1  score: 263.0 bits;  conditional E-value: 8.4e-80
  MSA_GH10_xylanases  51 qkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngk
klRgHtlvWhsQlPswvssik…adketllevlk 137
                            ++++++   + +++ ++f+s+t+eN+MK++ +ep++g+f++e+ad++++f+++ng
k+RgHtl+WhsQ+ +w+ +++       ke++ + +k
        k141_3972401   2 NRNVQDPDQIKVVLREFNSITAENAMKPQPTEPKKGEFNWEDADRIADFCRANGI
KMRGHTLMWHSQIGTWMYQDEkgnlLPKEEFYANMK 92
                            57888999999*********************************************
*******************998999999********* PP


  MSA_GH10_xylanases 138 nhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafe
aareadpnakLyiNDYnlesasaklegmvklvkkll 222
                            +hi+ +v+rYk+ vy WDVvNE++ +        lr+s+ y++ ge+++
+afe+a+eadp+a L++NDYn  ++ ak++ + +l+k+++
        k141_3972401  93
HHIQAIVNRYKDVVYCWDVVNEAVADSPVypgrpeLRNSPMYQIAGEEFIYKAFEYAHEADPKALLFYNDYNDAEP-
AKSQRIFNLLKRMK 182
                            ************************99864444456******************
```

```
*****************999.************** PP

  MSA_GH10_xylanases 223 eagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialel 272
                         +agvp+dG+G+q+H+++  ps++e+ +a++ +++     +++tELDi+++
        k141_3972401 183 DAGVPVDGVGMQAHYNVYGPSMKEVDDAIKLYSQVVKHIHLTELDIRINE 232
                         *****************************************544 PP


>> k141_3363962
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  261.4   0.1   2.6e-79   3.6e-79      37     272 ..     10     264 ..
7     269 .. 0.97


  Alignments for each domain:
  == domain 1  score: 261.4 bits;  conditional E-value: 2.6e-79
  MSA_GH10_xylanases  37 lkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfs
FegadelvnfakkngkklRgHtlvWhsQlPswvssi 125
                         lk a+k yf  G av++ ++++  ++ai+kk+f+s+t+eN+ K+ +i+p++g
++F  ad+++nf+++ng k+RgH l+WhsQ +w++++
        k141_3363962  10 LKDAYKGYFtiGVAVNKFNISDPAQTAIVKKQFNSVTAENAWKPGEIHPKEGVWN
FGLADSIANFCRENGIKMRGHCLCWHSQFADWMFTD 100
                         6889*************************************************
******************************* PP


  MSA_GH10_xylanases 126 k…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…
…lresvfyrvlgedyvkiafeaareadpnakLy 198
                         k    ++ke + ++l++hi+tvv+rYk+ vyaWDVvNE++ +dg
+r+s +++++g++++++afe+areadp+  L
        k141_3363962 101 KkgkpVKKEVFYQRLREHIHTVVNRYKDVVYAWDVVNEAMADDGRpfefvdgkmv
paspYRQSRHFKLCGDEFIAKAFEFAREADPTGVLM 191
                         999999*******************************988888888888
88899********************** PP


  MSA_GH10_xylanases 199
iNDYnlesasaklegmvklvkkllleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialel 272
                         +NDY+  ++  k+e ++++vkk++eagvpidGiG+q+H+++
p++++l+ka+n++++   ++itELD+++++
        k141_3363962 192 YNDYSCVDE-
GKRERIYNMVKKMKEAGVPIDGIGMQGHYNIYFPDEEKLEKAINRFSEIVNTIHITELDLRTNT 264
*****9988.9***************************************************9554 PP


>> k141_2686647
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
```

```
   1 !  256.9   0.3   6.2e-78   8.5e-78      50     274 ..       2     241 ..
1      269 [. 0.92


  Alignments for each domain:
  == domain 1  score: 256.9 bits;  conditional E-value: 6.2e-78
  MSA_GH10_xylanases   50 dqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkng
kklRgHtlvWhsQlPswvssik…adketllevl 136
                            +q++++++ ++a++ k+f+s+t+eN  K+ +i+p++g ++Fe ad++++f+++ng
k+RgH l+WhsQ  +w++++k    ++ke + ++l
        k141_2686647    2 NQRNVTDDAQKALVIKQFNSVTAENDWKPGEIHPKEGVWNFERADKIADFCRQNG
IKMRGHCLCWHSQFADWMFTDKngkpVKKEVFYQRL 92
                            5788999999************************************************
*******************999999********** PP


  MSA_GH10_xylanases  137 knhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlged
yvkiafeaareadpnakLyiNDYnlesasaklegmv 215
                            ++hi+tvv+rYk+ vyaWDVvNE++ +dg           +r+s
+++++g++++++af++areadpn+ L++NDY+  ++  k+e ++
        k141_2686647   93 REHIHTVVNRYKDVVYAWDVVNEAMADDGGfrfgrpgqepspYRQSRHFQLCGDE
FIAKAFQFAREADPNVLLFYNDYSCVDE-GKRERIY 182
                            ***************************9867777777788889***********
************************9988.9****** PP


  MSA_GH10_xylanases  216
klvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialelea 274
                            ++vkk+++agvpidGiG+q+H+++  p++a+l+ka+ ++ +
++itELD++++ e
        k141_2686647  183
NMVKKMKDAGVPIDGIGMQGHYNIYFPDEAQLEKAIVRFKEIVKHIHITELDLRMNNES 241
*************************************************77662 PP


>> k141_967616
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  254.6   0.1     3e-77   4.1e-77      48     270 ..       2     240 ..
1      242 [] 0.97


  Alignments for each domain:
  == domain 1  score: 254.6 bits;  conditional E-value: 3e-77
  MSA_GH10_xylanases   48 avdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakk
ngkklRgHtlvWhsQlPswvssik…adketlle 134
                            a +q+++++++++a++kk+f+s+t+eN  K+ +++p++g
++F++ad++++f++kng k+RgH l+WhsQ  +w++++k    ++ke + e
        k141_967616    2 ALNQRNVANEEQTALVKKEFNSVTAENDWKPGELHPQEGVWDFSKADKIADFCRK
NGIKMRGHCLCWHSQFADWMFTDKkgkdVKKEVFYE 92
                            678999************************************************
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***********************9999999****** PP


  MSA_GH10_xylanases 135 vlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvl
gedyvkiafeaareadpnakLyiNDYnlesasakle 212
                         +l++hi+tvv+rYk+ vyaWDVvNE++ +dg            +r+s
+++++g++++++afe+areadpn  L +NDY++ ++  k+e
         k141_967616   93 RLRDHIHTVVNRYKDVVYAWDVVNEAIADDGAprwglrpgeepspYRQSRHFKLC
GDEFIAKAFEFAREADPNGLLIYNDYSTVDP-GKRE 182
                          ***************************9888888888888899*********
**************************99.9*** PP


  MSA_GH10_xylanases 213
gmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDial 270
                         ++++vkk+++agvpidGiG+q+H+++  p+++ l +a++++ +l
++itELD+++
         k141_967616 183
RIYNMVKKMKDAGVPIDGIGMQGHYNIYFPDEELLDQAITRFKELVKHIHITELDLRM 240
*******************************************************95 PP


>> k141_2682329
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  254.6   0.6   3.1e-77   4.2e-77      63     252 ..      2     194 ..
1      195 [] 0.98


  Alignments for each domain:
  == domain 1  score: 254.6 bits;  conditional E-value: 3.1e-77
  MSA_GH10_xylanases  63 ikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQ
lPswvssikadketllevlknhiktvvgrYkgkvya 153
                         +kk+f+s+t+eN MK+e +ep++g+f++e+ad+++nfa++ng
klRgHtl+WhsQ+ w++++ ++ke++ +++knhi+ +v+rYk+ vy
         k141_2682329   2 VKKEFNSMTAENDMKPEPTEPREGEFNWENADRIANFARANGIKLRGHTLMWHSQ
IGRWMTAEGTTKEQFYARMKNHIQAIVSRYKDVVYC 92
                         89***************************************************
******************************** PP


  MSA_GH10_xylanases 154 WDVvNEilnedgs…lresvfyrvlgedyvkiafeaareadpnakLyiNDYnl
esasaklegmvklvkklleagvpidGiGsqsHlsag 240
                         WDVvNE+++++ +    +r+s  yr++g++++++af++a+eadp+a L++NDY++
++  k++ ++++vkk++++gvpidGiG+q+H+++
         k141_2682329  93
WDVVNEAMEDNPNatdpYRQSAMYRLCGDEFIEKAFQYAHEADPKALLFYNDYSTVDP-
HKRDRIYNMVKKMKAKGVPIDGIGMQAHYNIY 182
                         **********99888899*********************************
*99.9*************************** PP
```

43

```
   MSA_GH10_xylanases 241 apsvaelkkaln 252
                          ps+a+l +a++
       k141_2682329 183 YPSEARLDSAIT 194
                          *****9999885 PP


>> k141_2078378
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   253.5   0.8   6.7e-77   9.2e-77      74     273 ..       1     203 [.
1     223 [. 0.96


  Alignments for each domain:
  == domain 1  score: 253.5 bits;  conditional E-value: 6.7e-77
   MSA_GH10_xylanases  74 NsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikad
ketllevlknhiktvvgrYkgkvyaWDVvNEilned 164
                          N MK+e +ep++g+f++e+ad+++nfa++ng klRgHtl+WhsQ+  w++++
++ke++ +++knhi+ +v+rYk+ vy WDVvNE+++++
        k141_2078378    1 NDMKPEPTEPREGEFNWENADRIANFARANGIKLRGHTLMWHSQIGRWMTAEGTT
KEQFYARMKNHIQAIVSRYKDVVYCWDVVNEAMEDN 91
                          99****************************************************
********************************9 PP


   MSA_GH10_xylanases 165 gs…lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmv
klvkklleagvpidGiGsqsHlsagapsvaelkkal 251
                          ++    +r+s  yr++g++++++af++a+eadp+a L++NDY++ ++  k++
++++vkk++++gvpidGiG+q+H+++  ps+a+l +a+
        k141_2078378  92 ANatdpYRQSAMYRLCGDEFIEKAFQYAHEADPKALLFYNDYSTVDP-
HKRDRIYNMVKKMKAKGVPIDGIGMQAHYNIYYPSEARLDSAI 181
                          9888899****************************************99.9******
******************************** PP


   MSA_GH10_xylanases 252 nalaslgvevaitELDialele 273
                          + +        ++itE+Di+++ e
        k141_2078378 182 TLFKTIVKHIHITEFDIRVNEE 203
                          ******99**********5444 PP


>> k141_3977683
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   100.1   0.0      3e-30     4e-30      37     128 ..       4      96 ..
1     108 [. 0.93
   2 !   152.1   0.2   4.7e-46   6.4e-46     119     274 ..     182     342 ..
176     353 .. 0.91
```

```
  Alignments for each domain:
  == domain 1  score: 100.1 bits;  conditional E-value: 3e-30
  MSA_GH10_xylanases  37 lkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfs
FegadelvnfakkngkklRgHtlvWhsQlPswvssi 125
                        lk a+k yf  G av+ +++++s ++aii k+f+s+t+eN MK+ +i+p+ g
++F++ad++++f+++ng k+RgH lvWhsQ  +w++++
        k141_3977683    4 LKDAYKGYFkiGVAVTPRNVTDSLQAAIILKEFNSVTAENCMKPGEIHPQPGVWN
FAQADAIADFCRANGIKMRGHCLVWHSQFANWMFNK 94
                        6899*****************************************************
*****************************88 PP


  MSA_GH10_xylanases 126 kad 128
                         d
        k141_3977683  95 Y-D 96
                        6.3 PP


  == domain 2  score: 152.1 bits;  conditional E-value: 4.7e-46
  MSA_GH10_xylanases 119 PswvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…
.lresvfyrvlgedyvkiafeaareadpnakLyiND 201
                        P++ +   a+ke++ + l+ hi+ vv+rYk+ vy WDVvNE++++ ++
+r+s  y+++g++++ +af++a+eadpna L++ND
        k141_3977683 182 PKYAK---ATKEEFYDSLRAHIQVVVNRYKDVVYCWDVVNEAMSDANNpdapyeq
sFRQSTAYQLCGDEFILKAFQFAHEADPNATLFYND 269
                        44444…5789****************************997766666777
7****************************** PP


  MSA_GH10_xylanases 202
YnlesasaklegmvklvkklleagvpidGiGsqsHlsaga.psvaelkkalnalaslgvevaitELDialelea 274
                        Y+  ++ ak++ ++++vkkl+++g+pi GiG+q+H+++   p+ ++ +ka++++
+l  +++itE+D+++++ea
        k141_3977683 270 YSAWTP-
AKRTYIYNMVKKLQAEGAPITGIGMQGHYNIYDnPTIEDFEKAIQMYLELVDDIQITEFDVRINHEA 342
****99.************************988799************************76664 PP


>> k141_3525868
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  249.5   2.4   1.1e-75   1.5e-75      37     272 ..      13     310 ..
4     322 .. 0.95


  Alignments for each domain:
  == domain 1  score: 249.5 bits;  conditional E-value: 1.1e-75
  MSA_GH10_xylanases  37 lkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfs
FegadelvnfakkngkklRgHtlvWhsQlPswvssi 125
                        lk a+k+yf  G av+++++++  +++ii k+++s+t+eN MK+ +++p+ g
++Fe+ad ++nf++++g k+RgH+lvWhsQ  +w++++
```

45

```
         k141_3525868   13 LKDAYKNYFkiGVAVTERNVTDPVQSEIILKEYNSVTAENCMKPGELHPEPGVWD
FEKADIIANFCREHGIKMRGHNLVWHSQFCTWMFTH 103
                           7899**************************************************
******************************99 PP


  MSA_GH10_xylanases 126 k…ad
ketllevlknhiktvvgrYkgkvyaWDVvNEilned 164
                           +
a+ke++ + lk hi+tvv+rYk+ +y WDVvNE++++
         k141_3525868 104 HdengnpvverdaqgdtvwverrtfarpsgprpegaparmpamvttmvpkyvaAT
KEEFYDSLKVHIQTVVNRYKDVIYCWDVVNEAMSDS 194
                           999**************************************************
*****************************9875 PP


  MSA_GH10_xylanases 165 gs…lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasakl
egmvklvkklleagvpidGiGsqsHlsaga.psvae 246
                           +          +r+s+ y+++g++++k af +a+eadpn  L++NDY+  ++
ak++ ++++vkkl+++g+pi GiG+q+H+++   p+ ++
         k141_3525868 195 DNvnasyddsFRKSQAYQLCGDEFIKNAFIWAHEADPNCGLFYNDYSAWTP-
AKRTYIYNMVKKLQSEGAPITGIGMQGHYNIFDnPTLED 284
                           4334445555***********************************99.***
**************************987799*** PP


  MSA_GH10_xylanases 247 lkkalnalaslgvevaitELDialel 272
                           +ka+n++ +l  +++itE+Di+++
         k141_3525868 285 FEKAINMYLELVDDIQITEFDIRINE 310
                           **********************544 PP


>> k141_8086075
   #    score   bias   c-Evalue   i-Evalue hmmfrom   hmm to    alifrom   ali to
envfrom   env to     acc
 ---    ------  -----  ---------  --------- -------  -------     ------- -------
 ------- -------    ----
   1 !  248.5    0.0    2.3e-75    3.1e-75      104      337 ..       1      265 [.
1      267 [. 0.96


  Alignments for each domain:
  == domain 1  score: 248.5 bits;  conditional E-value: 2.3e-75
  MSA_GH10_xylanases 104 gkklRgHtlvWhsQlPswvssik…adketllevlknhiktvvgrYkgkvyaW
DVvNEilnedgs…lresvfyrvlge 178
                           g k+RgH l+WhsQ  +w++++k    ++ke + e+l++hi+tvv+rYk+
vyaWDVvNE++ +dg          +r+s +++++g+
         k141_8086075   1 GIKMRGHCLCWHSQFADWMFTDKkgkeVKKEVFYERLRDHIHTVVNRYKDVVYAW
DVVNEAMADDGGprwgrggqepspYRQSRHFKLCGD 91
                           679*******************99999999*************************
**********977777788888899********** PP


  MSA_GH10_xylanases 179 dyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGs
```

```
qsHlsagapsvaelkkalnalaslgvevaitELDia 269
                        +++++af++areadpna+L++NDY+  ++  k+e
++++vkk+++agvpidGiG+q+H+++  p++a l +a++++ +l    ++itELD++
        k141_8086075  92 EFIAKAFQFAREADPNAQLFYNDYSCVDP-
GKRERIYNMVKKMKDAGVPIDGIGMQGHYNIYFPDEALLDQAITRFKELVQHIHITELDLR 181
                        ************************99.9***********************
******************************** PP


  MSA_GH10_xylanases 270 lele…ateekleaqakdyvevvkaclevkkcv.gvtvWgvaD
kdsWls.eespllfdenynpKpaynaivk 337
                        ++ e              +++ +   q+++y+++++++++ k+++ +vt+W++
D+dsWl  ++ pl fdeny+pK+ y ai +
        k141_8086075 182 MNNEsggqlmfsrgeakpMPAYMGTLQNDQYARIFRVFRKHKDVIdNVTFWNLGD
RDSWLGvNNHPLPFDENYQPKACYRAIRD 265
                        88879***********9888899999*************************
****986899***************9976 PP


>> k141_8350670
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  236.4   0.3    1e-71   1.4e-71      44     235 ..      2     204 .]
1     204 [] 0.96


  Alignments for each domain:
  == domain 1  score: 236.4 bits;  conditional E-value: 1e-71
  MSA_GH10_xylanases  44 yf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadel
vnfakkngkklRgHtlvWhsQlPswvssik…ad 128
                        yf  G av++++ ++  + ++i ++f+s+t++N+MK++
+ep++g+f++e+ad++++f+++ng k+RgHtl+WhsQ+ +w+ +++
        k141_8350670   2 YFkiGVAVNNRNGTDPDQIKLILREFNSITADNAMKPQPTEPKKGEFNWEDADRI
ADFCRQNGIKMRGHTLMWHSQIGTWMYQDEkgnlLP 92
                        5666**********************************************
**************************99899999 PP


  MSA_GH10_xylanases 129 ketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlg
edyvkiafeaareadpnakLyiNDYnlesasakleg 213
                        k+++ + +k+hi+ +v+rYk+ vy WDVvNE++ +        lr+s+ y++
ge+++ +afe+a+eadpna L++NDYn  ++ ak++
        k141_8350670  93 KDQFYANMKHHIQAIVNRYKDVVYCWDVVNEAVADSPVypgrpeLRNSPMYQIAG
EEFIYKAFEYAHEADPNALLFYNDYNDAEP-AKSQR 182
                        *******************************99864444456***********
***********************999.***** PP


  MSA_GH10_xylanases 214 mvklvkklleagvpidGiGsqs 235
                        +++lvk++++agvp+dGiG+q+
        k141_8350670 183 IYNLVKRMKDAGVPVDGIGMQA 204


                               47
```

```
                    ********************6 PP

>> k141_9450604
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  233.3   0.1   9.2e-71   1.3e-70      88     337 ..       4     267 ..
1     269 [] 0.92


  Alignments for each domain:
  == domain 1  score: 233.3 bits;  conditional E-value: 9.2e-71
  MSA_GH10_xylanases  88 fsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllev
lknhiktvv…grYkg.kvyaWDVvNEilnedgs 166
                         s + a +  +f+++ng  lRgHt+vW+sQ+P+w+++++      ++k+ +
++l+n+ik+      + Y + +vy++DV+NE + +dg
        k141_9450604    4 VSLQRAAQTLKFCESNGIALRGHTFVWYSQTPDWFFKENfssngsyVSKDIMNQR
LENFIKDTFdalaKEYPNlEVYSYDVCNELFVNDGG 94
                         567889999**************************************************
*****987655558897658*********9977776 PP


  MSA_GH10_xylanases 167 .lr…esvfyrvlg…edyvkiafeaareadpn.akLyiNDYnlesasakleg
mvklvkklleagvpidGiGsqsHlsagapsvaelkk 249
                         lr   +s ++rv g    ++++  af +ar+++p+  kLyiNDYn + +
ak+++++++  kl+e+gv idGiG+qsHl++g ps + +k
        k141_9450604  95 gLRpgsNSGWTRVYGdtnDEFIINAFTYARKYAPKgCKLYINDYNEYIP-
AKTNDIYNIAMKLKEKGV-IDGIGMQSHLDVGYPSASVYKT 183
                         67766699**9998733368**********888758**********99.*****
*************7.9********************* PP


  MSA_GH10_xylanases 250 alnalaslgvevaitELDialeleateekleaqakdyvevvkaclevkkcv.gvt
vWgvaDkdsWlseespllfdenynpKpaynaivk 337
                         al+++ s+g+ev+itELDi+    t+ + ++qak +++v++++++ ++++
++tvWg+ D+ sW+s+++pllf++ y+pK+a++a+++
        k141_9450604 184 ALEKFLSTGLEVQITELDIT-----
TSGNYDSQAKLFADVFQMAIDHADQIpALTVWGTNDSISWRSSQNPLLFSSGYKPKKAFEAVMA 267
                         *******************…78889*********************9***
****************************986 PP

>> k141_8466112
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  226.3   2.1   1.3e-68   1.7e-68      39     214 ..       2     182 ..
1     183 [] 0.97


  Alignments for each domain:
```

```
== domain 1  score: 226.3 bits;  conditional E-value: 1.3e-68
  MSA_GH10_xylanases   39 aagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFe
gadelvnfakkngkklRgHtlvWhsQlPswvssika 127
                           +k+yf  G av+q+++++++++a+ik++f s+t+eN MK+e
+ep++g+f++egad+++nfa++ng klRgH l+WhsQ+  w++s++
        k141_8466112    2 DVYKDYFliGVAVNQRNVTNAEQQALIKREFSSMTAENDMKPEPTEPRQGQFNWE
GADRIANFARQNGIKLRGHCLMWHSQIGRWMTSDNP 92
                          579**************************************************
***************************** PP


  MSA_GH10_xylanases  128 dketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlge
dyvkiafeaareadpnakLyiNDYnlesasaklegm 214
                          +ke + +++k+hi+ vv+rYk+ vyaWDVvNE++ +d++     +r+sv
y+++g++++++afe+a++adpna L++NDYn  ++ +k++ +
        k141_8466112   93 TKEVFYQRMKSHIEAVVSRYKDVVYAWDVVNEAMTDDANaedpYRQSVMYKLCGD
EFIAKAFEFAHAADPNALLFYNDYNECDP-MKSQRI 182
                          *********************************99888999***********
**********************9999.888876 PP


>> k141_1693700
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 ! 222.9   0.1   1.3e-67   1.8e-67      89     338 ..      9     277 ..
3     279 .. 0.90


  Alignments for each domain:
  == domain 1  score: 222.9 bits;  conditional E-value: 1.3e-67
  MSA_GH10_xylanases   89 sFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllevl
knhiktvv…grYkgkvyaWDVvNEilnedgslr 168
                          +Fe+a   +fakkng  +RgHtlvWh+Q+P+w+++++        a++e
+le+l+++i+ v+    + Y g +yaWDVvNE+++e g++r
        k141_1693700    9 TFEHAIPYLEFAKKNGIAMRGHTLVWHNQTPKWFFHERynemfplASREVVLERL
ESYIHGVLdfvqTNYPGIIYAWDVVNEAVDE-GDFR 98
                          799999999*************************9999***************
*****99877779***************75.99** PP


  MSA_GH10_xylanases  169 esvfyrvlgedyvkiafeaare.adpnakLyiNDYnlesasaklegmv.klvkkl
leagvpidGiGsqsHlsagapsvaelkkalnalasl 257
                          +s +++++g+dyv +afe+a++ ++p + L++NDY +     k++ ++ +++k
l+++g+ +dG+G+qsHl + +p+ ++++ al+++ +l
        k141_1693700   99 KSIWTKTVGNDYVLKAFEFAKKyMAPGVDLFYNDYETALD-
WKRDFIIeNILKPLMDKGL-VDGMGMQSHLLMDHPDLNDYRTALEMYGAL 187
                          **********************89***********9977.88886661566777
77775.9*********************** PP


  MSA_GH10_xylanases  258 gvevaitELDialeleateekleaqakdyvevvkaclevkk…cv.gvtvWgv
```

49

```
aDkdsWls…eespllfdenynpKpaynaivka 338
                          g+ ++itELD++ + ++ ee +++  ++y+e +k++le kk     +v +vt+W++
D++sWl+      +++pllf  + ++K+ay+ +++a
        k141_1693700 188 GLKIHITELDMH-
NNDPGEESMKKLGERYQEFFKIYLEAKKsgkaNVtSVTFWNLLDENSWLTgfrreQSYPLLFKGKCEAKQAYYDVLEA
277
                          ************.6666678888888888888888776542222788*******
********99999899*****************9986 PP


>> k141_764324
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  222.4   2.2   1.9e-67   2.6e-67     134     338 ..       2     224 ..
1     226 [. 0.96


  Alignments for each domain:
  == domain 1  score: 222.4 bits;  conditional E-value: 1.9e-67
  MSA_GH10_xylanases 134 evlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkia
feaareadpnakLyiNDYnlesasaklegmvklvkk 220
                          +++knhi+ vv+rYk+ vyaWDVvNE++ +d +    +r+sv
y+++g++++++af++areadp+a L++NDYn  ++ +k++ ++++vkk
        k141_764324   2
QRMKNHIQAVVSRYKDVVYAWDVVNEAMTDDKNaedpYRQSVMYKLCGDEFIAKAFQFAREADPKALLFYNDYNECDP-
VKSKRIYNMVKK 91
                          79*****************************9998888899*****************
*******************99.*********** PP


  MSA_GH10_xylanases 221 lleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele..
…ateekleaqakdyvevvkaclevkk 298
                          ++++gvpidGiG+q+H+++  p+++e+ +a++ +      +++tELDi+++ e
+++++ ++ a++y++v+ ++++ k+
        k141_764324   92 MKDNGVPIDGIGMQGHYNIYGPTEKEVDDAITLYKTIVKHIHVTELDIRVNEEmg
gqlrfsregvtISDTVKQNLADQYARVFGVFRKHKD 182
                          *****************************************99**********776689
*********99899999999*************** PP


  MSA_GH10_xylanases 299 cv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivka 338
                          ++ +vt+W+++D+dsWl   ++pl fd++y+pK ay+ i ++
        k141_764324 183 VIdCVTFWNLSDRDSWLGaANYPLPFDSDYKPKLAYDYIKNM 224
                          *****************964789*****************99775 PP


>> k141_3957828
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
```

```
   1 !  219.2   0.1   1.8e-66   2.5e-66      114      337 ..       1      259 [.
1     261 [. 0.96


  Alignments for each domain:
  == domain 1  score: 219.2 bits;  conditional E-value: 1.8e-66
  MSA_GH10_xylanases 114 WhsQlPswvssik…adketllevlknhiktvvgrYkgkvyaWDVvNEilned
gs…lresvfyrvlgedyvkia 184
                          WhsQ  +w++++k     ++ke + ++l++hi+tvv+rYk+ vyaWDVvNE++
+d++               +r+s +++++g++++++a
          k141_3957828   1 WHSQFADWMFTDKngkpVKKEVFYQRLREHIHTVVNRYKDVVYAWDVVNEAMADD
NQfgprfgfgrpgqepspYRQSRHFQLCGDEFIAKA 91
                          *************999999*********************************
9888888888888888889**************** PP


  MSA_GH10_xylanases 185 feaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsa
gapsvaelkkalnalaslgvevaitELDialele.. 273
                          f++areadpn+ L++NDY+  ++   k+e ++++vkk+++agvpidGiG+q+H+++
ps+++l+ka+ ++ +     ++itELD++++ e
          k141_3957828   92 FQFAREADPNTLLFYNDYSCVDE-
GKRERIYNMVKKMKDAGVPIDGIGMQGHYNIYFPSEEQLEKAIVRFKEIVKHINITELDLRMNNEsg 181
                          ******************9988.9*****************************
****************************88879* PP


  MSA_GH10_xylanases 274
…ateekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk
337
                                          +++ +    q+++y++++k++++ ++++ +vt+W++ D+dsWl
++ pl fdeny+pK+   ai +
          k141_3957828 182
gqlmfsrgeakpMPAYMSTLQTDQYARLFKVFRKHADVIdNVTFWNLGDQDSWLGvNNHPLPFDENYRPKACLRAIRD
259
*********998999999********************************986899************9999865
PP


>> k141_3597594
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------   ------- -------
------- -------    ----
   1 !  220.1   3.1   9.3e-67   1.3e-66      137      337 ..       1      219 [.
1     222 [. 0.96


  Alignments for each domain:
  == domain 1  score: 220.1 bits;  conditional E-value: 9.3e-67
  MSA_GH10_xylanases 137 knhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafea
areadpnakLyiNDYnlesasaklegmvklvkklle 223
                          knhi+ vv+rYk+ vyaWDVvNE++ +d++    +r+sv
y+++g++++++afe+a++adpna L++NDYn   ++ +k++ ++++vkk+++
```

```
         k141_3597594    1
KNHIEAVVSRYKDVVYAWDVVNEAMTDDANaedpYRQSVMYKLCGDEFIAKAFEYAHAADPNALLFYNDYNECDP-
VKSQRIYNMVKKMKD 90
                          79*****************************99888999*******************
*****************99.************** PP


  MSA_GH10_xylanases 224 agvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele…
…ateekleaqakdyvevvkaclevkkcv. 300
                          agvpi+GiG+q+H+++  p+++++ kal+ + +    +++tELDi+ ++e
++++   ++ a++y++v++++++ k+++
         k141_3597594   91 AGVPIHGIGMQGHYNIYGPKEEDVDKALELYKKVVDHIHVTELDIRANQEmggql
afsrdgaaVNDSLKQHLADQYARVFRVFRKHKDVId 181
                          *******************************99**********766689***
******987888888899***************** PP


  MSA_GH10_xylanases 301 gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                          +vt+W+++D+dsWl  +++pl fd +y+pK ay+ i +
         k141_3597594 182 CVTFWNLSDRDSWLGqNNYPLPFDVDYKPKMAYEYIHD 219
                          **************963789****************9976 PP


>> k141_6262298
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  217.0   1.2   8.6e-66   1.2e-65      85     272 ..       2     208 ..
1     211 [. 0.96


  Alignments for each domain:
  == domain 1  score: 217.0 bits;  conditional E-value: 8.6e-66
  MSA_GH10_xylanases  85 rgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllev
lknhiktvvgrYkgkvyaWDVvNEilnedgs… 166
                          +g ++Fe ad++++f+++ng k+RgH l+WhsQ  +w++++k    ++ke +
e+l++hi+tvv+rYk+ vyaWDVvNE++ +d++
         k141_6262298    2 EGVWNFERADKIADFCRQNGIKMRGHCLCWHSQFADWMFTDKdgkdVSKEVFYER
LREHIHTVVKRYKDVVYAWDVVNEAMADDNQfgprf 92
                          789****************************************999999********
****************************9888888 PP


  MSA_GH10_xylanases 167 …lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasak
legmvklvkklleagvpidGiGsqsHlsagapsvae 246
                                   +r+s +++++g++++++af++areadpn+ L++NDY+  ++
k+e ++++vkk+++agvpidGiG+q+H+++  ps+++
         k141_6262298   93 gfgrpgqepspYRQSRHFQLCGDEFIAKAFQFAREADPNTLLFYNDYSCVDE-
GKRERIYNMVKKMKDAGVPIDGIGMQGHYNIYFPSEEQ 182
                          888888888889***********************************9988.9*
****************************** PP
```

```
  MSA_GH10_xylanases 247 lkkalnalaslgvevaitELDialel 272
                         l+ka+ ++ +    ++itELD++++
        k141_6262298 183 LEKAIVRFKEIVKHINITELDLRMNN 208
                         *******************9654 PP


>> k141_5897125
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  218.5   0.4     3e-66   4.1e-66      37     221 ..      6     204 ..
2     205 .] 0.97


  Alignments for each domain:
  == domain 1  score: 218.5 bits;  conditional E-value: 3e-66
  MSA_GH10_xylanases  37 lkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfs
FegadelvnfakkngkklRgHtlvWhsQlPswvssi 125
                         +k ++k+yf  G av+q+++++  + a+ikk+f+s+t+eN MK+ +i+p++g
++Fe ad+++nf+++ng klRgH l+WhsQ  +w++++
        k141_5897125   6 MKDSYKDYFtiGVAVNQRNVSNPDQIALIKKEFNSITAENDMKPGEIHPKEGVWN
FERADKIANFCRENGIKLRGHCLCWHSQFADWMFTD 96
                         7899****************************************************
********************************9 PP


  MSA_GH10_xylanases 126 k…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…l
resvfyrvlgedyvkiafeaareadpnakLyiNDYn 203
                         +     ++ke + e+l++hi+ vv+rYk+ vyaWDVvNE++ +dg
+r+s +++++g++++++af++areadpna L++NDY+
        k141_5897125  97 SkgkpVKKEVFYERLREHIHAVVNRYKDIVYAWDVVNEAMADDGRswpgreqspY
RQSRHFQLCGDEFIAKAFQFAREADPNALLFYNDYS 187
                         999999*********************************988888888889
9****************************** PP


  MSA_GH10_xylanases 204 lesasaklegmvklvkkl 221
                         ++  k+e ++++vkk+
        k141_5897125 188 CVDE-GKRERIYNMVKKM 204
                         9988.9**********98 PP


>> k141_6147756
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  218.0   0.0   4.3e-66   5.8e-66      80     267 ..      2     201 .]
1     201 [] 0.96


  Alignments for each domain:
  == domain 1  score: 218.0 bits;  conditional E-value: 4.3e-66
```

```
  MSA_GH10_xylanases  80 aiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adke
tllevlknhiktvvgrYkgkvyaWDVvNEilnedgs 166
                          +++p++g +++ gad+++n++++n+  lRgH l+WhsQ  +w+  +k    ++ke
+ e+l++hi+tvv+rYk+ vy WDVvNE++ + +
        k141_6147756    2 SVHPKEGVWNWGGADSVANYCRENNIPLRGHCLCWHSQFTDWMLYDKkgrmVKKE
VFYERLREHIHTVVNRYKDIVYCWDVVNEAIADRAF 92
                          689****************************************999999999***
***************************998753 PP


  MSA_GH10_xylanases 167 …lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasakle
gmvklvkklleagvpidGiGsqsHlsagapsvaelk 248
                              +r+s+ y+++g++++++afe+areadpna L++NDYn  ++  k++
++++vkk++e+gvpidGiG+q+H+++  ps++e++
        k141_6147756   93 grpgrpanpYRDSKLYQLCGDEFIAKAFEFAREADPNALLFYNDYNECDP-
GKRDRIYDMVKKMKEQGVPIDGIGMQGHYNIYGPSEEEIE 182
                          3355567789************************************99.9***
******************************** PP


  MSA_GH10_xylanases 249 kalnalaslgvevaitELD 267
                          +a++++++     +++tELD
        k141_6147756 183 DAIKKYSEIVNHIHVTELD 201
                          *****************9 PP


>> k141_8518009
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  217.7   1.0   5.2e-66   7.1e-66     121     337 ..       2     247 ..
1     249 [. 0.93


  Alignments for each domain:
  == domain 1  score: 217.7 bits;  conditional E-value: 5.2e-66
  MSA_GH10_xylanases 121 wvssik…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…
…lresvfyrvlgedyvkiafeaareadpnak 196
                          w+ ++k    ++ke + e+l++hi+tv++rYk+ vy WDVvNE++ ++
+res  y+++g++++++afe+areadp+a
        k141_8518009    2 WMLRDKkgnfVKKEVFYERLRDHIHTVMNRYKDIVYCWDVVNEAMADNQRpawgn
rpagspYRESDLYKLCGDEFIAKAFEFAREADPKAL 92
                          77777777778999****************************9987666666
7777899************************* PP


  MSA_GH10_xylanases 197 LyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkal
nalaslgvevaitELDialele…a 274
                          L++NDYn  ++  k++ + ++vkk+++agvpidGiG+q+Hl++ +ps+++
+a++++a l    ++itELDi+ + e             +
        k141_8518009   93 LFYNDYNAFDK-
GKSQRIFDMVKKMKDAGVPIDGIGMQGHLNIFNPSMEDFGNAIDKYATLVKHIQITELDIRANEEmggqlnfsrqgveI
```

182
```
                            ********988.9*****************************************
*****************66667999****999976 PP


  MSA_GH10_xylanases 275
teekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                            +   +  + ++++yv+++k +++  k++v   vt+W+++D+dsW+
+++pllfd+++n+K+ayna+++
        k141_8518009 183
KPWVKSLHTDQYVQLFKCLRKHKDVVdVVTFWNLSDRDSWVGtSNYPLLFDKDLNKKEAYNAVLN 247
6677788999****************99*************974889*****************98 PP


>> k141_6541486
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  215.9   0.0   1.9e-65   2.5e-65      93     330 ..      11     259 .]
2     259 .] 0.96


  Alignments for each domain:
  == domain 1  score: 215.9 bits;  conditional E-value: 1.9e-65
  MSA_GH10_xylanases  93 adelvnfakkngkklRgHtlvWhsQlPswvssik…adketllevlknhi
ktvv…grYkgkvyaWDVvNEilnedgs.lresv 171
                           a  l +fa+k + k+ gH lvWhsQ+P+ ++++        +++e ll
+++n+ik v+     ++Y g +++WDV+NE++++ ++ lr+s+
        k141_6541486  11 ARPLLDFAQKYNLKVHGHVLVWHSQTPDTLFHEGyeaskplVSREVLLGRMENYI
KGVLelteEKYPGVIVSWDVLNEAIDDGTNkLRNSN 101
                           566889**********************9998999*****************
***988989****************98877***** PP


  MSA_GH10_xylanases 172 fyrvlgedyvkiafeaare.adpnakLyiNDYnlesasaklegmvklvkklleag
vpidGiGsqsHlsagapsvaelkkalnalaslgvev 261
                           +++++gedy + af +ar+ a++ +kLy+NDYn+ +   kl g+ kl+k+l++ g
idG G+q H ++++p++++++++++a+lg+ +
        k141_6541486 102 WMKIIGEDYPNYAFAYARKyAAEGVKLYYNDYNTAYY-
GKLMGIEKLLKDLIADG-NIDGYGFQMHHGVSQPTMQMIEESVETIAKLGFSL 190
                           *****************88999***********99.9*************999
.7***************************** PP


  MSA_GH10_xylanases 262
aitELDialeleateekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWlseespllfdenynpKp 330
                           + ELD+   +   +te+ + +qak+y++++k+++ ++++  +v vWg++D+
sW+s+++pllfd + npKp
        k141_6541486 191 RVSELDVG-
TGSNTEASFTRQAKKYADIMKLLIRYSDQFeAVQVWGLTDTMSWRSRNFPLLFDGKGNPKP 259
********.67788999*********************9*****************************7 PP
```

55

```
>> k141_2110739
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom   env to      acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  213.6   0.1   9.2e-65   1.3e-64      88     330 ..      16     277 .]
6     277 .] 0.90


  Alignments for each domain:
  == domain 1  score: 213.6 bits;  conditional E-value: 9.2e-65
  MSA_GH10_xylanases  88 fsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllev
lknhiktvv…grYkgkvyaWDVvNEilnedgsl 167
                          +Fe+a    +fak++g  +RgHtlvWh+Q+P+w++ ++
ad++t+l++l+n+ik v+    + Y g +yaWDVvNEi++e g++
         k141_2110739   16 LTFENAIPYLEFAKEHGIAMRGHTLVWHNQTPKWFFCENynehfplADRDTMLSR
LENYIKGVLtfvqSNYPGVIYAWDVVNEIVDE-GDF 105
                          68999999**********************************99**************
******998777789***************975.99* PP


  MSA_GH10_xylanases 168 resvfyrvlgedyvkiafeaare.adpnakLyiNDYnlesasaklegmv.klvkk
lleagvpidGiGsqsHlsagapsvaelkkalnalas 256
                          r+s ++r++g+d+  +afe+ar+ + + + L++NDY +     k++ ++ +++k
l++++  +d +G+qsHl + +p+ +++kka++++ +
         k141_2110739 106 RKSLWTRTVGNDFFIKAFEYARRyVSDGVDLFYNDYETALD-
WKRDFIIaNVLKPLIDQK-LVDVMGMQSHLLMDHPDLDDYKKAIESYGA 194
                          ********************988999*********9977.8888655156666
66665.69************************** PP


  MSA_GH10_xylanases 257 lgvevaitELDialeleateekleaqakdyvevvkaclev…kkcv.gvtvWg
vaDkdsWls…eespllfdenynpKp 330
                          lg+ ++itELD++ + ++++e +++ a +y++ +k++l+    k+++
+vt+W+++D+dsWl+     +++pllf + ++K+
         k141_2110739 195 LGLKIHITELDMH-
NADPSDESMHSLALRYRDFFKIYLDAvrsgKANItSVTFWNLRDEDSWLTgfrreTSYPLLFKGKCEAKE 277
                          *************.77888999999999999998877643333777888******
********9999888999****9999985 PP

>> k141_2681456
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom   env to      acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  213.4   0.3     1e-64   1.4e-64      51     230 ..       2     196 .]
1     196 [] 0.96


  Alignments for each domain:
  == domain 1  score: 213.4 bits;  conditional E-value: 1e-64
  MSA_GH10_xylanases  51 qkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngk
```

```
klRgHtlvWhsQlPswvssik…adketllevlk 137
                    q+++ ++ +++++ k+f+s+t+eN MK+ +i+p++g +++e ad+++nf+++ng
k+RgH l+WhsQ  +w++++k    ++ke + e+l+
        k141_2681456    2 QRNVGDDAQKELVLKQFNSVTAENDMKPGEIHPKEGVWNWERADKIANFCRENGI
KMRGHCLCWHSQFADWMFTDKkgkpVKKEVFYERLR 92
                    6777888999**********************************************
*******************999999********** PP


  MSA_GH10_xylanases 138 nhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedy
vkiafeaareadpnakLyiNDYnlesasaklegmvk 216
                    +hi+tvv+rYk+ vyaWDVvNE++ +dg          +r+s
+++++g++++++afe+areadpn+ L++NDY+  ++  k+e +++
        k141_2681456   93 DHIHTVVNRYKDVVYAWDVVNEAMADDGGprwgrggqqpspYRQSRHFQLCGDEF
IAKAFEFAREADPNTLLFYNDYSCVDN-GKRERIYN 182
                    ***************************977777788888899**************
********************9977.9******* PP


  MSA_GH10_xylanases 217 lvkklleagvpidG 230
                    +vkk+++agvpidG
        k141_2681456 183 MVKKMKDAGVPIDG 196
                    *************9 PP


>> k141_3275240
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  213.1   0.0   1.3e-64   1.8e-64      24     212 ..      25     223 ..
3     225 .] 0.89


  Alignments for each domain:
  == domain 1  score: 213.1 bits;  conditional E-value: 1.3e-64
  MSA_GH10_xylanases  24 lesrqaaesldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsM
KweaiepsrgkfsFegadelvnfakkngkklRgHtl 112
                    +r+++e  d  lk a+k+yf  G av+++++++  + +++
++f+s+t+eN+MK++ +ep++g+f++e+ad+++nf++++g k+RgHtl
        k141_3275240   25 WGPRTIPEPTD-
GLKDAYKDYFkiGVAVNNRNVADPDQIKVVLREFNSITAENAMKPQPTEPRKGEFNWEDADKIANFCREHGIKMRGHTL
114
                    55666665555.799*****************************************
******************************** PP


  MSA_GH10_xylanases 113 vWhsQlPswvssik…adketllevlknhiktvvgrYkgkvyaWDVvNEilne
dgs…lresvfyrvlgedyvkiafeaareadp 193
                    +WhsQ+ +w+ +++      ke++ + +k+hi+ +v+rYk+ vy WDVvNE++ +
lr+s+ y++ ge+++ +afe+a+eadp
        k141_3275240 115 MWHSQIGTWMYQDEkgnlLPKEEFYANMKHHIQAIVNRYKDVVYCWDVVNEAVAD
SPVypgrpeLRNSPMYQIAGEEFIYKAFEYAHEADP 205
```

```
                           *************998999999******************************99
864444456*********************** PP

  MSA_GH10_xylanases 194 nakLyiNDYnlesasakle 212
                         na L++NDYn  ++ ak++
         k141_3275240 206 NALLFYNDYNDAEP-AKSQ 223
                         **********9988.7766 PP


>> k141_5782979
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  212.2   1.5   2.5e-64   3.4e-64     127     337 ..       8     242 ..
3     245 .. 0.93


  Alignments for each domain:
  == domain 1  score: 212.2 bits;  conditional E-value: 2.5e-64
  MSA_GH10_xylanases 127 adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresv
fyrvlgedyvkiafeaareadpnakLyiNDYnlesa 207
                         ++ke + ++l++hi+tvv+rYk+ vy WDVvNE++ e ++         +r+s+
++  g++++++afe+areadpna L++NDYn  ++
        k141_5782979   8 VKKEVFYARLRDHIHTVVNRYKDIVYCWDVVNEAMAESANpnrwnpnpspYRQSE
LFKNYGDEFIAKAFEFAREADPNALLFYNDYNAATP 98
                         5789999**************************9987777777888899****
*******************************99 PP


  MSA_GH10_xylanases 208 saklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgveva
itELDialele…ateekleaqakd 285
                         +k++ ++++vkk+++agvpidGiG+q+H+++  ps +++ +a++++++
+++itELD++ + e          ++      q+++
        k141_5782979  99 -SKRDLIYNMVKKMKDAGVPIDGIGMQGHYNIYGPSAEDIDAAITKYSEIVKNIH
ITELDVRANEEmggqlqfrrdkidIKPYIKTLQENQ 188
                         .9***************************************************
*******6666899******999866677788999* PP


  MSA_GH10_xylanases 286 yvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk
337
                         y++++++++ k++v +vt+W+v+D+dsWl  +++pllfd+++++K+a++ + +
        k141_5782979 189 YAQIFRVLRKHKDVVkCVTFWNVSDRDSWLGtNNYPLLFDKDLKAKKAFSVVKN
242
                         ***************************964889**************99876
PP


>> k141_9166542
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
```

```
------- ------- ----
   1 !   206.5   4.1   1.3e-62   1.8e-62      39     205 ..       8     181 ..
1     183 [] 0.90

  Alignments for each domain:
  == domain 1  score: 206.5 bits;  conditional E-value: 1.3e-62
  MSA_GH10_xylanases   39 aagkkyfGtavdqkelek…skeeaiikkdfgsltpeNsMKweaiepsrgkfsF
egadelvnfakkngkklRgHtlvWhsQlPswvssik 126
                          ++  +y+G++ +++ +     s+ e+i k++f+++++eN+MK++a+eps+gkfs+
+ d++v++a++ng+ +RgH+l WhsQ+P+wv++ k
        k141_9166542    8 EERGRYIGAILNSEWFGGrieSQFEQIHKAQFNAVVAENEMKFDATEPSEGKFSY
GNGDKMVKYAQQNGMRVRGHALAWHSQVPNWVNNYK 98
                          34446999999999988764535666677**************************
****************************** PP


  MSA_GH10_xylanases  127 adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs..lr..esvfyrvlg
edyvkiafeaareadpnakLyiNDYnle 205
                          +k++l +vlknhi++vvg++kg+v  WDVvNE++n++++    r
sv++++lg+d++  af +a++adp+a L++NDY +e
        k141_9166542   99 GQKDKLFKVLKNHIENVVGHWKGQVAEWDVVNEAVNDNNNhgWRssGSVWFETLG
ADFLDSAFVWAHAADPDAELCYNDYAIE 181
                          *****************************************999765522579******
***********************987 PP


>> k141_7127811
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   203.7   0.0   9.6e-62   1.3e-61      28     199 ..      21     199 .]
2     199 .] 0.92

  Alignments for each domain:
  == domain 1  score: 203.7 bits;  conditional E-value: 9.6e-62
  MSA_GH10_xylanases   28 qaaesldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKwea
iepsrgkfsFegadelvnfakkngkklRgHtlvWhs 116
                          +a    + lk a+k++f  G av+q+++++  ++a+i k+f+s+t+eN MK++
+ep +gkf++e ad+++nf++++g klRgH lvWh+
        k141_7127811   21 TA---CAEGLKDAYKNEFliGVAVNQRNVSDPMQSALICKEFNSITAENDMKPQP
TEPAEGKFNWERADRIANFCREHGIKLRGHCLVWHN 108
                          33…467899**********************************************
****************************** PP


  MSA_GH10_xylanases  117 QlPswvssik…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs.
…lresvfyrvlgedyvkiafeaareadpnakLyi 199
                          Q+ +w+ ++k    +dk+tll++l++hik +++rYk+ +y WDVvNE++ +d +
+r+s  y++ g+d+++ af+aar+adp+a L++
        k141_7127811  109 QIGDWIYTDKngneVDKKTLLKRLRKHIKAIISRYKDVIYCWDVVNEAITDDPKa
```

```
enhFRQSRLYKIAGDDFIREAFKAARKADPKALLFY 199
                          ********999999******************************99877
777****************************98 PP


>> k141_3919179
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  201.4   0.1   4.5e-61   6.2e-61      69      235 ..       1      181 []
1      181 [] 0.97


  Alignments for each domain:
  == domain 1  score: 201.4 bits;  conditional E-value: 4.5e-61
  MSA_GH10_xylanases  69 sltpeNsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvs
sik…adketllevlknhiktvvgrYkgkvyaWD 155
                         s+t+eN+ K+ +i+p++g+++F  ad+++nf+++ng k+RgH l+WhsQ
+w++++k    ++ke + ++l++hi+tvv+rYk+ vyaWD
        k141_3919179   1 SVTAENAWKPGEIHPKEGEWNFGLADSIANFCRENGIKMRGHCLCWHSQFADWMF
TDKkgkeVKKEVFYQRLREHIHTVVNRYKDVVYAWD 91
                         69****************************************************
*99999999************************* PP


  MSA_GH10_xylanases 156 VvNEilnedgs…lresvfyrvlgedyvkiafeaareadpnakLyi
NDYnlesasaklegmvklvkklleagvpidGiGsqs 235
                         VvNE++n+d+            +r+s +++++g++++++afe+areadp+  L
+NDY++ ++   k+e ++++vkk+++agvpidGiG+q+
        k141_3919179  92
VVNEAINDDNMmfprpgvtpspYRQSRHFKLCGDEFIAKAFEFAREADPTGVLIYNDYSTVDP-
GKRERIYEMVKKMKDAGVPIDGIGMQG 181
                         ********98777777778889************************
******99.9*******************96 PP


>> k141_4551951
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  200.4   0.3   9.5e-61   1.3e-60      34      195 ..      18      185 .]
4      185 .] 0.94


  Alignments for each domain:
  == domain 1  score: 200.4 bits;  conditional E-value: 9.5e-61
  MSA_GH10_xylanases  34 dallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg
kfsFegadelvnfakkngkklRgHtlvWhsQlPswv 122
                         + lk  +k+ f  G  v+q+++++ +++a+ik++f+s+t eN MK+e
+eps+g+f++++ad++++f+++ng klRgH l+WhsQ+ +w+
        k141_4551951  18 SQGLKDVYKDCFmvGVSVNQRNVTNPEQQALIKQEFNSITCENDMKPEPTEPSEG
```

```
NFNWRNADRIADFCRANGIKLRGHCLMWHSQIGKWM 108
                             45789999*99999*******************************
******************************* PP


  MSA_GH10_xylanases 123
ssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaareadpna
195
                             + ++ +ke + ++++nhi+tvv+rYk+ vyaWDVvNE++ +d +    +r+sv
y+++g+++++af++areadp+a
        k141_4551951 109
TDDNPTKEVFYQRMRNHIHTVVNRYKDIVYAWDVVNEAITDDRNaedtYRQSVMYKLCGDEFIAKAFQYAREADPKA
185
**********************************998766667***********************86 PP


>> k141_2382513
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  198.3   0.3   4.1e-60   5.6e-60     145     335 ..      1     215 [.
1     219 [. 0.96


  Alignments for each domain:
  == domain 1  score: 198.3 bits;  conditional E-value: 4.1e-60
  MSA_GH10_xylanases 145 grYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaare
adpnakLyiNDYnlesasaklegmvklvkklleagv 226
                             +rYk+ vyaWDVvNE++++ g           +res
y+++g++++++afe+a+eadpna L +NDYn  ++ ak++ ++++vkk++eagv
        k141_2382513   1
NRYKDVVYAWDVVNEAMSDAGRgfrgqepnpYRESRAYKLCGDEFIAKAFEFAHEADPNAILVYNDYNAFQP-
AKRDRIYNMVKKMQEAGV 90
                             59**************99987777788889*********************
***************99.**************** PP


  MSA_GH10_xylanases 227 pidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele…
…ateekleaqakdyvevvkaclevkkcv.gv 302
                             pi GiG+q+H++a  ps++e+++a++++++l   ++itELDi+l+ e
a+++ +  qa++yv+++++++k+++ +v
        k141_2382513  91 PISGIGMQGHYNAYGPSEDEVEEAIKKYSELVKHIQITELDIRLNEEmggqlqfs
rgnnatAPAHLVTMQADRYVKLFRLYRKYKDVIdNV 181
                             *****************************************6666799*****
****9999999********************* PP


  MSA_GH10_xylanases 303 tvWgvaDkdsWls.eespllfdenynpKpaynai 335
                             t+W+v+D+dsW+  ++ pl +den++pK  y+a+
        k141_2382513 182 TFWNVSDRDSWVGvNNHPLPYDENLKPKRVYYAL 215
                             **********986899**************986 PP
```

```
>> k141_3934167
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  196.4   0.0   1.6e-59   2.1e-59     140     337 ..       1     228 [.
1     230 [. 0.96


  Alignments for each domain:
  == domain 1  score: 196.4 bits;  conditional E-value: 1.6e-59
  MSA_GH10_xylanases 140 iktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlged
yvkiafeaareadpnakLyiNDYnlesasaklegmv 215
                         i+t+++rYk+ vyaWDVvNE++ +dg              +r+s
+++++g++++++af++areadp++ L++NDY+  ++  k+e ++
        k141_3934167    1 IQTIMKRYKDVVYAWDVVNEAMADDGGgprwgfgrggqepspYRQSRHFQLCGDE
FIAKAFQFAREADPDVLLFYNDYSCVDE-GKRERIY 90
                         89**********************977777878888888899**************
**********************9988.9****** PP


  MSA_GH10_xylanases 216 klvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDial
ele…ateekleaqakdyvevvka 292
                         ++vkk+++agvpidGiG+q+H+++  ps+++l+ka+ ++ +
++itELD++++ e         +++ ++  q+++y++++k+
        k141_3934167   91 NMVKKMKDAGVPIDGIGMQGHYNIYFPSEEQLEKAIVRFKEIVKHINITELDLRM
NNEsggqlmfsrgeakpQPAYMATLQNDQYARLFKI 181
                         ****************************************************8
8879***********998999*************** PP


  MSA_GH10_xylanases 293 clevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                         +++ ++++ +vt+W++ D+dsWl  ++ pl fdeny+pK+ y ai +
        k141_3934167 182 FRKHADVIdNVTFWNLGDRDSWLGvNNHPLPFDENYRPKACYRAIRD 228
                         ********************986899***************9975 PP


>> k141_8098396
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  196.9   0.0   1.1e-59   1.5e-59      83     315 ..       8     260 ..
4     264 .. 0.91


  Alignments for each domain:
  == domain 1  score: 196.9 bits;  conditional E-value: 1.1e-59
  MSA_GH10_xylanases  83 psrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…ad
ketllevlknhiktvv…grYkgkvyaWDVvNEi 160
                         p++   +F+ +d+l  fa+ +g  lR HtlvWh+Q+P w++++k         a
+e ll++l+n+i++v+     +r+ g vy+WDVvNE+
        k141_8098396    8 PRHAAVDFARVDALLSFARDHGIALRYHTLVWHNQTPVWFFKEKwendwnapaAP
```

```
REILLARLENYIRDVMrhvnTRFPGVVYTWDVVNEA 98
                        7778899**********************************9***9999999
****************888889************** PP


  MSA_GH10_xylanases 161 lnedgs…lr.esvfyrvlgedyvkiafeaare.adpnakLyiNDYnlesasa
klegmvklvkklleagvpidGiGsqsHlsagapsva 245
                        ++         +r +s+++  +g d++  af+aare a+p   L++NDYn  ++
+k++++++++k ll++++ +d +G+q+H+     +v+
        k141_8098396   99 IEPGQGgpglFRtRSPWFAFTGRDFLPAAFRAAREnAAPGQTLCYNDYNAFDP-
VKRDAIIEMLKPLLAENL-VDTMGMQGHYVLPDLNVS 187
                        *9754446777768********************989**************99.*
**************9986.9************** PP


  MSA_GH10_xylanases 246
elkkalnalaslgvevaitELDialele..ateekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls 315
                        +++ a +a+aslg+ +++tELDi+ + +  a +++l +   +++ +++k + +
+ +vt+Wgv+D+dsWl+
        k141_8098396 188
ACETAARAYASLGLKLQVTELDIHCNSNdeAHAAALTDAYRSWFSMMKKLSQEGLEIeAVTFWGVTDADSWLP 260
***********************444422666677777777788888888888999**************97 PP


>> k141_9008962
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  196.8   0.0   1.2e-59   1.6e-59     145      337 ..      1      217 [.
1      220 [. 0.94


  Alignments for each domain:
  == domain 1  score: 196.8 bits;  conditional E-value: 1.2e-59
  MSA_GH10_xylanases 145 grYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaare
adpnakLyiNDYnlesasaklegmvklvkklleagv 226
                        +rYk+ vyaWDVvNE++ +++          +res
+++++g++++++afe+a+eadpna L++NDYn  ++ k++ ++++vkk++eagv
        k141_9008962    1
NRYKDIVYAWDVVNEAIADQAFgrpgrpanpYRESTHFKLCGDEFIAKAFEFAHEADPNALLFYNDYNAADP-
GKRDRIYNMVKKMQEAGV 90
                        59*************998644455677789*********************
****************.9************** PP


  MSA_GH10_xylanases 227 pidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele…
…ateekleaqakdyvevvkaclevkkcv.gv 302
                        pi GiG+q+H+++  ps++++ +a++++++l    ++itELD+++++e
++   +  q ++y++++++++ k+++ +v
        k141_9008962   91 PITGIGMQGHYNIYGPSEEDIDAAITKYSELVKHIHITELDLRTNTEqggqlrfs
rgeatpQAPYIATLQGDQYARIFRIFRKHKDVIdNV 181
                        *******************************************777789******
```

```
                  ***98766678999********************** PP

  MSA_GH10_xylanases 303 tvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                         t+W+++D+dsWl  ++ pl fdeny+pK +y+ i +
        k141_9008962 182 TFWNLSDRDSWLGvNNHPLPFDENYKPKRSYQIIKN 217
                         ***********986899**************98876 PP


>> k141_6886796
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  196.8   1.9   1.2e-59   1.6e-59      33     190 ..      3     166 .]
1     166 [] 0.97


  Alignments for each domain:
  == domain 1  score: 196.8 bits;  conditional E-value: 1.2e-59
  MSA_GH10_xylanases  33 ldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsr
gkfsFegadelvnfakkngkklRgHtlvWhsQlPsw 121
                         + + lk  +k+yf  G av+q+++++++++a+ik++f s+t+eN MK+e
+ep++g+f++egad+++nfa++ng klRgH l+WhsQ+  w
          k141_6886796   3 MAQGLKDVYKDYFliGVAVNQRNVTNAEQQALIKREFSSMTAENDMKPEPTEPRQ
GQFNWEGADRIANFARQNGIKLRGHCLMWHSQIGRW 93
                          5677899**************************************************
******************************** PP


  MSA_GH10_xylanases 122
vssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaare 190
                         ++ ++ +ke + +++knhi+ vv+rYk+ vyaWDVvNE++ +d++    +r+sv
y+++g++++++afe+a++
          k141_6886796  94
MTDDNPTKEVFYQRMKNHIEAVVSRYKDVVYAWDVVNEAMTDDANaedpYRQSVMYKLCGDEFIAKAFEYAHA 166
*****************************************99888999****************85 PP


>> k141_5776680
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  196.3   0.4   1.6e-59   2.2e-59     147     337 ..      1     209 [.
1     212 [. 0.96


  Alignments for each domain:
  == domain 1  score: 196.3 bits;  conditional E-value: 1.6e-59
  MSA_GH10_xylanases 147 YkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaareadpnakL
yiNDYnlesasaklegmvklvkklleagvpidGiGs 233
                         Yk+ vy WDVvNE++++d++    +r+s  yr++g++++++afe+a+eadp+a
L++NDY++ ++  k++ ++++vkk++++g+pidGiG+
```

64

```
       k141_5776680    1
YKDVVYCWDVVNEAISDDANatdpYRQSAMYRLCGDEFIEKAFEYAHEADPKALLFYNDYSTVDP-
HKRDRIYNMVKKMKAKGIPIDGIGM 90
                             9****************9888999****************************
********99.9********************* PP

  MSA_GH10_xylanases 234 qsHlsagapsvaelkkalnalaslgvevaitELDialele…at
eekleaqakdyvevvkaclevkkcv.gvtvWgvaDk 310
                             q+H+++  ps+a+l +a++ +       ++itE+Di+++ e
+t++  +  a++y++ ++++++ k+++ +vt+W++ D+
         k141_5776680   91 QGHYNIYYPSEARLDSAITLFKTVVKHIHITEFDIRVNEEmggglmfsregatVT
DSIKQYLADQYARCFRVFRKHKDVIdCVTFWNLGDR 181
                             ***********************99***********777789*********9888
8888999************************* PP

  MSA_GH10_xylanases 311 dsWls.eespllfdenynpKpaynaivk 337
                             dsWl  +++pl +deny+pK ay+ i +
         k141_5776680 182 DSWLGaRNYPLPWDENYQPKLAYEYIHD 209
                             ***964789**************9976 PP


>> k141_363992
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  196.3   1.2   1.6e-59   2.2e-59     102     256 ..      2     159 ..
1     165 [] 0.97


  Alignments for each domain:
  == domain 1  score: 196.3 bits;  conditional E-value: 1.6e-59
  MSA_GH10_xylanases 102 kngkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvyaWDV
vNEilnedgs…lresvfyrvlgedyvkiafeaa 188
                             +ng klRgHtl+WhsQ+  w++++ ++ke++ +++knhi+ +v+rYk+
vyaWDVvNE++++d++     +r+s  yr++g++++++af++a
         k141_363992    2 QNGIKLRGHTLMWHSQIGRWMTAEGTTKEQFYARMKNHIQAIVSRYKDVVYAWDV
VNEAMSDDANatdpYRQSAMYRLCGDEFIEKAFQYA 92
                             89****************************************************
********9888999******************* PP

  MSA_GH10_xylanases 189
readpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalas 256
                             +eadp+a L++NDY++ ++   k++ ++++vkk++++g+pidGiG+q+H+++
ps+a+l +a++ +
         k141_363992   93 HEADPKALLFYNDYSTVDP-
HKRDRIYNMVKKMKAKGIPIDGIGMQAHYNIYYPSEARLDSAITLFKT 159
****************99.9**************************************99865 PP


>> k141_8769892
```

```
    #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  196.1   0.2   1.9e-59   2.6e-59      46     216 ..       1     183 [.
1     184 [] 0.94


  Alignments for each domain:
  == domain 1  score: 196.1 bits;  conditional E-value: 1.9e-59
  MSA_GH10_xylanases  46 GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfa
kkngkklRgHtlvWhsQlPswvssik…adketl 132
                          G av+ ++++++ ++++i ++f+s+t+eN MK+ +i+p +g
++Fe+ad++++f+++ng  lRgH l+WhsQ  +w++ +k     ++ke +
        k141_8769892   1 GVAVNPTNVSNQAQMDLIVQEFNSITAENVMKPGEIHPAEGVWNFEAADRVADFC
RQNGIRLRGHCLCWHSQFCEWMFVDKkgrpVKKEVF 91
                          789999*************************************************
*********************999999***** PP


  MSA_GH10_xylanases 133 levlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlge
dyvkiafeaareadpnakLyiNDYnlesasaklegm 214
                          ++l++hi+tvv+rYk+ vyaWDVvNE++ +++        +r+s
++++g++++++afe+a+eadp+a L++NDYn +++  k++ +
        k141_8769892  92 YQRLREHIHTVVNRYKDVVYAWDVVNEAIADQAFaapgqepnpYRNSRLFQLCGD
EFIAKAFEFAHEADPTALLFYNDYNETDP-GKRDRI 181
                          ***************************998754444446778***********
*********************99.788777 PP


  MSA_GH10_xylanases 215 vk 216
                          ++
        k141_8769892 182 YN 183
                          76 PP


>> k141_4984645
    #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  195.5   1.5     3e-59     4e-59     133     314 ..       4     204 .]
1     204 [] 0.93


  Alignments for each domain:
  == domain 1  score: 195.5 bits;  conditional E-value: 3e-59
  MSA_GH10_xylanases 133 levlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyv
kiafeaareadpnakLyiNDYnlesasaklegmvkl 217
                          + +k+hi+ vv+rYk+ vy WDVvNE++ +        lr+s+ y++ ge+++
+afe+a++adpna L++NDYn  ++ ak++ + +l
        k141_4984645   4 YANMKHHIEAVVNRYKDVVYCWDVVNEAVADSPVwpgrseLRDSPMYQIAGEEFI
YKAFEYAHAADPNALLFYNDYNDAEP-AKSKRIFNL 93
```

66

```
                          578*************************99754444455***************
**********************999.********* PP

  MSA_GH10_xylanases 218 vkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialel
e…ateekleaqakdyvevvkacle 295
                          vk++++agvp+dGiG+q+H+++  p+++e+ +a++ ++      +++tELDi+++
+           +++ +  q+++yv+++k++++
        k141_4984645   94 VKRMKDAGVPVDGIGMQAHYNVYGPTMEEVDNAIKLYSTVVKHIHLTELDIRVNE
DmggglrfrqgatqVADWERTLQQDQYVNLFKVLRK 184
                          *********************************************99**********666
679******99887666677889************* PP

  MSA_GH10_xylanases 296 vkkcv.gvtvWgvaDkdsWl 314
                          k+++ +vt+W+v+DkdsWl
        k141_4984645 185 HKDVIdCVTFWNVSDKDSWL 204
                          ******************6 PP


>> k141_5834011
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------   ------- -------
------- -------    ----
   1 !  195.3   0.0   3.3e-59   4.5e-59      98     268 ..      1     183 []
1     183 [] 0.97


  Alignments for each domain:
  == domain 1  score: 195.3 bits;  conditional E-value: 3.3e-59
  MSA_GH10_xylanases  98 nfakkngkklRgHtlvWhsQlPswvssik…adketllevlknhiktvvgrYk
gkvyaWDVvNEilnedgs…lresvfyrv 175
                          nf+++ng klRgH l+WhsQ  +w+++++   ++ke + e+l++hi+
vv+rYk+ vyaWDVvNE++ +dg       +r+s ++++
        k141_5834011   1 NFCRENGIKLRGHCLCWHSQFADWMFTDSkgkpVKKEVFYERLREHIHAVVNRYK
DIVYAWDVVNEAMADDGRgwpgreqspYRQSRHFQL 91
                          79**************************9999999********************
****************9888888888899******* PP

  MSA_GH10_xylanases 176 lgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidG
iGsqsHlsagapsvaelkkalnalaslgvevaitEL 266
                          +g++++++af +areadpna L +NDY+  ++  k+e
++++vkk+++agvpidGiG+q+H+++  p+++ l +a++++ +l   ++itEL
        k141_5834011  92 CGDEFIAKAFIFAREADPNATLIYNDYSCVDP-
GKRERIYNMVKKMKDAGVPIDGIGMQGHYNIYFPEEELLDQAITRFRELVNHIHITEL 181
                          *****************************99.9*********************
****************************** PP

  MSA_GH10_xylanases 267 Di 268
                          D+
        k141_5834011 182 DL 183
```

```
                               *6 PP


>> k141_345001
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  193.3   0.2   1.4e-58   1.9e-58     102     272 ..       2     181 ..
1     184 [] 0.94


  Alignments for each domain:
  == domain 1  score: 193.3 bits;  conditional E-value: 1.4e-58
  MSA_GH10_xylanases 102 kngkklRgHtlvWhsQlPswvssik…adketllevlknhiktvvgrYkgkvy
aWDVvNEilnedgs…lresvfyrvlgedyvk 182
                         ++g klRgH l+WhsQ+ +w+ +++      ke++ +++k+hi+ vv+rYk+
vyaWDVvNE++ +        +r+s+ +++ ge+++
        k141_345001   2 QHGIKLRGHCLMWHSQIGTWIYQDEkgnlLPKEEFYKRMKSHIQAVVNRYKDVVY
AWDVVNEAVADSPVragqspMRQSPMFQIAGEEFIY 92
                         799********************99899999***********************
**********98654444468*************** PP


  MSA_GH10_xylanases 183 iafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHl
sagapsvaelkkalnalaslgvevaitELDialel 272
                         +afe+a+eadpna L++NDYn  ++  k++ +
+l++++++agvp++G+G+q+H+++ +p++ae+ +a++++       ++itELD+++++
        k141_345001  93 KAFEYAHEADPNALLFYNDYNDAEP-
GKAQRIFELLQRMKAAGVPVHGLGMQGHYNIYSPTEAEIDNAISKYKTVVNHIHITELDVRVNT 181
                         *********************999.9***************************
*******************99**********655 PP


>> k141_2725076
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  191.4   0.9   5.3e-58   7.2e-58      81     241 ..       1     173 [.
1     176 [] 0.96


  Alignments for each domain:
  == domain 1  score: 191.4 bits;  conditional E-value: 5.3e-58
  MSA_GH10_xylanases  81 iepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adket
llevlknhiktvvgrYkgkvyaWDVvNEilnedgs. 166
                         ++p++g +++e+ad+++nf+++ng k+RgH l+Wh Q  +w++++k     ++ke
+ ++l++hi+ vv+rYk+ vyaWDVvNE++++ g
        k141_2725076   1 LHPQEGVWKWEKADAIANFCRQNGIKMRGHCLCWHAQFADWMFTDKngkpVKKEV
FYARLREHIHAVVNRYKDVVYAWDVVNEAMSDAGRg 91
                         58***********************************************999999****
****************************99987 PP


                                   68
```

```
   MSA_GH10_xylanases 167 …lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasakleg
mvklvkklleagvpidGiGsqsHlsaga 241
                                    +res   +++g++++++afe+a+eadpna L +NDYn  ++ ak++
++++vkk++eagvpi GiG+q+H+++
        k141_2725076   92 wrgqepnpYRESTAWKLCGDEFIAKAFEFAHEADPNAILVYNDYNAFQP-
AKRDRIYNMVKKMQEAGVPITGIGMQGHYNSYG 173
                            7777888899*******************************99.*****
**********************9865 PP


>> k141_8362774
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  191.3   0.1   5.6e-58   7.7e-58      44     200 ..      26     188 .]
9     188 .] 0.92


  Alignments for each domain:
  == domain 1  score: 191.3 bits;  conditional E-value: 5.6e-58
  MSA_GH10_xylanases  44 yfGtavdqkelek..skeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadel
vnfakkngkklRgHtlvWhsQlPswvssik…ad 128
                          +G+a  +   e+  + e+++++++f s+t+eN+MK+e ++p++g+f+++
ad++v+f +++g+k+ gH lvWh Q+P+w+++++    ad
        k141_8362774   26 HVGAALGKWVYEQtpNAESDVVAANFSSITAENEMKPERVQPREGEFHWDSADKF
VAFGERHGMKIIGHCLVWHYQTPDWFFKNAdgskAD 116
                          44777666555443367899******************************
**************************9989999** PP


  MSA_GH10_xylanases 129
ketllevlknhiktvvgrYkgkvyaWDVvNEilnedgslresvfyrvlgedyvkiafeaareadpnakLyiN 200
                          +etl++++++hi+ vvgrYkg+v  WDVvNE++++ g l  s++ + +ged+++
af++a+eadp+a Ly+N
        k141_8362774 117
RETLIARMRTHIHAVVGRYKGRVHGWDVVNEAFDDAGALHPSPWRDGIGEDFIELAFRFAHEADPDAELYYN 188
**********************************************************************9 PP


>> k141_2943029
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  190.9   0.7   7.2e-58   9.8e-58      31     186 ..      10     171 ..
3     172 .] 0.97


  Alignments for each domain:
  == domain 1  score: 190.9 bits;  conditional E-value: 7.2e-58
  MSA_GH10_xylanases  31 esldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiep
```

```
srgkfsFegadelvnfakkngkklRgHtlvWhsQlP 119
                         ++l + lk a+k+yf  G av+q+++++ +++a+ikk+f+s+t+eN MK++
+ep++g+f++e+ad+++nfa++ng klRgH l+WhsQ+
        k141_2943029   10 TMLAQGLKDAYKDYFmiGVAVNQRNVTTPEQQALIKKEFNSMTAENDMKPQPTEP
KEGEFNWEAADRIANFARQNGIKLRGHCLMWHSQIG 100
                         5788999***************************************************
********************************** PP


  MSA_GH10_xylanases 120
swvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafe 186
                         +w+  ++ +ke + +++knhi+ vv+rYk+ vy WDVvNE++ +d +
+r+s+ y+++g++++++af+
        k141_2943029 101
EWMLGDNPTKEVFYQRMKNHIQAVVTRYKDVVYCWDVVNEAMTDDKNavdpYRQSPMYKLCGDEFIAKAFQ 171
**********************************************99989999*****************8 PP


>> k141_6418135
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !  190.6   0.0   9.2e-58   1.3e-57     136     337 ..       1     231 [.
1     234 [. 0.95


  Alignments for each domain:
  == domain 1  score: 190.6 bits;  conditional E-value: 9.2e-58
  MSA_GH10_xylanases 136 lknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvl
gedyvkiafeaareadpnakLyiNDYnlesasakle 212
                         l++hi+tvv+rYk+ vyaWDVvNE++ +dg            +r+s
+++++g++++++afe+areadp+  L +NDY+  ++  k+e
        k141_6418135   1 LRDHIHTVVNRYKDVVYAWDVVNEAMADDGRpfefvdgkmvpaspYRQSRHFKLC
GDEFIAKAFEFAREADPTGVLIYNDYSCVDN-GKRE 90
                         689***************************98888888888888899*********
************************9977.9*** PP


  MSA_GH10_xylanases 213 gmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELD
ialele…ateekleaqakdyvev 289
                         ++ +vkk+++agvpidGiG+q+H+++  p++++l+ka++++++
++itELD+++++e        ++   +  q+++y+++
        k141_6418135  91 RIYTMVKKMKDAGVPIDGIGMQGHYNIYFPDEDQLEKAIQRFSEIVNTIHITELD
LRTNTEsggqlrfsrgevkpQAPYIATLQEDQYARL 181
                         ********************************************************
**887799*********98766778999******** PP


  MSA_GH10_xylanases 290 vkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                         +k+++++k+++ +vt+W+++DkdsWl  ++ pl  den+++K +++ i +
        k141_6418135 182 FKIFRKYKNVIkNVTFWNLSDKDSWLGlGNHPLPIDENFKAKRSFQVIRD 231
                         **************************87999**************99976 PP


                                    70
```

```
>> k141_9437986
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  190.0   0.0   1.4e-57   1.9e-57      87     243 ..       1     160 [.
1     164 [] 0.97

  Alignments for each domain:
  == domain 1  score: 190.0 bits;  conditional E-value: 1.4e-57
  MSA_GH10_xylanases  87 kfsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllevlk
nhiktvvgrYkgkvyaWDVvNEilnedgslresvfy 173
                          +f+Fe +d++v++ ++ g ++ gH l+WhsQ+ +w+++++    ++ e
l++++k+hi  v+grYkgk++ WDVvNE++ edgs+r+s +y
        k141_9437986    1 EFDFELSDKFVEYGEAAGLTMTGHCLIWHSQTADWMFKDEkgglVSPEVLKQRMK
DHIYAVAGRYKGKLKGWDVVNEAIIEDGSYRNSYYY 91
                          69*****************************************999999**********
******************************** PP

  MSA_GH10_xylanases 174
rvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagaps 243
                          ++lge+++  af++a+eadp+a Ly+NDY ++++
+++g+v+l+++l+e+g++id iG+q+H+++  p+
        k141_9437986   92 QILGEEFIPWAFQCAHEADPDAELYYNDYGMHEP-
GRRDGVVRLIRQLKERGLRIDAIGMQGHMGMDYPT 160
*****************************99.99***************************998765 PP


>> k141_2976020
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  189.6   0.1   1.9e-57   2.6e-57      81     230 ..       1     153 []
1     153 [] 0.98

  Alignments for each domain:
  == domain 1  score: 189.6 bits;  conditional E-value: 1.9e-57
  MSA_GH10_xylanases  81 iepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketllev
lknhiktvvgrYkgkvyaWDVvNEilnedgs…l 167
                          +ep++g+f++++ad++++f+++ng k+RgH l+WhsQ+  w+  ++ +ke +
e++++hi+ +v+rYk+ vy WDVvNE++++d +    +
        k141_2976020    1 TEPREGQFNWTNADRIADFCRANGIKMRGHCLMWHSQIGRWMLGDNPTKEVFYER
MRKHIHAIVTRYKDVVYCWDVVNEAISDDPNaqdpY 91
                          79*************************************************
**************************99888899 PP


  MSA_GH10_xylanases 168
```

```
resvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidG 230
                       r+s+ y+++g++++++af++areadpn+ L++NDY+  +a  k+e
++++vkk+++agvpidG
        k141_2976020  92 RQSPMYKLCGDEFIAKAFQYAREADPNTLLFYNDYSCVDA-
HKRERIYNMVKKMKAAGVPIDG 153
*******************************999.9*******************9 PP


>> k141_7696858
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  188.0   0.1   5.5e-57   7.5e-57     147      336 ..      1      207 [.
1     210 [. 0.96


  Alignments for each domain:
  == domain 1  score: 188.0 bits;  conditional E-value: 5.5e-57
  MSA_GH10_xylanases 147 YkgkvyaWDVvNEilnedgs..lresvfyrvlgedyvkiafeaareadpnakLyi
NDYnlesasaklegmvklvkklleagvpidGiGsqs 235
                           Yk+ vy WDVvNE++++ g+  +r+s+ y+++g++++++afe+areadp+  L
+NDY+  ++  k+e ++++vkk+++agvpidGiG+q+
        k141_7696858   1
YKDIVYCWDVVNEAMSDGGEnpYRNSKLYQLCGDEFIAKAFEFAREADPTGVLIYNDYSCVDE-
GKRERIYNMVKKMKDAGVPIDGIGMQG 90
                           9***************9999*****************************
****9988.9*********************** PP


  MSA_GH10_xylanases 236 HlsagapsvaelkkalnalaslgvevaitELDialele…ate
ekleaqakdyvevvkaclevkkcv.gvtvWgvaDkd 311
                           H+++   p++++l+ka+n++++    ++itELD+++++e            +++
++   q+++y++++k++++ k+++ +vt+W+++Dkd
        k141_7696858  91 HYNIYFPDEDQLEKAINRFSEIVNIIHITELDLRTNTEsggqlmfargevkpQPA
YMATLQEDQYNRLFKVFRKHKDVIkNVTFWNLSDKD 181
                           *******************************888799***********99899
9*********************** PP


  MSA_GH10_xylanases 312 sWls.eespllfdenynpKpaynaiv 336
                           sWl  ++ pl fden+++K + + i
        k141_7696858 182 SWLGtGNHPLPFDENFKAKRSLQIIR 207
                           **974799***********998775 PP


>> k141_3033986
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  183.7   0.8   1.1e-55   1.6e-55      62      194 ..      2      138 .]
1     138 [] 0.98
```

```
  Alignments for each domain:
  == domain 1  score: 183.7 bits;  conditional E-value: 1.1e-55
  MSA_GH10_xylanases  62 iikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhs
QlPswvssikadketllevlknhiktvvgrYkgkvy 152
                         ++kk+f+s+t+eN MK+e +ep++g+f++e+ad+++nfa++ng
klRgHtl+WhsQ+  w++++ ++ke++ +++knhi+ +v+rYk+ vy
        k141_3033986    2 LVKKEFNSMTAENDMKPEPTEPREGEFNWENADRIANFARANGIKLRGHTLMWHS
QIGRWMTAEGTTKEQFYARMKNHIQAIVSRYKDVVY 92
                         79**************************************************
******************************* PP


  MSA_GH10_xylanases 153 aWDVvNEilnedgs…lresvfyrvlgedyvkiafeaareadpn 194
                            WDVvNE++++d++    +r+s  yr++g++++++af++areadpn
        k141_3033986   93 CWDVVNEAISDDANatdpYRQSAMYRLCGDEFIEKAFQYAREADPN 138
                         **************9888999*********************97 PP


>> k141_2060042
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  182.5   0.0   2.6e-55   3.6e-55      85      280 ..      1      210 [.
1      234 [. 0.88


  Alignments for each domain:
  == domain 1  score: 182.5 bits;  conditional E-value: 2.6e-55
  MSA_GH10_xylanases  85 rgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllevl
knhiktvvgrYkgkvyaWDVvNEilnedgs… 166
                         +gkfsF+ ad++v++a++ g k+R H+ vWh+Q+P+w+  +    a  e + e++
h k +++rY  +vyaWDVvNE+  +d
        k141_2060042    1 EGKFSFDRADAIVAMAREMGVKIRAHAPVWHNQTPAWMYLDGdrpAAPELICERI
DAHSKAMCERYGRDVYAWDVVNEATRDDVPdpvknp 91
                         689**********************************99867777899*****
**********************998743334444 PP


  MSA_GH10_xylanases 167 …lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvk
lvkklleagvpidGiGsqsHlsagapsvaelkkaln 252
                            +r+s++y+++g+ +++ af+    +++p+a+L++NDY+   + ak++
+v+l+++l+e+g+++dGiG+q H  a   + +e+k++++
        k141_2060042   92 gessvYRHSEYYKLCGTGFIEAAFRSMDRYAPDAQLFYNDYSECVP-
AKRDRIVSLIRNLREKGCRVDGIGMQQHHFAAP-DYDEIKRSIE 180
                         557789****************************************999.********
*******************88765.8********* PP


  MSA_GH10_xylanases 253 alaslgvevaitELDia..leleateekle 280
                            +a lg+ +++tELD++    +++  +++l+
        k141_2060042 181 IYAGLGLRIHVTELDVSmmATMNRGTRRLK 210
```

```
                        ****************5334444445555 PP


>> k141_8989385
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  181.0   1.0   7.3e-55     1e-54      74     219 ..       1     149 []
1     149 [] 0.98


  Alignments for each domain:
  == domain 1  score: 181.0 bits;  conditional E-value: 7.3e-55
  MSA_GH10_xylanases  74 NsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikad
ketllevlknhiktvvgrYkgkvyaWDVvNEilned 164
                         N MK+e +ep++g+f++egad+++nfa++ng klRgH l+WhsQ+  w+++++
+ke + +++knhi+ vv+rYk+ vyaWDVvNE++ +d
        k141_8989385   1 NDMKPEPTEPRQGQFNWEGADRIANFARQNGIKLRGHCLMWHSQIGRWMTEDNPT
KEVFYQRMKNHIEAVVSRYKDVVYAWDVVNEAMTDD 91
                         99****************************************************
*******************************99 PP


  MSA_GH10_xylanases 165
gs…lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvk 219
                         ++    +r+sv y+++g++++ +afe+a +adpn  L++ DY   ++ +k +
++++vk
        k141_8989385  92 ANaqdpYRQSVMYKLCGDEFIDMAFEYALAADPNELLFYYDYFECDP-
VKCQRIYNMVK 149
9888899****************************99999.********997 PP


>> k141_2722401
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  177.3   0.7     1e-53   1.4e-53     125     273 ..       4     155 ..
1     174 [. 0.93


  Alignments for each domain:
  == domain 1  score: 177.3 bits;  conditional E-value: 1e-53
  MSA_GH10_xylanases 125 ikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrv
lgedyvkiafeaareadpnakLyiNDYnlesasakl 211
                         ++ +ke + +++k+hi+ vv+rYk+ vyaWDVvNE++ +d++    +r+sv
y+++g++++++afe+a++adpna L++NDYn  ++ +k+
        k141_2722401   4 DNPTKEVFYQRMKSHIEAVVNRYKDVVYAWDVVNEAMTDDANaqdpYRQSVMYKL
CGDEFIAKAFEYAHAADPNALLFYNDYNECDP-VKS 93
                         56789999*******************************999888899********
****************************99.*** PP



                                  74
```

```
  MSA_GH10_xylanases 212
egmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele 273
                          + + ++vkk+++agvpi+GiG+q+H+++  ps++++ kal+ + +
++itELDi+ ++e
        k141_2722401  94
QRIFNMVKKMKDAGVPIHGIGMQGHYNIYGPSEEDIDKALTLYKQVVSHIHITELDIRANQE 155
*********************************************************5544 PP


>> k141_8400597
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  177.2   0.7     1e-53    1.4e-53      66     201 ..      2     147 .]
1     147 [] 0.95


  Alignments for each domain:
  == domain 1  score: 177.2 bits;  conditional E-value: 1e-53
  MSA_GH10_xylanases  66 dfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPs
wvssik…adketllevlknhiktvvgrYkgkvy 152
                           +f+s+t+eN+MK++ +ep++g+f++e+ad+++nf+++ng k+RgHtl+WhsQ+
+w+ +++       ke++ + +k+hi+ vv+rYk+ vy
        k141_8400597   2 EFNSITAENAMKPQPTEPRKGEFNWEDADRIANFCRANGIKMRGHTLMWHSQIGT
WMYQDEkgnlLPKEEFYANMKHHIDAVVNRYKDVVY 92
                           8*****************************************************
****998999999********************** PP

  MSA_GH10_xylanases 153 aWDVvNEilnedgs…lresvfyrvlgedyvkiafeaareadpnakLyiND
201
                           WDVvNE++ +        lr+s+  ++ ge+++ +afe+a+eadp+a L++ND
        k141_8400597  93 CWDVVNEAVADSPVwpgrseLRDSPMWKIAGEEFIYKAFEYAHEADPDALLFYND
147
                           *********99754444455*****************************9
PP


>> k141_1740359
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  176.6   0.1   1.7e-53    2.3e-53      27     184 ..     22     189 .]
2     189 .] 0.89


  Alignments for each domain:
  == domain 1  score: 176.6 bits;  conditional E-value: 1.7e-53
  MSA_GH10_xylanases  27 rqaaesldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKwe
aiepsrgkfsFegadelvnfakkngkklRgHtlvWh 115
                           rq  + + + +k ++k+yf  G av+++++  ++a+ik++f+s+t+eN+MK++
```

```
+ep++g f++e+ad+++nf+++ng klRgHtl+Wh
        k141_1740359   22 RQ--QPITNGMKDTYKDYFmiGVAVNNRNVTDPDQMALIKREFNSITAENAMKPQ
PTEPEKGVFNWEEADRIANFCRQNGIKLRGHTLMWH 110
                          33..458899********************************************
******************************** PP


  MSA_GH10_xylanases 116
sQlPswvssik…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkia
184
                          sQ+  w+  +        ke++ + +k+hi+ vv+rYk+ vyaWDVvNE++++
+r+s+ +++ ge+++ +a
        k141_1740359 111
SQVGRWMYMDDkgnlLPKEEFYANMKHHIEAVVNRYKDVVYAWDVVNEAVQDSPVrngqspMRQSPMFQIAGEEFIYKA
189
********9988888899**********************************98543333478***************876
PP


>> k141_6095884
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to   alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  172.7   0.1   2.6e-52   3.5e-52     167     337 ..      2     186 ..
1     189 [. 0.95


  Alignments for each domain:
  == domain 1  score: 172.7 bits;  conditional E-value: 2.6e-52
  MSA_GH10_xylanases 167 lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkkl
leagvpidGiGsqsHlsagapsvaelkkalnalasl 257
                          +r+sv y+++g++++++afe+a++adpna L++NDYn  ++ +k++
++++vkk+++agvpi+GiG+q+H+++  p+++e+ kal+ + +
        k141_6095884   2 YRQSVMYKLCGDEFIAKAFEYAHAADPNALLFYNDYNECDP-
VKSQRIYNMVKKMKDAGVPIHGIGMQGHYNIYGPKEEEVDKALELYKKV 91
                          79****************************************99.***********
********************************* PP


  MSA_GH10_xylanases 258 gvevaitELDialelele…ateekleaqakdyvevvkaclevkkc
v.gvtvWgvaDkdsWls.eespllfdenynpKpayn 333
                          +++tELDi+ ++e               ++++  +  a++y++v++++++
k+++ +vt+W+++D+dsWl   +++pl fd +y+pK ay+
        k141_6095884  92 VSHIHVTELDIRANQEmggqlafsrdgatVNDSLKQFLADQYARVFRVFRKHKDV
IdCVTFWNLSDRDSWLGqNNYPLPFDVDYKPKMAYE 182
                          ************766689*********977777778889***************
***************963789**************9 PP


  MSA_GH10_xylanases 334 aivk 337
                          i +
        k141_6095884 183 YIRD 186


                                    76
```

9876 PP

>> k141_2071297
   #   score bias c-Evalue i-Evalue hmmfrom   hmm to   alifrom ali to
envfrom env to   acc
 ---   ------ ----- --------- --------- ------- -------   ------- -------
------- -------   ----
   1 ! 172.5   0.3   2.9e-52   3.9e-52   52   191 ..   2   149 .]
1   149 [] 0.96

  Alignments for each domain:
  == domain 1 score: 172.5 bits; conditional E-value: 2.9e-52
  MSA_GH10_xylanases 52 kelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngkk
lRgHtlvWhsQlPswvssik…adketllevlkn 138
                          +++++ ++a+i ++f+s+t+eN MK++ +ep++g+f+F++ad+++nf+++ng
lRgH l+Wh Q+ +w+ +++   ke++ +++++
        k141_2071297   2 RNVTNPDQQALILQNFNSITAENDMKPQPTEPRQGQFNFNNADRIANFCRENGIR
LRGHCLMWHAQIGEWIYKDAagnlLPKEEMFRRMRD 92
                         677888999**
******************9898889********** PP

  MSA_GH10_xylanases 139
hiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaarea 191
                         hi+tvvgrYk+ vyaWDVvNE++ +d +   +r+s+ y++
g++++++af++area
        k141_2071297 93
HIHTVVGRYKDIVYAWDVVNEAMTDDKNaedpYRQSPMYQIAGDEFIAKAFQYAREA 149
*********************9998888899*****************986 PP

>> k141_85666
   #   score bias c-Evalue i-Evalue hmmfrom   hmm to   alifrom ali to
envfrom env to   acc
 ---   ------ ----- --------- --------- ------- -------   ------- -------
------- -------   ----
   1 ! 171.2   0.0   7.4e-52   1e-51   164   334 ..   10   195 ..
5   199 .. 0.93

  Alignments for each domain:
  == domain 1 score: 171.2 bits; conditional E-value: 7.4e-52
  MSA_GH10_xylanases 164 dgslresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklv
kklleagvpidGiGsqsHlsagapsvaelkkalnal 254
                         ++ +r+s+ +++ ge+++ +afe+a+eadpna L++NDYn ++ k++ +
+lv+++++agvpidGiG+q+H+++ +p+ +e+ +a++++
        k141_85666 10 QSPMRQSPMFQIAGEEFIYKAFEYAHEADPNALLFYNDYNDAEP-
GKSQRIFELVQRMKAAGVPIDGIGMQGHYNIYSPTAEEIDAAITKY 99
                         5569**999.9*********
******************************* PP

77

```
  MSA_GH10_xylanases 255 aslgvevaitELDialele…ateekleaqakdyvevvkacle
vkkcv.gvtvWgvaDkdsWls.eespllfdenynpK 329
                              s    ++itELDi+++++             ++ +   q+++yv+++k++++
+++v +vt+W+v D+dsWl  ++spllfd++y+pK
         k141_85666 100 KSIVKHIHITELDIRVNTDqggqlnfsrgqstpLEAWQTALQNDQYVNLFKVLRK
HADVVdCVTFWNVGDRDSWLGaNNSPLLFDTEYQPK 190
                              ***************777789*******9998755666778999***********
*******************964899*********** PP


  MSA_GH10_xylanases 330 payna 334
                          +y
         k141_85666 191 RSYFL 195
                          **965 PP


>> k141_3223482
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  169.8   0.0   1.9e-51   2.6e-51     156     337 ..      1     206 [.
1     209 [. 0.93


  Alignments for each domain:
  == domain 1  score: 169.8 bits;  conditional E-value: 1.9e-51
  MSA_GH10_xylanases 156 VvNEilnedgs…lresvfyrvlgedyvkiafeaareadpnakLyiND
YnlesasaklegmvklvkklleagvpidGiGsqsHl 237
                              VvNE++ +d            +r+s  y+++g++++++af++areadpna
L++NDY++ ++  k+e ++ +vk+++eagvpidGiG+q+H+
         k141_3223482   1
VVNEAIADDVRtrpgteanpYRQSRLYQLCGDEFIAKAFQFAREADPNALLFYNDYSTVDP-
GKRERIYTMVKQMKEAGVPIDGIGMQGHF 90
                              7888888775444445666798888888888888888888888888888888
****99.9*********************** PP


  MSA_GH10_xylanases 238 sagapsvaelkkalnalaslgvevaitELDialele…ateek
leaqakdyvevvkaclevkkcv.gvtvWgvaDkdsW 313
                              ++  p+++ l  a++++a+l   ++itELD+++++e            +++
+  q+++y+++++++++ k+++ +vt+W+++D+dsW
         k141_3223482  91 NIYYPDEELLDTAISRFAELVKHIHITELDLRTNTEsggqlmfargevvpQPSYI
ATIQEDQYARIFRVFRKHKDVIdNVTFWNLSDRDSW 181
                              *******************************888799**********9888899
999****************************** PP


  MSA_GH10_xylanases 314 ls.eespllfdenynpKpaynaivk 337
                          l  ++ pl fdeny++K++++ i +
         k141_3223482 182 LGvNNHPLPFDENYKAKSSFTVIRD 206
                          986899*************99976 PP
```

```
>> k141_8814130
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  167.7   0.2   8.1e-51   1.1e-50     152     325 ..      1     202 [.
1     203 [] 0.91


  Alignments for each domain:
  == domain 1  score: 167.7 bits;  conditional E-value: 8.1e-51
  MSA_GH10_xylanases 152 yaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaareadp
nakLyiNDYnlesasaklegmvklvkklleagvpid 229
                         y WDVvNE++ ++                    +res
+y+++g++++++afe+a+eadpna L++NDYn   ++  k++ ++++vkk+++agvpi+
        k141_8814130    1
YCWDVVNEAIADNVRpnfvngkfepgnpYRESRHYQLCGDEFIAKAFEFAHEADPNALLFYNDYNECDP-
GKRDRIYNMVKKMQDAGVPIH 90
                         68*******99875444445556677789***************************
************99.9******************* PP


  MSA_GH10_xylanases 230 GiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele…
…ateekleaqakdyvevvkaclevkkcv.gvtvW 305
                         GiG+q+H+++  ps++++ +a++++++l    +++tELD+++++e
++       q ++y+++++++++ k+++ +vt+W
        k141_8814130  91 GIGMQGHYNIYGPSEEDIDAAITKYSELVKHIHVTELDLRTNTEmggqlrfsrge
akpMAPYLQTLQDDQYNRIFRIFRKHKDVIdCVTFW 181
                         ****************************************777789********9
986445555678899******************** PP


  MSA_GH10_xylanases 306 gvaDkdsWls.eespllfden 325
                         +++D+dsWl   ++ pl fden
        k141_8814130 182 NLSDRDSWLGvNNHPLPFDEN 202
                         ********986899*****98 PP


>> k141_3254317
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  166.6   0.0   1.8e-50   2.5e-50     165     337 ..     16     203 ..
13     205 .. 0.95


  Alignments for each domain:
  == domain 1  score: 166.6 bits;  conditional E-value: 1.8e-50
  MSA_GH10_xylanases 165 gslresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvk
klleagvpidGiGsqsHlsagapsvaelkkalnala 255
                         + +res   y+++g++++++afe+a+eadpna L +NDYn   ++ ak++
++++vkk++eagvpi GiG+q+H++a  ps++e+++a+++++
```

```
        k141_3254317  16 NPYRESRAYQLCGDEFIAKAFEFAHEADPNAILVYNDYNAFQP-
AKRDRIYNMVKKMQEAGVPITGIGMQGHYNAYGPSEEEVEEAIKKYS 105
                         558**************************************99.**********
******************************* PP


  MSA_GH10_xylanases 256 slgvevaitELDialele…ateekleaqakdyvevvkaclev
kkcv.gvtvWgvaDkdsWls.eespllfdenynpKp 330
                         +l   +++tELDi+l+ e           a+ + +  q+++y
+++++++++k+++ +vt+W+v+D+dsW+   ++ pl fden++pKp
        k141_3254317 106 ELVKHIQVTELDIRLNEEmggqlqfsrgnagaAPGHLVTMQTDRYIKLFRLYRKY
KDIIdNVTFWNVSDRDSWVGvNNHPLPFDENLRPKP 196
                         **************6666799**********989999******************
******************986899*********** PP


  MSA_GH10_xylanases 331 aynaivk 337
                         y+a+ +
        k141_3254317 197 VYYALKN 203
                         **98765 PP


>> k141_5481546
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  165.9   0.0   2.9e-50      4e-50      40     238 ..       2     225 ..
1     226 [] 0.95


  Alignments for each domain:
  == domain 1  score: 165.9 bits;  conditional E-value: 2.9e-50
  MSA_GH10_xylanases  40 agkkyfGtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg…
…kfsFegadelvnfakkngkklRgHtlvWhs 116
                         agk  +G+a+ q  ++++k +++ik++f+ ltpeN++K++a+ + +g
+F++a  l nfak+ng k+ gH l+Whs
        k141_5481546   2 AGKFDIGSAAPQMVFRDTKWTNLIKEQFNILTPENELKPDAVLDVNGsrklvtet
gdetaaAVHFDAAKPLLNFAKENGIKVHGHVLIWHS 92
                         578889***********************************99999999*****
******************************* PP


  MSA_GH10_xylanases 117 QlPswvssik…adketllevlknhiktvv…grYkgkvyaWDVvNEi
lnedgs.lresvfyrvlgedyvkiafeaareadpn. 194
                         Q+P+ ++++        ++ e +l +++n+i +v     + Y g
v++WDV+NE++++ ++ lr+s++ r++gedy ++a+e+ar+++p+
        k141_5481546  93 QTPEAFFREGdatskpfVSWEVMLGRMENFIMSVFtslnENYPGVVVSWDVLNEA
IDDGSNwLRNSNWLRIVGEDYPNKAYEYARKYAPEg 183
                         ***99998878999999999**********999888899**************
**99889**********************88764 PP


  MSA_GH10_xylanases 195 akLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHls 238
```

```
                                    + Ly+NDYn+   +   kl+g+v+l+k+l+ +g  idG G+q H s
            k141_5481546 184 TLLYYNDYNTAIP-GKLHGIVRLLKSLIPEG-NIDGYGFQMHHS 225
                                    789*********99.9***************99.6*********76 PP


>> k141_5245547
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  165.1   0.2   5.2e-50     7e-50      92     229 ..      2     148 .]
1     148 [] 0.95


  Alignments for each domain:
  == domain 1  score: 165.1 bits;  conditional E-value: 5.2e-50
  MSA_GH10_xylanases  92 gadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllevlknhikt
vvgrYkgkvyaWDVvNEilnedgs…lresvf 172
                            +ad+++nf++++g k+RgHtl+WhsQ+ +w+ +++      ke++ + +k+hi+
vv+rYk+ vy WDVvNE++ +         lr+s+
        k141_5245547   2 DADKIANFCREHGIKMRGHTLMWHSQIGTWMYQDEqgnlLPKEEFYANMKHHIQA
VVNRYKDIVYCWDVVNEAVADSPVypgrpeLRNSPM 92
                            79*****************************998888899*************
*****************99864444456****** PP


  MSA_GH10_xylanases 173
yrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpid 229
                            y++ ge+++ +afe+a+eadp+a L++NDYn  ++ ak++ +
+lvk++++agvp+d
        k141_5245547  93 YQIAGEEFIYKAFEYAHEADPDALLFYNDYNDAEP-
AKSQRIFNLVKRMKDAGPVD 148
******************************999.*****************98 PP


>> k141_1676112
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  164.7   0.0   6.6e-50     9e-50     127     274 ..     10     165 ..
1     177 [. 0.92


  Alignments for each domain:
  == domain 1  score: 164.7 bits;  conditional E-value: 6.6e-50
  MSA_GH10_xylanases 127 adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvf
yrvlgedyvkiafeaareadpnakLyiNDYnlesas 208
                            ++ke + e+l++hi+tvv+rYk+ vyaWDVvNE++ +d          +r+s
y+++g++++++af++areadpna L++NDY++ ++
        k141_1676112  10 VKKEVFYERLRDHIHTVVNRYKDVVYAWDVVNEAIADDVRtrpgteanpYRQSRL
YQLCGDEFIAKAFQFAREADPNALLFYNDYSTVEP- 99
                            679999****************************99655556677889*****
```

81

```
********************************99. PP

  MSA_GH10_xylanases 209
aklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialelea 274
                             k+e ++++vkk++eagvpidGiG+q+H+++  p+++ l  a++++a+l
++itELD+++++e
        k141_1676112 100
GKRERIYDMVKKMKEAGVPIDGIGMQGHYNIYYPDEELLDTAISRFAELVKHIHITELDLRTNTES 165
9*********************************************************66654 PP


>> k141_770369
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  163.9   0.2   1.2e-49   1.6e-49      35     178 ..      15     168 ..
8     169 .] 0.96


  Alignments for each domain:
  == domain 1  score: 163.9 bits;  conditional E-value: 1.2e-49
  MSA_GH10_xylanases  35 allkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgk
fsFegadelvnfakkngkklRgHtlvWhsQlPswvs 123
                             + lk a+++yf  G av+q+++++  ++a+i ++f+s+t+eN MK++
+ep++g+f+F+ ad+++nf+++ng k+RgH l+Wh Q+ +w+
        k141_770369   15 QGLKDAYRDYFtiGVAVNQRNVTNPDQQALICREFNSVTAENDMKPQPTEPRQGQ
FDFTRADRIANFCRQNGIKMRGHCLMWHAQIGDWMY 105
                             56899****************************************************
******************************** PP


  MSA_GH10_xylanases 124
sik…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlge 178
                             +++      k+++ +++++hi+ vv+rYk+ vy WDVvNE++ +d +
+r+sv y++ g+
        k141_770369 106
KDEqgnlLPKDEFFKRMREHIHAVVNRYKDVVYCWDVVNEAMTDDKNaedpYRQSVMYQIAGD 168
*998888899****************************9998888899********997 PP


>> k141_9388058
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  161.8   0.5      5e-49   6.8e-49     129     273 ..       2     161 ..
1     172 [. 0.93


  Alignments for each domain:
  == domain 1  score: 161.8 bits;  conditional E-value: 5e-49
  MSA_GH10_xylanases 129 ketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…l
```

82

```
resvfyrvlgedyvkiafeaareadpnakLyiNDYn 203
                          ke + ++l++hi+tvv+rYk+ vyaWDVvNE++++ g
+res +y+++g++++++afe+a+eadpna L++NDYn
        k141_9388058    2 KEVFYARLREHIHTVVNRYKDVVYAWDVVNEAISDGGGfggfggfgrpgqqpnpY
RESTHYKLCGDEFIAKAFEFAHEADPNAILFYNDYN 92
                          678899*****************************99866667777777788889
******************************** PP


  MSA_GH10_xylanases 204
lesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele 273
                            ++   k++ ++++vkk+++agvpi GiG+q+H+++  ps++++++a+n++++l
++itELD+++++e
        k141_9388058   93 EADP-
GKRDRIYNMVKKMQDAGVPITGIGMQAHYNIYGPSEEDIEAAINKYSELVKHIHITELDLRTNTE 161
**99.9***********************************************************6554 PP


>> k141_1004518
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  163.0   0.0   2.2e-49     3e-49     166     337 ..       6     192 ..
2     194 .. 0.95


  Alignments for each domain:
  == domain 1  score: 163.0 bits;  conditional E-value: 2.2e-49
  MSA_GH10_xylanases 166 slresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkk
lleagvpidGiGsqsHlsagapsvaelkkalnalas 256
                           +r+s+ +++ ge+++ +afe+a+eadpna L++NDYn  ++  k++ +
+l++++++agvp++G+G+q+H+++ +p+++e+ +a++++
        k141_1004518    6 PMRQSPMFQIAGEEFIYKAFEYAHEADPNALLFYNDYNDSEP-
GKAQRIFELLQRMKAAGVPVHGLGMQGHYNIYSPTEQEIDNAISKYKT 95
                          59*************************************9999.9***********
******************************* PP


  MSA_GH10_xylanases 257 lgvevaitELDialele…ateekleaqakdyvevvkaclevk
kcv.gvtvWgvaDkdsWls.eespllfdenynpKpa 331
                           ++itELD+++++e            +++ + +  a++y++++k++++
++++ +vt+W+++D+dsWl    ++pllfd++y+pK+a
        k141_1004518   96 VVNHIHITELDVRVNTEqgggglrfsqgatinVPSYQQSLFADQYNRIFKVFRKHA
DVIdCVTFWNLSDRDSWLGaANYPLLFDSEYRPKNA 186
                          *99**********88878*********99887777888889**************
****************964789************* PP


  MSA_GH10_xylanases 332 ynaivk 337
                          y ++ +
        k141_1004518 187 YRTVKN 192
                          *99976 PP
```

```
>> k141_1687580
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  162.0   0.0   4.6e-49   6.2e-49     111     251 ..       1     153 [.
1     155 [] 0.95

  Alignments for each domain:
  == domain 1  score: 162.0 bits;  conditional E-value: 4.6e-49
  MSA_GH10_xylanases 111 tlvWhsQlPswvssik…adketllevlknhiktvvgrYkgkvyaWDVvNEil
nedgs…lresvfyrvlgedyvkiafeaa 188
                         +l+WhsQ  +w++ +k    ++ke + ++l++hi tvv+rYk+ vyaWDVvNE++
+++          +r+s  y+++g++++++afe+a
        k141_1687580   1 NLCWHSQFCDWMFVDKkgkpVTKEVFYKRLREHIFTVVNRYKDVVYAWDVVNEAM
ADQAFafpgmepnpYRNSRLYQLCGDEFIAKAFEFA 91
                         59***********999999*****************************
998655555566779***************** PP

  MSA_GH10_xylanases 189
readpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkal 251
                         +eadp+a L++NDYn  ++  k++ + ++vkk+++agvpi+GiG+q+H+++
ps+++l++a+
        k141_1687580  92 HEADPDALLFYNDYNEADP-
GKRDRIFNMVKKMQDAGVPIHGIGMQGHYNIYGPSEEDLEAAI 153
*****************99.9********************************99997 PP

>> k141_2899687
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  161.9   0.0   4.8e-49   6.6e-49     176     333 ..       2     173 .]
1     173 [] 0.96

  Alignments for each domain:
  == domain 1  score: 161.9 bits;  conditional E-value: 4.8e-49
  MSA_GH10_xylanases 176 lgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidG
iGsqsHlsagapsvaelkkalnalaslgvevaitEL 266
                         +g++++++af++areadpna L++NDYn  ++ +k++
++++vkk+++agvpidGiG+q+H+++  p+++e+ +a++ +       +++tEL
        k141_2899687   2 CGDEFIAKAFQFAREADPNALLFYNDYNECDP-
VKSKRIYNMVKKMKDAGVPIDGIGMQGHYNIYGPTEKEVDDAISLYKTVVKHIHVTEL 91
                         79***************************99.*********************
************************999******* PP

  MSA_GH10_xylanases 267 Dialele…ateekleaqakdyvevvkaclevkkcv.gvtvWgv
```

84

```
aDkdsWls.eespllfdenynpKpayn 333
                            Di+++ e              +t+++ ++ a++y++v++a+++ k+++ +vt+W++
D+dsWl   ++pl fd++y+pK ay+
       k141_2899687   92 DIRVNEEmggqlrfsregvnVTDSVKQHLADQYARVFRAFRKHKDVIdCVTFWNL
GDRDSWLGaANYPLPFDSEYKPKMAYE 173
                            ***776689***********999999999*****************************
******964789***************5 PP
```

```
>> k141_8453879
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  159.0   0.2   3.7e-48   5.1e-48     133     300 ..       4     201 ..
1     204 [] 0.94


  Alignments for each domain:
  == domain 1  score: 159.0 bits;  conditional E-value: 3.7e-48
  MSA_GH10_xylanases 133 levlknhiktvvgrYkgkvyaWDVvNEilnedgs…lres
vfyrvlgedyvkiafeaareadpnakLyiNDYnles 206
                            e+l++hi+tvv+rYk+ vy WDVvNE++++ g             +res
+y+++g++++++afe+a+eadpna L++NDY+   +
       k141_8453879   4 YERLREHIHTVVNRYKDVVYCWDVVNEAISDGGGfggfggfgrrpgqapspYRES
RHYKLCGDEFIAKAFEFAHEADPNALLFYNDYSCVD 94
                            689************************9987667777777777888889***
*****************************998 PP


  MSA_GH10_xylanases 207 asaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvev
aitELDialele…ateekleaqa 283
                            +  k+e ++++vkk+++agvpi+GiG+q+H+++  p+++ l ka++++++l
++itELD++++ e         +++ +   q+
       k141_8453879  95 E-
GKRERIYNMVKKMQDAGVPIHGIGMQGHYNIYFPDEELLDKAITRFSELVKHIHITELDLRMNNEsggqlmfsrgeakpQ
PAYMSTLQT 184
                            8.9***********************************************
********888799*********99888899999** PP


  MSA_GH10_xylanases 284 kdyvevvkaclevkkcv 300
                            ++y++++k++++ k+++
       k141_8453879 185 DQYARIFKVLRKHKDVI 201
                            **********999887 PP


>> k141_6119917
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  160.2   1.5   1.6e-48   2.2e-48      37     165 ..      10     144 ..
```

```
    4    145 .] 0.98

  Alignments for each domain:
  == domain 1  score: 160.2 bits;  conditional E-value: 1.6e-48
  MSA_GH10_xylanases  37 lkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfs
FegadelvnfakkngkklRgHtlvWhsQlPswvssi 125
                         lk a+k+yf  G av+q+++++  + +iikk+f+s+t+eN  K+
+i+p++g+++Fe+ad+++nf+++ng k+RgH l+WhsQ  +w++++
        k141_6119917   10 LKDAYKNYFtiGVAVNQTNVTDPAQIEIIKKQFNSVTAENDWKPGEIHPKEGEWN
FEKADKIANFCRENGIKMRGHCLCWHSQFADWMFTD 100
                         6899*****************************************************
****************************** PP

  MSA_GH10_xylanases 126 k…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedg 165
                         k    ++ke + e+l++hi+tvv+rYk+ vyaWDVvNE++ +dg
        k141_6119917 101 KkgkpVKKEVFYERLRDHIHTVVNRYKDVVYAWDVVNEAMADDG 144
                         999999*****************************988 PP


>> k141_9355598
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  159.7   0.0   2.2e-48    3e-48     46     203 ..      3     172 .]
1     172 [] 0.92

  Alignments for each domain:
  == domain 1  score: 159.7 bits;  conditional E-value: 2.2e-48
  MSA_GH10_xylanases  46 GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfa
kkngkklRgHtlvWhsQlPswvssik…adketll 133
                         G+av+ + + +   +++i ++f+slt+eN+MK+e +ep +g+f Fe
ad++v++a++ g  +RgH+ vWh+Q+P w+ ++    a  e +
        k141_9355598   3 GAAVSPAVIGE--
RRDLIMRHFNSLTAENEMKYEPTEPAEGEFRFERADAVVALAREMGIRIRGHAPVWHNQTPLWMYREGdgpAAPERIY
91
                         77777777774..899***************************************
*********************9988888999*** PP

  MSA_GH10_xylanases 134 evlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlg
edyvkiafeaareadpnakLyiNDYn 203
                         +++  h + +++rY ++vyaWDVvNE+  +d           +r+s+++r++g
+++ af+    +++p+a+L++NDYn
        k141_9355598  92 DRIDRHSRAICERYGSDVYAWDVVNEAARDDMPppsalsgqdpvYRDSEYFRLCG
SGFIEAAFRSMDRYAPDAQLFYNDYN 172
                         ***********************998853444555557779**********
**********************9 PP


>> k141_8034862
```

```
    #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  157.0   0.0   1.5e-47   2.1e-47     167     330 ..       1     179 [.
1     180 [] 0.95


  Alignments for each domain:
  == domain 1  score: 157.0 bits;  conditional E-value: 1.5e-47
  MSA_GH10_xylanases 167 lresvfyrvlg.edyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkk
lleagvpidGiGsqsHlsagapsvaelkkalnalas 256
                         lr+s++ ++ g ++++++afe+a+eadp+a L++NDYn    +
ak+++++++++vk++++agvpidGiG+q+H+++ +ps ++++ a++++++
        k141_8034862   1 LRRSQWKQIAGgDEFIRKAFEFAHEADPDALLFYNDYNAAVP-
AKRDKIYNMVKEMKAAGVPIDGIGMQGHFNVYEPSLEDIETAIEKYSE 90
                         699*****996378**************************99.***********
******************************* PP


  MSA_GH10_xylanases 257 lgvevaitELDialele…ateekleaqakdyvevvkaclevkk
cv.gvtvWgvaDkdsWls.eespllfdenynpKp 330
                         ++ tELDi+l+ e            t ek + +++y+  +++++
++++   vt+W+v+D+dsW+  +++pllfd++ npK+
        k141_8034862  91 IVDHIQFTELDIRLNREmggqlnmnrqgeeLTPEKKQMFEDKYTGFFDILRRHAD
VIdVVTFWNVTDADSWVGvSNYPLLFDRDANPKD 179
                         *************66667899*****999978888899999**************
**99*************986899***********7 PP


>> k141_5145849
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  156.0   0.0     3e-47   4.1e-47     116     260 ..       1     148 []
1     148 [] 0.96


  Alignments for each domain:
  == domain 1  score: 156.0 bits;  conditional E-value: 3e-47
  MSA_GH10_xylanases 116 sQlPswvssik…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs
lresvfyrvlgedyvkiafeaareadpnakLyiNDY 202
                         sQ   w++ ++    ++ e l++++k+hi+t+++rYkg+v+ +DVvNE++
+dgs+r s fy++lge+++  af++a eadp+a Ly+NDY
        k141_5145849   1 SQCAPWFFVDAkgklVKPEVLKQRMKDHITTIMTRYKGRVTGYDVVNEAILDDGS
YRPSLFYQILGEEFIPWAFQCAMEADPDAELYYNDY 91
                         67777888887778788899*********************************
******************************* PP


  MSA_GH10_xylanases 203
nlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgve 260
```

```
                               ++ ++   k+ g+v ++kkl+e+g++id +G+qsH+++ +ps +e +++++a+
++gv+
        k141_5145849  92 SMAEP-
GKRAGVVGVIKKLKERGIRIDAVGLQSHMGMDHPSWEEFEASIKAFIEAGVD 148
***99.9***********************************************996 PP


>> k141_6755562
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  155.6   1.7     4e-47   5.5e-47      37     164 ..       2     135 ..
1     140 [. 0.97


  Alignments for each domain:
  == domain 1  score: 155.6 bits;  conditional E-value: 4e-47
  MSA_GH10_xylanases  37 lkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfs
FegadelvnfakkngkklRgHtlvWhsQlPswvssi 125
                         lk a+k+yf  G av+++++++  ++++i ++++s+t+eN+MK++++ep+++
f++e+ad++++f+++ng k+RgHtl+WhsQ+  w+ ++
        k141_6755562   2 LKDAYKDYFkiGVAVNNRNVNDPDQVKVILREYNSITAENAMKPQETEPQKDVFT
WENADRIADFCRQNGIKMRGHTLMWHSQIGRWMYQD 92
                         5889*****************************************************
**********************************9 PP


  MSA_GH10_xylanases 126 k…adketllevlknhiktvvgrYkgkvyaWDVvNEilned 164
                         +       +ke++ + +k+hi+ +v+rYk+ vy WDVvNE++ +
        k141_6755562  93 EngnlLSKEEFYANMKHHIQAIVNRYKDVVYCWDVVNEAVADS 135
                         9999999****************************9875 PP


>> k141_3918953
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  155.3   0.4   4.8e-47   6.5e-47      62     187 ..       3     138 .]
1     138 [] 0.94


  Alignments for each domain:
  == domain 1  score: 155.3 bits;  conditional E-value: 4.8e-47
  MSA_GH10_xylanases  62 iikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhs
QlPswvssik…adketllevlknhiktvvgrYk 148
                         +i ++f+s+t+eN+MK++ +ep++g f++e+ad+++nf++++g
+RgHtl+WhsQ+ +w+ +++     ke++ + +k+hi+ v++rYk
        k141_3918953   3 VILREFNSITAENAMKPQPTEPEKGVFNWEDADRIANFCREHGIRMRGHTLMWHS
QIGTWMYQDAngnlLPKEEFYANMKHHIQAVMNRYK 93
                         7899*****************************************************
********99888889999**************** PP
```

```
  MSA_GH10_xylanases 149 gkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafea 187
                          + vy WDVvNE++ +          lr+s+ y++ ge+++ +afe+
         k141_3918953   94 DVVYCWDVVNEAVADSPVwpgrseLRDSPMYKIAGEEFIYKAFEY 138
                          *************99754444455******************96 PP


>> k141_381421
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  155.0   0.8   6.2e-47   8.5e-47     117     271 ..     23     182 ..
18     185 .] 0.93


  Alignments for each domain:
  == domain 1  score: 155.0 bits;  conditional E-value: 6.2e-47
  MSA_GH10_xylanases 117 QlPswvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…
…lresvfyrvlgedyvkiafeaareadpnakLyi 199
                         +P++v +    +k+++ + l+ hi+tvv+rYk+ +y WDVvNE++++ ++
+r+s+ y+++g++++k af +a+eadpna L++
        k141_381421   23 KVPKYVAA---
SKQEFYDSLRVHINTVVNRYKDVIYCWDVVNEAMSDANNpdapyedsFRKSQAYQLCGDEFIKNAFIWAHEADPNAGLFY
110
                        57999984…56**************************9977666677
777***************************** PP


  MSA_GH10_xylanases 200
NDYnlesasaklegmvklvkklleagvpidGiGsqsHlsaga.psvaelkkalnalaslgvevaitELDiale 271
                         NDY+  ++ ak++ ++++vkkl+++g+pi GiG+q+H+++    p+ ++ +
a++++ +l  +++itE+Di+++
        k141_381421 111 NDYSAWTP-
AKRTYIYNMVKKLQAEGAPITGIGMQGHYNIFDnPTLEDFETAIKMYLELVDDIQITEFDIRIN 182
******99.**************************987799*********************944 PP


>> k141_5473247
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  154.6   0.9   8.1e-47   1.1e-46     103     269 ..      1     178 [.
1     187 [. 0.92


  Alignments for each domain:
  == domain 1  score: 154.6 bits;  conditional E-value: 8.1e-47
  MSA_GH10_xylanases 103 ngkklRgHtlvWhsQlPswvssik…adketllevlknhiktvv…g
rYkgkvyaWDVvNEilnedgslresvfyrvlgedyv 181
                         n+ ++RgHtlvW+sQ+P+w++++         +++e ll+++++ i++v       +
Y +  ya+DVvNE+  edg++r+ ++++++g+dy+
```

```
        k141_5473247    1 NNFSMRGHTLVWYSQTPEWLFHEDfdankdyVTREVLLARMESMIRQVFenlteQ
GYIDLFYAYDVVNEAWMEDGTMRKNHWSEIIGDDYL 91
                        6889*****************999999999999***************9777777
79999************************** PP


  MSA_GH10_xylanases 182 kiafeaareadp.nakLyiNDYnlesasaklegmvklvkklleag..vpidGiGs
qsHlsagapsvaelkkalnalaslgvevaitELDia 269
                        af +a +++p ++ Ly+NDYn +   +k++++vk vk+l++++
idG+G+q+Hl ++  s +++ +++++la++g+ +++tELD+
        k141_5473247   92 WYAFYYADKYAPeSIDLYYNDYNEQ---
YKTDALVKFVKTLVDEKgnYLIDGVGFQAHLYTSD-SLHAYFNTVDTLAETGLKLQLTELDVC 178
                        *********6652689*******98…78***********98642278******
******99.89999*******************97 PP


>> k141_5899885
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  153.7   0.1   1.5e-46     2e-46     127     273 ..       7     166 ..
2     172 .. 0.94


  Alignments for each domain:
  == domain 1  score: 153.7 bits;  conditional E-value: 1.5e-46
  MSA_GH10_xylanases 127 adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…l
resvfyrvlgedyvkiafeaareadpnakLyiNDYn 203
                        ++ke + ++l++hi+tvv+rYk+ vyaWDVvNE++ +dg
+r+s +++++g++++++afe+areadp+  L +NDY+
        k141_5899885    7 VKKEVFYQRLREHIHTVVNRYKDVVYAWDVVNEAMADDGRpfefvngkmvpaspY
RQSRHFKLCGDEFIAKAFEFAREADPTGVLIYNDYS 97
                        5789999*****************************98888888888888899
********************************* PP


  MSA_GH10_xylanases 204
lesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele 273
                        ++  k+e ++++vkk+++agvpidGiG+q+H+++  p++a+l+ka+n++++
++itELD+++++e
        k141_5899885   98 CVDE-
GKRERIYNMVKKMKDAGVPIDGIGMQGHYNIYFPDEAQLEKAINRFSEIVKIIHITELDLRTNTE 166
9988.9*********************************************************6554 PP


>> k141_6547853
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  153.6   0.1   1.6e-46   2.2e-46      26     166 ..      21     167 ..
1     175 [. 0.87
```

```
   Alignments for each domain:
   == domain 1  score: 153.6 bits;  conditional E-value: 1.6e-46
   MSA_GH10_xylanases  26 srqaaesldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKw
eaiepsrgkfsFegadelvnfakkngkklRgHtlvW 114
                           +r +        lk a+k+yf  G av++ ++++  ++aiikk++ s+t+eN+ K+
+i+p++g ++F  ad+++nf+++ng k+RgH l+W
         k141_6547853  21 GRPVDYAAGPGLKDAYKDYFtiGVAVNKFNISDPVQTAIIKKQYSSVTAENAWKP
GEIHPKEGVWNFGLADSIANFCRENGIKMRGHCLCW 111
                           3333334455799*********************************
****************************** PP


   MSA_GH10_xylanases 115
hsQlPswvssik…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs 166
                           hsQ +w++++k    ++ke + ++l++hi+tvv+rYk+ vyaWDVvNE++ +dg
         k141_6547853 112
HSQFADWMFTDKkgkpVKKEVFYQRLREHIHTVVNRYKDVVYAWDVVNEAMADDGR 167
***********999999********************************96 PP


>> k141_3957880
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
  ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  152.5  0.9   3.6e-46   4.9e-46    117    269 ..     47     204 ..
41     207 .] 0.92


   Alignments for each domain:
   == domain 1  score: 152.5 bits;  conditional E-value: 3.6e-46
   MSA_GH10_xylanases 117 QlPswvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…
…lresvfyrvlgedyvkiafeaareadpnakLyi 199
                           +P++v +   +ke++ + l+ hi+ vv+rYk+ +y WDVvNE++++  +
+r+s+ y+++g++++k af +a+eadpna L++
         k141_3957880  47 KVPKYVAA---
SKEEFYDSLRAHINVVVNRYKDVIYCWDVVNEAMSDSDDvnasyedsFRKSQAYQLCGDEFIKNAFIWAHEADPNAGLFY
134
                           68999984…569***************************8865444556
6669***************************** PP


   MSA_GH10_xylanases 200
NDYnlesasaklegmvklvkklleagvpidGiGsqsHlsaga.psvaelkkalnalaslgvevaitELDia 269
                           NDY+  ++ ak++ ++++vkkl+++g+pi GiG+q+H+++   p+ ++
+ka+n++ +l  +++itE+Di+
         k141_3957880 135 NDYSAWTP-
AKRTYIYNMVKKLQAEGAPITGIGMQGHYNIFDnPTLDDFEKAINMYLELVDDIQITEFDIR 204
******99.*****************************987799************************9 PP


>> k141_5915145
```

```
    #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  152.5   0.0   3.6e-46   4.9e-46     107     258 ..       2     163 ..
1     164 [] 0.92


  Alignments for each domain:
  == domain 1  score: 152.5 bits;  conditional E-value: 3.6e-46
  MSA_GH10_xylanases 107 lRgHtlvWhsQlPswvssik…adketllevlknhiktvv…grYkgk
vyaWDVvNEilnedgslresvfyrvlgedyvkiafe 186
                           +RgHtlvWh+Q+P+w++ ++        +d+et+l++l+n+ik v+    + Y g
+yaWDVvNE+++ +g++r+s +++++g+d+v +afe
        k141_5915145    2
MRGHTLVWHNQTPKWFFCEHynesfpyTDRETMLARLENYIKGVLgfiqSEYPGVIYAWDVVNEAVD-
NGDFRKSLWTKTVGNDFVIKAFE 91
                           9****************99999*********************9777789****
**********96.79******************** PP


  MSA_GH10_xylanases 187
aare.adpnakLyiNDYnlesasakle.gmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslg 258
                           +ar+ a+p + L++NDY +    k++  +++++k l+e+g+ +dG+G+qsHl +
+p+ ++++kal+ + +lg
        k141_5915145   92 FARKyAAPGVDLFYNDYETALD-WKRDfIIANILKPLQEKGL-
VDGMGMQSHLLMDHPQFDDYRKALEIYGALG 163
****999***********9977.7777356677777777775.9*************************9988 PP


>> k141_729729
    #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  152.1   0.3   4.8e-46   6.5e-46      98     237 ..       3     152 ..
1     153 [] 0.97


  Alignments for each domain:
  == domain 1  score: 152.1 bits;  conditional E-value: 4.8e-46
  MSA_GH10_xylanases  98 nfakkngkklRgHtlvWhsQlPswvssik…adketllevlknhiktvv.
…grYkgkvyaWDVvNEilnedgslresvfyrvlg 177
                           +fak++g  +RgHtlvWh+Q+P+w++ ++       ad+et+l++l+++i+ v+
+ Y g +yaWDVvNEi++e g +r+s +++ +g
        k141_729729    3
EFAKEKGIAMRGHTLVWHNQTPKWFFCQNynehfplADRETILKRLESYIHGVMdfvqTNYPGIIYAWDVVNEIVDE-
GAFRKSIWTQAVG 92
                           89*************************9999*********************9
9989***************975.89*********** PP


  MSA_GH10_xylanases 178
```

```
edyvkiafeaare.adpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHl 237
                         ed+  +afe+a++ ++p + L++NDY + ++  k++ ++++v k l ++
+dG+G+qsHl
        k141_729729  93 EDFFIKAFEFAKKnVAPGVDLFYNDYETAQP-
WKRDYIIEHVLKPLMEKKLVDGMGMQSHL 152
***********9989**************99.*************************8 PP


>> k141_6539735
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  151.8   0.0   5.7e-46   7.8e-46      46     222 ..      2     205 ..
1     212 [. 0.90


  Alignments for each domain:
  == domain 1  score: 151.8 bits;  conditional E-value: 5.7e-46
  MSA_GH10_xylanases  46 Gtavdqk..elekskeeaiikkdfgsltpeNsMKweaiepsrg…
kfsFegadelvnfakkngkklRgHtlvWhsQlPswv 122
                         G+a+ q+  +l ++k ++i+  +f  ltpeN++K++++ + ++
++ ++a  l +fa+kng k+ gH lvWhsQ+P+ +
        k141_6539735   2 GAAAPQYvfNLGQEKLQEIVLDHFSILTPENELKPDSVLDVQKskglakddetav
AIKLNAAKPLLKFAQKNGLKVHGHVLVWHSQTPEAF 92
                         55555552245668999*****************988888888*********
*****************************999 PP


  MSA_GH10_xylanases 123 ssik…adketllevlknhiktvv…grYkgkvyaWDVvNEilnedgs
.lr.esvfyrvlgedyvkiafeaare.adpnakLyi 199
                         +++         +++e +l +l+n+i++v+    + Y g +++WDVvNE++n+ ++
lr +s++ r++ged+v++afe+ar+ a++ + Ly+
        k141_6539735  93 FHEGydtskpfVSREIMLGRLENYIREVLtqteEEYPGVIVSWDVVNEAINDGTN
wLRqDSKWVRIIGEDFVSKAFEYARKyAAEGVLLYY 183
                         98888999**99***************9888889****************999
86658*****************88899***** PP


  MSA_GH10_xylanases 200 NDYnlesasaklegmvklvkkll 222
                         NDYn+ ++  kl g++kl++ l+
        k141_6539735 184 NDYNTAYT-GKLLGITKLLNMLI 205
                         ******99.99999999998776 PP


>> k141_4184415
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  151.6   0.0   6.5e-46   8.8e-46      88     240 ..     17     179 ..
6     181 .] 0.92
```

```
  Alignments for each domain:
  == domain 1  score: 151.6 bits;  conditional E-value: 6.5e-46
  MSA_GH10_xylanases  88 fsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllev
lknhiktvv…grYkgkvyaWDVvNEilnedgsl 167
                           +Fe+a     +fak+ng  +RgHtlvWh+Q+P+w++
ad+et+l++l+++ik v+    + Y g +yaWDVvNE ++ dg +
       k141_4184415   17 LNFEAARPYLEFAKANGIAMRGHTLVWHNQTPKWFFCVDyneskalADRETILAR
LESYIKGVLefvqTEYPGVIYAWDVVNECVD-DGGF 106
                           589****************************************998889999***********
******998777789**************96.788* PP


  MSA_GH10_xylanases 168
resvfyrvlgedyvkiafeaare.adpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsag 240
                           r+sv++  +ged+  +afe+ar+ a+p + L++NDY + +   k++ +++ v k
l ++  +dG+G+qsHl +
       k141_4184415 107 RKSVWSSAVGEDFFIKAFEFARKyAAPGVALFYNDYETSQD-
WKRDFIIESVLKPLMEKGLVDGMGLQSHLLMD 179
***********************999***********9977.99999998887766666679********9765 PP


>> k141_7073722
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  150.9   0.2   1.1e-45   1.4e-45     117     240 ..       1     127 [.
1     129 [] 0.97


  Alignments for each domain:
  == domain 1  score: 150.9 bits;  conditional E-value: 1.1e-45
  MSA_GH10_xylanases 117 QlPswvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…l
resvfyrvlgedyvkiafeaareadpnakLyiNDYn 203
                           Q+  w++ ++ +ke + +++k hi+ vv+rYk+ vy WDVvNE++ +d +
+r+s  y+++g++++++afe+a+eadpna L++NDYn
       k141_7073722   1 QIGRWMTDDNPTKEVFYQRMKIHIEAVVNRYKDVVYCWDVVNEAMTDDPKaedpY
RQSAMYKLCGDEFIAKAFEFAHEADPNALLFYNDYN 91
                           7889*********************************************9988999
********************************** PP


  MSA_GH10_xylanases 204 lesasaklegmvklvkklleagvpidGiGsqsHlsag 240
                           ++ +k++ + ++vkk+++agvpidGiG+q+H+++
       k141_7073722  92 ECDP-VKSQRIFNMVKKMKDAGVPIDGIGMQGHYNIY 127
                           **99.**********************9975 PP


>> k141_99796
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
```

```
   1 !  149.7   0.1   2.5e-45   3.4e-45     127     273 ..       7     166 ..
2     179 .. 0.93

  Alignments for each domain:
  == domain 1  score: 149.7 bits;  conditional E-value: 2.5e-45
  MSA_GH10_xylanases 127 adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…l
resvfyrvlgedyvkiafeaareadpnakLyiNDYn 203
                        ++ke + e+l++hi+tvv+rYk+  yaWDVvNE++ +dg
+r+s +++++g++++++afe+areadp+  L +NDY+
          k141_99796   7 VKKEVFYERLRDHIHTVVNRYKDVGYAWDVVNEAMADDGRpfefvdgkmvkaspY
RQSRHFELCGDEFIAKAFEFAREADPTGVLIYNDYS 97
                        5789999***************************98888888888888889
99************************** PP


  MSA_GH10_xylanases 204
lesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialele 273
                        + ++  k+e ++++vkk++eagvpidGiG+q+H+++  p++++l+ka++++++
++itELD+++++e
          k141_99796  98 TIDN-
GKRERIYEMVKKMKEAGVPIDGIGMQGHYNIYFPDEDQLEKAIERFSEIVNTIHITELDLRTNTE 166
9977.9************************************************************6665 PP


>> k141_7842613
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  149.9   0.0   2.1e-45   2.9e-45     167     329 ..      11     188 ..
5     189 .] 0.95

  Alignments for each domain:
  == domain 1  score: 149.9 bits;  conditional E-value: 2.1e-45
  MSA_GH10_xylanases 167 lresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkkl
leagvpidGiGsqsHlsagapsvaelkkalnalasl 257
                        +r+s +++++g++++++afe+areadp+  L +NDY++ ++  k+e ++
+vkk+++agvpidGiG+q+H+++  p++++l+ka+n++ +
        k141_7842613  11 YRQSRHFKLCGDEFIAKAFEFAREADPTGVLIYNDYSTVDN-
GKRERIYTMVKKMKDAGVPIDGIGMQGHYNIYFPDEEQLEKAINRFKEI 100
                        8***********************************9977.9***********
******************************** PP


  MSA_GH10_xylanases 258 gvevaitELDialele…ateekleaqakdyvevvkaclevkk
cv.gvtvWgvaDkdsWls.eespllfdenynpK 329
                        ++itELD+++++e            ++   + q+++y++++k++++
++++ +vt+W+++DkdsWl  ++ pl fden+++K
        k141_7842613 101 VNIIHITELDLRTNTEsggqlmfsrgeakpQAPYIATLQEDQYARLFKIFRKHAD
VIkNVTFWNLSDKDSWLGvNNHPLPFDENFKAK 188
                        *9**********888799*********98766778999*****************
```

```
****************986899**********99 PP


>> k141_2698953
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !  150.0   0.0   2.1e-45   2.8e-45     128     245 ..       3     123 ..
1     125 [] 0.96


  Alignments for each domain:
  == domain 1  score: 150.0 bits;  conditional E-value: 2.1e-45
  MSA_GH10_xylanases 128 dketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlge
dyvkiafeaareadpnakLyiNDYnlesasaklegm 214
                           dke + +++knhi+ vv+rYk+ vy WDVvNE+++++       +resv
y+++g++++++af++areadpna L++NDYn   ++ +k++ +
        k141_2698953   3 DKEVFYQRMKNHIQAVVTRYKDVVYCWDVVNEAMSDNPRsphpYRESVMYKLCGD
EFIAKAFQYAREADPNALLFYNDYNECDP-VKSQRI 92
                           89999********************************988889************
***************************99.****** PP


  MSA_GH10_xylanases 215 vklvkklleagvpidGiGsqsHlsagapsva 245
                           +++vk+++++gvpidGiG+q+H+++  p+++
        k141_2698953  93 YEMVKRMKAQGVPIDGIGMQGHYNIYGPTEE 123
                           ***********************9987665 PP


>> k141_2362932
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !  148.4   0.0   6.2e-45   8.4e-45     179     337 ..       2     175 ..
1     177 [. 0.96


  Alignments for each domain:
  == domain 1  score: 148.4 bits;  conditional E-value: 6.2e-45
  MSA_GH10_xylanases 179 dyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGs
qsHlsagapsvaelkkalnalaslgvevaitELDia 269
                           +++++af++areadp++ L++NDY+  ++  k+e
++++vkk+++agvpidGiG+q+H+++  ps+++l+ka+ ++ +     ++itELD++
        k141_2362932   2 EFIAKAFQFAREADPDVLLFYNDYSCVDE-
GKRERIYNMVKKMKDAGVPIDGIGMQGHYNIYFPSEEQLEKAIVRFKEIVKHINITELDLR 91
                           8***********************9988.9*************************
********************************* PP


  MSA_GH10_xylanases 270 lele…ateekleaqakdyvevvkaclevkkcv.gvtvWgvaD
kdsWls.eespllfdenynpKpaynaivk 337
                           ++ e              +++ +   q+++y++++k++++ ++++ +vt+W++
```

```
DkdsWl  ++ pl fdeny+pK+   ai +
       k141_2362932   92 MNNEsggqlmfsrgeakpMPAYMSTLQTDQYARLFKVFRKHADVIdNVTFWNLGD
KDSWLGvNNHPLPFDENYRPKQCMRAIRD 175
                           88879**********998999999***************************
****986899************9999865 PP


>> k141_3542624
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------   ------- -------
------- -------    ----
   1 !  145.9   2.5   3.5e-44   4.8e-44      48     163 ..       2     121 ..
1     125 [. 0.97


  Alignments for each domain:
  == domain 1  score: 145.9 bits;  conditional E-value: 3.5e-44
  MSA_GH10_xylanases  48 avdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakk
ngkklRgHtlvWhsQlPswvssik…adketlle 134
                         av++++++   + +++ ++f+s+t+eN+MK++
+ep++g+f++e+ad+++nf+++ng k+RgHtl+WhsQ+ sw+ ++       +ke+l +
       k141_3542624    2 AVNNRNVADPDQIKVVLREFNSITAENAMKPQPTEPKKGEFNWEDADRIANFCRQ
NGIKMRGHTLMWHSQIGSWMYQDDkgnlLSKEELYA 92
                         7889999999****************************************
*******************99999999******* PP


  MSA_GH10_xylanases 135 vlknhiktvvgrYkgkvyaWDVvNEilne 163
                         +k+hi+ +v+rYk+ vy WDVvNE++ +
       k141_3542624   93 NMKHHIQAIVNRYKDVVYCWDVVNEAVAD 121
                         ************************987 PP


>> k141_8990501
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------   ------- -------
------- -------    ----
   1 !  145.4   0.2   5.2e-44   7.1e-44     191     335 ..       1     159 [.
1     163 [. 0.94


  Alignments for each domain:
  == domain 1  score: 145.4 bits;  conditional E-value: 5.2e-44
  MSA_GH10_xylanases 191 adpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsva
elkkalnalaslgvevaitELDialele… 273
                         adpna L++NDYn  ++ ak++ +++lvk++++agvp+dGiG+q+H+++
p+++e+ +a++ ++      +++tELDi+++ +
       k141_8990501    1 ADPNALLFYNDYNDAEP-
AKSQRIYNLVKRMKDAGVPVDGIGMQAHYNVYGPTMKEVDDAIKLYSTVVDHIHLTELDIRINEDmggglrfn 90
                         69***********999.*********************************
***********999**********666679****** PP


                                    97
```

```
    MSA_GH10_xylanases 274
…ateekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynai 335
                                  +++ +   q+++yv+++k++++ k+++ +vt+W+v+DkdsWl
+++pllfdeny+pK+ay a+
         k141_8990501  91
qgqatVSDWERTLQQDQYVQLFKVLRKHKDVIdCVTFWNVSDKDSWLGvRNYPLLFDENYKPKQAYLAV 159
99988777788899******************************986899**************988 PP


>> k141_81645
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  145.3   0.0   5.6e-44   7.6e-44      81     230 ..       2     165 ..
1     166 [] 0.93


  Alignments for each domain:
  == domain 1  score: 145.3 bits;  conditional E-value: 5.6e-44
  MSA_GH10_xylanases  81 iepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adketl
levlknhiktvvgrYkgkvyaWDVvNEilnedgs.. 166
                            +ep++g+f Fe ad + ++a++ g k+R H+ vWh+Q+P+w+ ++    a+ e +
+++  h k +++rY+g+vyaWDVvNE+   +d
          k141_81645    2 TEPEEGRFRFERADVIFALAREMGVKVRAHAPVWHNQTPDWMCRDGdspASPELI
YARIDAHSKALCQRYNGDVYAWDVVNEATRDDPLdp 92
                            89*****************************************9988888999**
**************************99986444 PP


  MSA_GH10_xylanases 167
…lresvfyrvlgedyvkiafe.aareadpnakLyiNDYnlesasaklegmvklvkklleagvpidG 230
                                  +r+s++y+++g+ +++ af+ +a+ a+p+a+L++NDYn   +
k++ +v l+++l+e+g+++dG
          k141_81645   93 akapdespvYRNSEYYHLCGAGFIEAAFRsMAKYAAPDAQLFYNDYNECLP-
EKRDRIVTLIRNLQEKGCRVDG 165
4556667889******************845777***************99.9********************9 PP


>> k141_6568681
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  144.6   0.0      9e-44   1.2e-43     180     335 ..       1     171 [.
1     175 [. 0.94


  Alignments for each domain:
  == domain 1  score: 144.6 bits;  conditional E-value: 9e-44
  MSA_GH10_xylanases 180 yvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsq
sHlsagapsvaelkkalnalaslgvevaitELDial 270
```

```
                              ++++afe+areadpna L++NDY++ ++  k+e
++++vkk++eagvpidGiG+q+H+++  p+++ l ka++++++    ++itELD+++
        k141_6568681    1 FIAKAFEFAREADPNALLFYNDYSTVDP-
GKRERVYEMVKKMKEAGVPIDGIGMQGHYNIYFPDEELLDKAITRFSEIVSHIHITELDLRT 90
                         89**********************99.9***********************
*******************************8 PP


  MSA_GH10_xylanases 271 ele…ateekleaqakdyvevvkaclevkkcv.gvtvWgvaDk
dsWls.eespllfdenynpKpaynai 335
                         ++e                   +  +   q+++y++++k+++  k+++
+vt+W+++DkdsWl  ++ pl fdeny++K +   i
        k141_6568681   91 NTEsggqlafsrgearpLAGYMQTLQEDQYARIFKVLRRHKDVIdNVTFWNLSDK
DSWLGaNNHPLPFDENYKAKRSLRII 171
                         88799********998756677788999**************************
***964889***********998766 PP


>> k141_8720743
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  144.3   0.0   1.1e-43   1.5e-43     154     270 ..      1     116 [.
1     123 [. 0.97


  Alignments for each domain:
  == domain 1  score: 144.3 bits;  conditional E-value: 1.1e-43
  MSA_GH10_xylanases 154 WDVvNEilnedgslresvfyrvlgedyvkiafeaareadpnakLyiNDYnlesas
aklegmvklvkklleagvpidGiGsqsHlsagapsv 244
                         WDVvNE++ ++g++r+s++y+++g d++k af +a++adp+a Ly+NDY++  +
ak++++vklvk+l++ag++id +G+qsH + + p+
        k141_8720743    1 WDVVNEAILDNGEYRQSPYYKIIGPDFIKLAFIFAHQADPDAELYYNDYSMSIP-
AKRNAVVKLVKELKAAGCRIDAVGMQSHNGFNYPNL 90
                         **************************************************99.
******************************* PP


  MSA_GH10_xylanases 245 aelkkalnalaslgvevaitELDial 270
                         ++++++++a+ ++gv+v+ tELD+++
        k141_8720743   91 EDYENSIKAFIAAGVDVQFTELDVNM 116
                         *********************93 PP


>> k141_1664273
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  144.0   0.0   1.3e-43   1.8e-43     176     335 ..      2     176 ..
1     178 [] 0.95
```

```
  Alignments for each domain:
  == domain 1  score: 144.0 bits;  conditional E-value: 1.3e-43
  MSA_GH10_xylanases 176 lgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidG
iGsqsHlsagapsvaelkkalnalaslgvevaitEL 266
                         +g++++++afe+areadp+  L +NDY+  ++  k+e ++
+vkk+++agvpidGiG+q+H+++  p++++l+ka+n++ +     ++itEL
         k141_1664273    2 CGDEFIAKAFEFAREADPTGVLIYNDYSCVDN-
GKRERIYTMVKKMKDAGVPIDGIGMQGHYNIYFPDEEQLEKAINRFKEIVNIIHITEL 91
                         79**********************9977.9*********************
*****************************9******* PP


  MSA_GH10_xylanases 267 Dialele…ateekleaqakdyvevvkaclevkkcv.gvtvWg
vaDkdsWls.eespllfdenynpKpaynai 335
                         D+++++e                ++    +  q+++y++++k++++ ++++
+vt+W+++DkdsWl  ++ pl fden+++K + + i
         k141_1664273   92 DLRTNTEsggqlmfsrgeakpQAPYIATLQEDQYARLFKIFRKHADVIkNVTFWN
LSDKDSWLGvNNHPLPFDENFKAKRSLQII 176
                         ***888799*********98766778999*************************
*******986899***********998866 PP


>> k141_3339881
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  141.8   0.1   6.3e-43   8.6e-43     145     272 ..       1     140 [.
1     143 [] 0.94


  Alignments for each domain:
  == domain 1  score: 141.8 bits;  conditional E-value: 6.3e-43
  MSA_GH10_xylanases 145 grYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafe
aareadpnakLyiNDYnlesasaklegmvklvkkll 222
                         +rYk+ vy WDVvNE++ +dg              +r+s
+++++g++++++af++areadpna L++NDY++ ++  k+e ++++vkk++
         k141_3339881    1
NRYKDVVYCWDVVNEAMADDGGfrgprrggeepspYRQSRHFKLCGDEFIAKAFQFAREADPNALLFYNDYSTVDP-
GKRERIYNMVKKMK 90
                         59****************9766777777777888899*****************
*******************99.9************* PP


  MSA_GH10_xylanases 223 eagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDialel 272
                         +agvpidGiG+q+H+++  ps+++l ka++++++l    ++itELD++++
         k141_3339881   91 DAGVPIDGIGMQGHYNIYFPSEEQLDKAITRFSELVKHINITELDLRMNN 140
                         *******************************************9654 PP


>> k141_8387005
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
```

```
   ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !  142.5   0.2   3.9e-43   5.4e-43      77     191 ..       1     119 []
1     119 [] 0.98


  Alignments for each domain:
  == domain 1  score: 142.5 bits;  conditional E-value: 3.9e-43
  MSA_GH10_xylanases  77 KweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadket
llevlknhiktvvgrYkgkvyaWDVvNEilnedgs. 166
                          K+e +ep++g+f++++ad+++n+a++ng klRgH l+WhsQ+   ++++
+ke++ e++knhi+ +v+rYk+ +y WDVvNE+++++++
        k141_8387005   1 KPEPTEPQEGQFNWDNADRIANYARQNGIKLRGHCLMWHSQIGRLMTAEGSNKEQ
FYERMKNHIQAIVTRYKDVIYCWDVVNEAIEDNANa 91
                        8899*************************************************
*****************************9988 PP


  MSA_GH10_xylanases 167 …lresvfyrvlgedyvkiafeaarea 191
                           +r+s  yr++g++++++af++area
        k141_8387005  92 tdpYRQSAMYRLCGDEFIEKAFQFAREA 119
                        8899*****************986 PP


>> k141_2242540
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !  141.6   0.1   7.3e-43   9.9e-43     191     337 ..       2     162 ..
1     165 [. 0.94


  Alignments for each domain:
  == domain 1  score: 141.6 bits;  conditional E-value: 7.3e-43
  MSA_GH10_xylanases 191 adpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsva
elkkalnalaslgvevaitELDialele… 273
                          adpna L++NDYn  ++ +k++ + ++vkk+++agvpi+GiG+q+H+++
p+++++ kal+ + +    +++tELDi+ ++e
        k141_2242540   2 ADPNALLFYNDYNECDP-
VKSQRIFNMVKKMKDAGVPIHGIGMQGHYNIYGPKEEDIDKALELYKQVVSHIHVTELDIRANQEmggqlafs 91
                        8**************99.*********************************
***********************766689****** PP


  MSA_GH10_xylanases 274
…ateekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                           ++++  ++ a++y++v++++++ k+++ +vt+W+++D+dsWl  +++pl
fd +y+pK ay+ i +
        k141_2242540  92
rdgaaVNDSLKQHLADQYARVFRVFRKHKDVIdCVTFWNLSDRDSWLGqNNYPLPFDVDYKPKMAYEYIRD 162
***987888888899****************************963789**************99876 PP




                                   101
```

```
>> k141_5128900
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  141.1   0.0   1.1e-42   1.4e-42     112     268 ..      2     169 .]
1     169 [] 0.96


  Alignments for each domain:
  == domain 1  score: 141.1 bits;  conditional E-value: 1.1e-42
  MSA_GH10_xylanases 112 lvWhsQlPswvssik…adketllevlknhiktvv…grYkgkvyaWD
VvNEilnedgs.lresvfyrvlgedyvkiafeaare 190
                         lvWhsQ+P+ +++++       +++e +l +l+n+ik v+    + Y g
v++WDV+NE++++ ++ lr+s++ +++g+dy + a+e+ar+
        k141_5128900    2 LVWHSQTPEAFFHESydtkkpfVTREVMLGRLENYIKGVMeylnENYPGVVVSWD
VLNEAIDDGSNwLRNSNWRKIIGDDYPNRAYEYARR 92
                         9********999998899***99******************999889*********
*******99889*********************** PP


  MSA_GH10_xylanases 191
adpn.akLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDi
268
                            ++p+ +kLy+NDYn+  + +kl+g+++l+k+l+ +g  idG G+q H sa+ ps
++++a+n+ a lg+ + + ELD+
        k141_5128900   93 YAPEgTKLYYNDYNTAIP-SKLNGIMRLLKSLIPEG-
NIDGYGFQMHHSASFPSIGQIRSAVNTVAGLGIRLRVSELDV 169
776549***********99.9*************99.6***********************************8
PP


>> k141_2744974
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  140.5   0.4   1.6e-42   2.2e-42     143     290 ..      1     170 [.
1     171 [] 0.91


  Alignments for each domain:
  == domain 1  score: 140.5 bits;  conditional E-value: 1.6e-42
  MSA_GH10_xylanases 143 vvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiafeaar
eadpnakLyiNDYnlesasaklegmvklvkklleag 225
                        vv+rYk+ vy WDVvNE++++ ++         +r+s  y+++g++++
+af++a+eadpna L++NDY+  ++ ak++ ++++vkkl+++g

IOPub message rate exceeded.
The notebook server will temporarily stop sending output
to the client in order to avoid crashing it.
To change this limit, set the config variable
```

```
`--NotebookApp.iopub_msg_rate_limit`.

Current values:
NotebookApp.iopub_msg_rate_limit=1000.0 (msgs/sec)
NotebookApp.rate_limit_window=3.0 (secs)



  MSA_GH10_xylanases 172 fyrvlged…yvkiafeaareadpnakLyiNDYnlesasaklegmvklvkkll
eagvpidGiGsqsHlsagapsvaelkkalnalaslg 258
                          +r++ e+     vk  f aa+e +p+a L iND+n+ +a       ++l++
lleagvpi  +G+qsH + g +  ++l++ l+++++
         k141_4537008  91 ITRICKEKgrvgLVKEVFAAAKESNPDAVLLINDFNTSEA------
YAELIEALLEAGVPISAVGIQSHQHQGYWGLEKLNRVLERFSRFS 175
                          7777776544458*********************966…899******
******************************** PP


  MSA_GH10_xylanases 259 vevaitE 265
                         + ++ tE
         k141_4537008 176 LPIHFTE 182
                          ******9 PP


>> k141_417097
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   91.4   0.0   1.4e-27   1.9e-27      36     144 ..      81     212 ..
62     214 .] 0.94


  Alignments for each domain:
  == domain 1  score: 91.4 bits;  conditional E-value: 1.4e-27
  MSA_GH10_xylanases  36 llkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg..
…kfsFegadelvnfakkngkklRgH 110
                         +lk a+kk f  Gta++ +e++ + +++++ k+f+s+t++N++K++a+ +++
+  ga  + nf+++n+  +RgH
         k141_417097  81 SLKDAYKKHFkiGTATTVAEISPKATQKLVIKHFNSVTAGNELKPDALLDQKAtl
aeaeetgdytnpIVKVGGAGPILNFCAENDIPVRGH 171
                         68999***9999****************************************9999*
*******999988899******************* PP


  MSA_GH10_xylanases 111 tlvWhsQlPswvssik…adketllevlknhiktvv 144
                         tlvWhsQ+P w++++k        +dk+t+l++++n+ik+v
         k141_417097 172 TLVWHSQTPIWFFKEKfdesgkwVDKDTMLKRMENYIKNVF 212
                         ***********************************96 PP


>> k141_164929
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
```

```
envfrom  env to    acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   90.7   0.0   2.2e-27     3e-27     107     337 ..      1     243 [.
1     246 [. 0.83

  Alignments for each domain:
  == domain 1  score: 90.7 bits;  conditional E-value: 2.2e-27
  MSA_GH10_xylanases 107 lRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvyaWDVvNEil
nedgs…lresvfyrvlge.dyvkiafeaaread 192
                            ++gH l+Wh      w+ + + ++e l + + + i+  ++ +kg +  WDV+NE++
+   + lg    vk  f aa+e+d
       k141_164929    1 VKGHPLCWHTACAPWLMQYS-NEEILRRQI-
ERIHRDMSAFKGVIGLWDVINEVVIMPVFdkydNAITRICKDLGRvGIVKEVFAAAKETD 89
                            68**************988.666666666.579*****************87
5433211003334445555565258999********* PP

  MSA_GH10_xylanases 193 pnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvael
kkalnalaslgvevaitELDia..lele… 273
                            p+a L iND+n+ +         +l+++lleagvpi  iG+qsH + g +
++l++ l+++++ g+ ++ tE  +
       k141_164929   90 PDAVLLINDFNTSKH------
YEELIEDLLEAGVPIGTIGIQSHQHQGYWGLEKLNDVLERFSRFGLPIHFTENTLIsgDI-Mpahivdln 173
                            ************955…67899*****************************
*****************76542322.146778899 PP

  MSA_GH10_xylanases 274
…ateekleaqakdyvevvkaclevkkcvgvtvWgvaDkdsWlseespllfdenynpKpaynaivk 337
                               t e  e+qa++  e+  ++ + + + ++t W++ D   Wl+  s
+++++n   Kp+y+a+ +
       k141_164929 174 dwqvdewpSTPEGEERQAREISEMYTVLFSHPLVDAITPWDFNDG-
CWLKAPSGFVHQDN-SLKPSYDALRQ 243
999**99988899999********99999999888********95.8*******999877.57999998765 PP


>> k141_1399820
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   90.6   0.7   2.4e-27    3.3e-27     155     316 ..      6     172 ..
1     196 [. 0.84

  Alignments for each domain:
  == domain 1  score: 90.6 bits;  conditional E-value: 2.4e-27
  MSA_GH10_xylanases 155 DVvNEil..nedgs..lresvf.yrvlgedyvkiafeaareadpnakLyiNDYnl
esasaklegmvklvkklleagvpidGiGsqsHlsag 240
                            DVvNE++  +++g+  ++es      +g d++  afe+a+e  p+a L +NDYn+
+  + +++ ++lv++l++ag+pid  G qsH   +
```

```
        k141_1399820    6
DVVNEAVgmHQQGNplMKESLGgEGQTGYDWLINAFEMAHERWPDAILIYNDYNTFQ--
YDTDAYIDLVRTLRDAGAPIDAYGCQSHDVDN 94
                          9****97335667698889987678**********************9
95..599********************6665 PP


  MSA_GH10_xylanases 241 apsvaelkkalnalaslgv.evaitELDialeleateekleaqakdyvevvkacl
evkkcvgvtvWgvaDkdsWls…e 316
                          s+++l++++ ++ ++     + itELDi+        +  ++q+++y++++ ++
e + c gvt+Wg      +W++        +
        k141_1399820   95 I-SKSNLQNSMARIQDAVKmPMYITELDIN------
VQDDNQQKAQYESIFPVMWEADYCAGVTIWGYVYGATWVDhsglyrngS 172
                          5.9***********998777**********…344578999**********
******************9555555542 PP


>> k141_6478272
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   90.1   0.9   3.4e-27   4.7e-27      77     213 ..      3     167 ..
1     168 [] 0.81


  Alignments for each domain:
  == domain 1  score: 90.1 bits;  conditional E-value: 3.4e-27
  MSA_GH10_xylanases  77 Kweaiepsrg…kfsFegadelvnfakkngkklRgHtlvWhsQlP
swvssik…adketllevlknhiktvv… 144
                          K++ai ++++              f++ +  +  +f+++ng
lRgHt+vW+sQ+P+w+++++      ++k+ + ++l++ ik+
        k141_6478272   3 KPDAIINQQQcqqkgnnvntqvVFNWGT-
QQTLKFCENNGIPLRGHTFVWYSQTPDWFFRENfnnwgnyVSKSIMDKRLESLIKNTFelln 92
                          5555555555555555565555889865.67789*****************
***************99************99884444 PP


  MSA_GH10_xylanases 145
grYkg.kvyaWDVvNEilnedgs.lr…esvfyrvlged.yvkiafeaareadp.nakLyiNDYnlesasakleg 213
                          Y    + ++D+ NE + ++g  +r   +s++++v g+d +v  af +ar+++p
kLy+ND+n + + ak+++
        k141_6478272  93
RDYPRlLIHSYDIANELFINNGGgmRgadNSNWFKVYGDDsFVINAFTYARRYAPiGCKLYLNDFNEYIP-AKTND 167
4564415889******986666557766699*******8769**********888469*********999.88876 PP


>> k141_7803464
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   89.6   0.1   4.6e-27   6.2e-27     231     336 ..      1     121 [.
```

```
1      124 [. 0.93

  Alignments for each domain:
  == domain 1  score: 89.6 bits;  conditional E-value: 4.6e-27
  MSA_GH10_xylanases 231 iGsqsHlsagapsvaelkkalnalaslgvevaitELDialele…
.ateekleaqakdyvevvkaclevkkcv.gvtvWgv 307
                           iG+q+H+++  p+++e+ +a++ ++      +++tELDi+++ +
+++ +   q+++yv+++k++++ k+++ +vt+W+v
        k141_7803464    1 IGMQAHYNVYGPTMEEVDNAIKLYSTVVKHIHLTELDIRVNEDmggglrfnrgga
nVADWERTLQQDQYVNLFKVLRKHKDVIdCVTFWNV 91
                           9************************99**********666679*********9
8777778899*********************** PP


  MSA_GH10_xylanases 308 aDkdsWls.eespllfdenynpKpaynaiv 336
                           +DkdsWl   ++pllfdeny+pK+ay+a+
        k141_7803464   92 SDKDSWLGaANYPLLFDENYKPKQAYTAVK 121
                           ******964789***************985 PP


>> k141_6822803
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   56.3   0.5   6.4e-17   8.8e-17     106     168 ..       4      81 ..
1      86 [. 0.86
   2 !   36.8   1.2   5.5e-11   7.5e-11     158     224 ..      88     155 .]
84     155 .] 0.88


  Alignments for each domain:
  == domain 1  score: 56.3 bits;  conditional E-value: 6.4e-17
  MSA_GH10_xylanases 106
klRgHtlvWhsQlPswvssik…adketllevlknhiktvv…grYkgkvyaWDVvNEilnedgs.lr
168
                            k+RgH lvWhsQ+P+w++++      ++ e++ ++ + +i++v+      +
Yk+  y WDVvNE++++ +  +r
        k141_6822803    4
KVRGHVLVWHSQTPEWFFHEDydktkpyVSAEEMDKRQEWYIREVLthfvgedSPYKDLFYGWDVVNEAVSDATGtYR
81
89*****************99989999999999*************9666666666999***********88654154
PP


  == domain 2  score: 36.8 bits;  conditional E-value: 5.5e-11
  MSA_GH10_xylanases 158
NEilnedgslresvfyrv.lgedyvkiafeaareadp.nakLyiNDYnlesasaklegmvklvkkllea 224
                           NE l++d++  +s + +v   e+++  af++a++++p +  Ly+NDYn   +a
k+eg+v l+k ++e+
        k141_6822803   88 NEDLSNDTHGNNSSWWHVyQSEEFIINAFKYANKYAPaDLELYYNDYNECMA-
KKREGIVALLKAVKEQ 155
```

```
999******99998866616799***********6663799********999.9**********99875 PP


>> k141_1962144
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   88.7   0.0   8.9e-27   1.2e-26      78     265 ..      33     217 ..
30     233 .. 0.86


  Alignments for each domain:
  == domain 1  score: 88.7 bits;  conditional E-value: 8.9e-27
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEilnedgs.. 166
                          w   ep +g+  + ++ +++ + ++++ +++gH l+Wh     w+ + + ++e l
+ l+  i+  v+ +kg +  WDV+NE++
        k141_1962144  33 WGRYEPVEGQTVYPETMAAARWLREKDVQVKGHPLCWHTACAPWLMQYS-
NEEILRRQLE-RIHRDVSAFKGVIGLWDVINEVVIMPVFdk 121
                         6678999999999999999***************************988.77777
77775.699999***************975433211 PP


  MSA_GH10_xylanases 167 ..lresvfyrvlge.dyvkiafeaareadpnakLyiNDYnlesasaklegmvklv
kklleagvpidGiGsqsHlsagapsvaelkkalnal 254
                           +   + lg   vk+ f aa+e+dp a L iND+n+ +a
+l+++llea+vpi  iG+qsH + g +  ++l++ l+++
        k141_1962144 122 ydNAITRICKELGRvPLVKKVFDAAKETDPGAVLLINDFNTSKA------
YEHLIEDLLEAEVPISAIGIQSHQHQGYWGLDKLNDVLERF 206
                         00333444555565259***********************966…67889
******************************** PP


  MSA_GH10_xylanases 255 aslgvevaitE 265
                         ++ g+ ++ tE
        k141_1962144 207 SRFGLPIHFTE 217
                         **********9 PP


>> k141_8337506
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   88.1   2.2   1.4e-26   1.9e-26     117     204 ..      52     144 ..
47     147 .] 0.90


  Alignments for each domain:
  == domain 1  score: 88.1 bits;  conditional E-value: 1.4e-26
  MSA_GH10_xylanases 117 QlPswvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…
…lresvfyrvlgedyvkiafeaareadpnakLyi 199
                         +P++vs+   +ke++ + lk+hi tvv+rYk+ +y WDVvNE++++ ++
```

```
+r+s+ y+++g++++k af +a+eadpna L++
        k141_8337506  52 KVPKYVSA---
TKEEFYDSLKSHIYTVVNRYKDVIYCWDVVNEAMSDANNidasyedsFRKSQAYQLCGDEFIKNAFIWAHEADPNAGLFY
139
                            68999995…569****************************9876655667
7779************************** PP


  MSA_GH10_xylanases 200 NDYnl 204
                            NDY+
        k141_8337506 140 NDYSA 144
                            ***85 PP


>> k141_2401341
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !   87.1   0.0   2.7e-26   3.6e-26      60      175 ..       3     143 .]
1      143 [] 0.91


  Alignments for each domain:
  == domain 1  score: 87.1 bits;  conditional E-value: 2.7e-26
  MSA_GH10_xylanases  60 eaiikkdfgsltpeNsMKweaiepsrg…kfsFegadelvnfakk
ngkklRgHtlvWhsQlPswvssik…adket 131
                            +++ik +   ltpeN++K++++ +              +F++a  l
++a+k+g+k+ gH lvWhsQ+P+ ++++         +++e
        k141_2401341   3 MQLIKDQCSILTPENELKPDSVLDVSRsrrlaeedetavAVHFDAAKPLLDYARK
TGTKVHGHVLVWHSQTPEAFFHEGydtskplVTREV 93
                            6899***************9987666689**********9***************
*****************99998888999******** PP


  MSA_GH10_xylanases 132 llevlknhiktvv…grYkgkvyaWDVvNEilnedgs.lr.esvfyrv 175
                            +l +l+n+i++v+    + Y g +++WDVvNE++++ ++ +r  s++++v
        k141_2401341  94 MLGRLENYIREVLtqteEMYPGVIVSWDVVNEAIDDGTNwIRkGSKWTQV 143
                            ************9777778****************999875525888775 PP


>> k141_1105734
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !   85.5   0.1   8.4e-26   1.1e-25     148      310 ..       2     197 ..
1      210 [. 0.80


  Alignments for each domain:
  == domain 1  score: 85.5 bits;  conditional E-value: 8.4e-26
  MSA_GH10_xylanases 148 kgkvyaWDVvNEilnedgs…lres…vfyrvlgedyvkiafea
are…adpnakLyiNDYnlesasaklegmvklvk 219
```

```
                               g +y WDVvNE++ + +s                 +r+    f+  +g+dyv+ af
+ar+     ++ ++kL++NDYn+ +   k++++v+l+k
        k141_1105734    2
PGVIYCWDVVNEAIGDSASdwratdprhiriVRDGgpnYFQAYVGDDYVEYAFFCARNtvekLGADIKLFYNDYNMFMM-
EKRNAAVELIK 91
                             5889**********99988655555555544444233258899**********99
9977778999***********99.9********** PP


  MSA_GH10_xylanases 220 kllea…gvp.idGiGsqsHlsaga…psvaelkkalnalaslgveva
itELDia.leleateekleaqakdyvevvkaclevk 297
                             +++++   g p idG+G+q+ ++            + ++++
++++++s+g+ev++tE+ ++ ++  +++e+++ + + + ev+  +   +
        k141_1105734   92 SIQSYdpdGRPlIDGLGMQGYIGGYGtqsgclqeSHISDIRTSIRTYSSMGLEVQ
LTEMAVRnFDKSKAAEHADYYGRLFSEVFMKANTEE 182
                             *998622244459*****9998765556667777667899***************
*******77777888888888899999886665555 PP


  MSA_GH10_xylanases 298 kcv..gvtvWgvaDk 310
                             k    +v +Wg+ D+
        k141_1105734 183 KAPltAVCIWGLVDA 197
                             544489*****9986 PP


>> k141_8164561
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   86.2   0.0   5.2e-26   7.2e-26      59     164 ..       6     136 ..
1      139 [. 0.93


  Alignments for each domain:
  == domain 1  score: 86.2 bits;  conditional E-value: 5.2e-26
  MSA_GH10_xylanases  59 eeaiikkdfgsltpeNsMKweaiepsrg…kfsFegadelvnf
akkngkklRgHtlvWhsQlPswvssik…ad 128
                             ++++k++f  ltpeN++K++++ +  g                  F++a+ l
fa++ng k+ gHtl+Wh+Q+P  ++++          ++
        k141_8164561   6 LMKLMKEQFSILTPENELKPDSVLDVAGsqklvretgdetsvAVRFDAANGLLRF
ASNNGLKVHGHTLLWHNQTPVTFFHEGydsenplVT 96
                             57889*****************99999999***********9************
******************988877779999**** PP


  MSA_GH10_xylanases 129 ketllevlknhiktvv…grYkgkvyaWDVvNEilned 164
                             +e +l +++n+ik v+    + Y g v++WDV+NE++++
        k141_8164561  97 REVMLGRMENYIKGVMeymqETYPGVVVSWDVLNEAIDDG 136
                             ***************888889**************874 PP


>> k141_6868187
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
```

```
envfrom   env to    acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   85.6   0.0   7.6e-26     1e-25      78     250 ..      52     221 ..
23     223 .] 0.87


  Alignments for each domain:
  == domain 1  score: 85.6 bits;  conditional E-value: 7.6e-26
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEilnedgslr 168
                            w   ep++gk  + ++ +++++ + ng +++gH l+Wh     w+ + + ++e l
+ l+  i+  v+ Ykg +  WDV+NE++      r
        k141_6868187  52 WGRYEPEEGKTAYPETMAAAKWLRDNGVQVKGHPLCWHTACAPWLLKYS-
NEEILRRQLE-RIHRDVSAYKGVINLWDVINEVVIMPVFDR 140
                            77889************************************888.77777
76665.699999**************987766544 PP


  MSA_GH10_xylanases 169 .esvfyrvlged…yvkiafeaareadpnakLyiNDYnlesasaklegmvklv
kklleagvpidGiGsqsHlsagapsvaelkka 250
                            +    +r++ e+     v+  f aa+e+dp+a L iND+n+ +a
++l+++llea+vpi  iG+qsH + g +  ++l+
        k141_6868187 141 yDNAITRICIEKgrvgLVREVFAAAKETDPDAVLLINDFNTSEA------
YAQLIEDLLEADVPISAIGIQSHQHQGYWGLEKLNTV 221
                            26666666655333348**********************966…899**
******************99998776666655 PP


>> k141_5933602
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to    acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   85.7   0.1   7.1e-26   9.8e-26     233     335 ..       1     118 [.
1     120 [] 0.93


  Alignments for each domain:
  == domain 1  score: 85.7 bits;  conditional E-value: 7.1e-26
  MSA_GH10_xylanases 233 sqsHlsagapsvaelkkalnalaslgvevaitELDialele…a
teekleaqakdyvevvkaclevkkcv.gvtvWgvaD 309
                            +q+H+++  p+++e+ ka++ ++     +++tELDi+++ +
+++ +   q+++yv+++k++++ k+++ +vt+W+v+D
        k141_5933602   1 MQAHYNVYGPTMEEVDKAIQLYSTVVKHIHLTELDIRVNEDmggglrfrqgasqV
SDWERTLQQDQYVNLFKVLRKHKDVIdCVTFWNVSD 91
                            7************************99**********666679*******99987
77788899************************ PP


  MSA_GH10_xylanases 310 kdsWls.eespllfdenynpKpaynai 335
                            kdsWl  +++pllfdeny+pK+ay a+
        k141_5933602  92 KDSWLGtNNYPLLFDENYKPKQAYLAV 118
```

```
                              ****964889**************987 PP

>> k141_4348153
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !   85.4   1.3   8.8e-26   1.2e-25     130     240 ..        2     117 ..
1     120 [. 0.86

  Alignments for each domain:
  == domain 1  score: 85.4 bits;  conditional E-value: 8.8e-26
  MSA_GH10_xylanases 130 etllevlknhiktvvgr…YkgkvyaWDVvNEilnedgslresvfyrvlged
yvkiafeaareadp.nakLyiNDYnlesasaklegm 214
                         +++l++++n +kt  ++    Y +  ya+D+vNE+  e+gs+re
++++++g+dy+  af +a +++p ++ Ly+NDYn +    k++ +
       k141_4348153   2 DEMLSRMENMMKTGFEQleelgYIDLFYAYDIVNEAWMENGSMRENNWSKIIGDD
YLWYAFYYADKYAPeSIDLYYNDYNEQ---FKTQTL 89
                         67889999999988855444449999*****************************
***********6652689*******98…799*** PP

  MSA_GH10_xylanases 215 vklvkkllea..gvpidGiGsqsHlsag 240
                         ++ v++l+++  +  idG+G+q+Hl +
       k141_4348153  90 IDFVNTLKDEdgNYLIDGVGFQAHLYTT 117
                         *****9997632578*********9765 PP

>> k141_7416581
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !   85.4   0.0   8.7e-26   1.2e-25     208     313 ..        6     126 .]
1     126 [] 0.95

  Alignments for each domain:
  == domain 1  score: 85.4 bits;  conditional E-value: 8.7e-26
  MSA_GH10_xylanases 208 saklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgveva
itELDialele…ateekleaqak 284
                         + k+e ++++vkk+++agvpidGiG+q+H+++  p++++l  a++++ +l
++itELD++++ e           ++  +   q++
       k141_7416581   6 NGKRERIYNMVKKMKDAGVPIDGIGMQGHYNIYFPDEDQLDLAITRFKELVKHIH
ITELDLRMNNEsggqlmfsrgeakpMPGYMGTLQTD 96
                         479***************************************************
*******88879*********999877888899*** PP

  MSA_GH10_xylanases 285 dyvevvkaclevkkcv.gvtvWgvaDkdsW 313
                         +y++++k++++ ++++ +vt+W++ D+dsW
       k141_7416581  97 QYARLFKVFRKHADVIdNVTFWNLGDQDSW 126
```

```
                              *************************** PP


>> k141_328913
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   85.2   0.1     1e-25   1.4e-25     163     269 ..       2     107 ..
1     116 [. 0.89


  Alignments for each domain:
  == domain 1  score: 85.2 bits;  conditional E-value: 1e-25
  MSA_GH10_xylanases 163 edgslresvfyrvlgedyvkiafeaareadp.nakLyiNDYnlesasaklegmvk
lvkkllleag..vpidGiGsqsHlsagapsvaelkka 250
                         edgs+r+ ++y+++gedy+  af +a +++p ++ Ly+NDYn +   +k e++++
v++l++ +    idGiG+q+Hl +   + +++ +
        k141_328913   2 EDGSMRQNHWYDIIGEDYIWYAFYFADKYAPeSIDLYYNDYNEQ---
YKDEALCDFVQTLVDDDgrYLIDGIGMQAHLFTAD-DLNTYLEG 88
                         89***************************6652689*******98…7899****
****997652267**********999.79999999 PP


  MSA_GH10_xylanases 251 lnalaslgvevaitELDia 269
                         ++ la++g+ ++itELD+
        k141_328913  89 VDGLAKTGLKLQITELDLG 107
                         ****************86 PP


>> k141_5146991
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   85.2   0.6   1.1e-25   1.4e-25      67     169 ..       9     108 ..
2     137 .] 0.85


  Alignments for each domain:
  == domain 1  score: 85.2 bits;  conditional E-value: 1.1e-25
  MSA_GH10_xylanases  67 fgsltpeNsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPsw
vssikadketllevlknhiktvvgrYkgkvyaWDVv 157
                         ++++t+eN+ Kw +ie +rg+++++g d++ n+ak+ng + ++H+lvW sQ
P+w++  +   +  ++++ n+++ v ++Y + +   DVv
        k141_5146991   9
WNQITAENECKWASIEGTRGRYNWSGCDAAYNWAKNNGGHFKFHALVWGSQYPNWLNGLS--
AADTKTAITNWMDAVKQHYPD-LEMIDVV 96
                         79******************************************************
*9877..66667899**********86.8899*** PP


  MSA_GH10_xylanases 158 NEilnedgslre 169
                         NE+++  gs+ +


                              112
```

```
         k141_5146991  97 NEAIKSGGSYHS 108
                          ******999764 PP


>> k141_8183010
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   85.1   0.3   1.1e-25   1.5e-25     137     232 ..       1     100 [.
1     101 [] 0.90


  Alignments for each domain:
  == domain 1  score: 85.1 bits;  conditional E-value: 1.1e-25
  MSA_GH10_xylanases 137 knhiktvv…grYkgkvyaWDVvNEilnedgs.lresvfyrvlgedyvkiafe
aareadp.nakLyiNDYnlesasaklegmvklvkkl 221
                          +n+ik v       +Y g +++WDV+NE++++ ++ lr+s++ +++gedy + af
+ar+++p +++Ly+NDYn+   + kl g+v l+k+l
        k141_8183010    1
ENYIKAVFeateAQYPGIIVSWDVLNEAIDDGTNkLRNSNWKKIIGEDYPNYAFAYARKYAPeSVRLYYNDYNTAIP-
GKLAGIVTLLKSL 90
                          57888888666679****************98877******************
****665279**********99.9*********** PP


  MSA_GH10_xylanases 222 leagvpidGiG 232
                          +e g  idG G
        k141_8183010  91 IEDG-NIDGYG 100
                          *999.689987 PP


>> k141_8660669
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   84.8   0.0   1.3e-25   1.8e-25     231     337 ..       1     122 [.
1     125 [. 0.93


  Alignments for each domain:
  == domain 1  score: 84.8 bits;  conditional E-value: 1.3e-25
  MSA_GH10_xylanases 231 iGsqsHlsagapsvaelkkalnalaslgvevaitELDialele…
.ateekleaqakdyvevvkaclevkkcv.gvtvWgv 307
                          iG+q+H+++  p+++++ kal+ + +    +++tELDi+ ++e
++++   ++ a++y++v++++++ k+++ +vt+W++
        k141_8660669    1 IGMQGHYNIYGPKEEDVDKALELYKKVVDHIHVTELDIRANQEmggqlafsrdga
aVNDSLKQHLADQYARVFRVFRKHKDVIdCVTFWNL 91
                          9****************************99**********766689*********9
87888888899*********************** PP


  MSA_GH10_xylanases 308 aDkdsWls.eespllfdenynpKpaynaivk 337
```

```
                              +D+dsWl  +++pl fd +y+pK ay+ i +
          k141_8660669  92 SDRDSWLGqNNYPLPFDVDYKPKMAYEYIRD 122
                             ******963789**************99876 PP


>> k141_4173172
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   84.6   0.1   1.5e-25   2.1e-25      33     159 ..      23     169 .]
8     169 .] 0.91


  Alignments for each domain:
  == domain 1  score: 84.6 bits;  conditional E-value: 1.5e-25
  MSA_GH10_xylanases  33 ldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsr
g…kfsFegadelvnfakkngkklRgHtlvWh 115
                            da lk a  kyf  G++ +  ++++s  + +  ++++s+  eN+ K++a+
++g     k s +    ++ +f++kng  +RgHtlvWh
        k141_4173172  23 ADAGLKLAFGKYFrvGNIFNGMNVRNSALQGLALTNYNSIECENETKPDATLVQN
GstdtniKVSLNSCASIFDFCAKNGIGVRGHTLVWH 113
                            567788888899999***********9999999*******************999
98999889999*********************** PP


  MSA_GH10_xylanases 116
sQlPswvssik…adketllevlknhiktvv…grYkg.kvyaWDVvNE 159
                           sQ+P+w++++        ++ +t+ ++++++ik++      ++Y
++ya+DV+NE
        k141_4173172 114
SQTPQWFFKEGfnnngawVNSSTMDKRMESYIKNMFnaiqTQYPTlDLYAYDVCNE 169
*********9999999*9999*************99866667885448********9 PP


>> k141_7444673
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   84.4   0.2   1.8e-25   2.5e-25     151     253 ..       2     108 ..
1     112 [. 0.91


  Alignments for each domain:
  == domain 1  score: 84.4 bits;  conditional E-value: 1.8e-25
  MSA_GH10_xylanases 151 vyaWDVvNEilnedgs.lr…esvfyrvlged.yvkiafeaareadpn.akLyi
NDYnlesasaklegmvklvkklleagvpidGiGsqs 235
                           vya+DV NE + +dg  +r   +s++ rv g+d +v++af +ar+++p+
kL++NDYn + +  k++++++  kl+e gv idGiG+qs
        k141_7444673   2
VYAYDVANELFLNDGGgMRpadNSNWVRVYGDDsFVTKAFTYARKYAPKgCKLFLNDYNEYIP-
NKTNDIYNMAMKLKELGV-IDGIGMQS 90


                                  114
```

```
                        9********98777665777769********877***********888758****
******99.9***************7.9******* PP

  MSA_GH10_xylanases 236 Hlsagapsvaelkkalna 253
                         Hl+++ +   +++k++l++
         k141_7444673  91 HLDVNIKVLQSIKQQLKN 108
                         ******999999999985 PP


>> k141_8366699
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   84.5   0.1   1.7e-25   2.3e-25     180     287 ..       1     108 [.
1     111 [] 0.91


  Alignments for each domain:
  == domain 1  score: 84.5 bits;  conditional E-value: 1.7e-25
  MSA_GH10_xylanases 180 yvkiafeaareadpn.akLyiNDYnlesasaklegmvklvkklleagvpidGiGs
qsHlsaga…psvaelkkalnalaslgvevaitEL 266
                         +vk+af +ar+++p+  kL++NDYn +    k++ ++++ k+l e gv
+dG+G+qsH++a++       +++ +a++++ s g ev+itEL
         k141_8366699   1 FVKQAFTYARQYAPEgCKLFYNDYNEYWD-HKRDCIYRMCKELYEDGV-
LDGVGMQSHINANWggfSGYDNYVAAMKKYLSIGCEVQITEL 89
                         8**********777648********9977.****************8.8*****
*******98876789999****************** PP

  MSA_GH10_xylanases 267 Dialeleateekleaqakdyv 287
                         Di+ +e+ +  +++qak+y
         k141_8366699  90 DIS--VENGTYSAQDQAKKYC 108
                         ***..7777788999999996 PP


>> k141_2038176
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   84.3   0.0     2e-25   2.7e-25      96     264 ..       9     174 .]
3     174 .] 0.83


  Alignments for each domain:
  == domain 1  score: 84.3 bits;  conditional E-value: 2e-25
  MSA_GH10_xylanases  96 lvnfakkngkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgk
vyaWDVvNEilnedgs…lresvfyrvlge.dyv 181
                         + f ++++ k++gH l+Wh    +w+ +   d++t+l+     i+  v+ +kg
+  WDV+NE++        +   + lg    v
         k141_2038176   9 TASFLQSKNVKVKGHPLCWHTVCADWLMKY--
DNQTILSKQLARIDREVQGFKGLIDMWDVINEVVIMPVFdkydNAITRICQELGRvPLV 97
```

```
                                  5678899*******************965..577777777789**********
**********97543321100333445566665259* PP


  MSA_GH10_xylanases 182 kiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsH
lsagapsvaelkkalnalaslgvevait 264
                              k+ f  a++ +p+a L +ND+n+    k e   +l++  l+agvpi  iG+qsH
+ g + +++l++ l+++++ g+ ++ t
        k141_2038176  98 KKVFDEAHACNPDAVLLLNDFNTSV---KYE---
ELIEGCLDAGVPITAIGIQSHQHQGYWGREKLEDVLTRFSRFGLPIHFT 174
                              *******************994…455…677899**************
*********************998876 PP


>> k141_475762
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to    acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   84.3   0.0   1.9e-25   2.6e-25     208     338 ..      3     144 ..
1     146 [. 0.89


  Alignments for each domain:
  == domain 1  score: 84.3 bits;  conditional E-value: 1.9e-25
  MSA_GH10_xylanases 208 saklegmvklvkklleagvpidGiGsqsHlsaga…psvaelkkalnalas
lgvevaitELDia..leleateekleaqakdyvevv 290
                              +ak+   +++ vk+++++g+pi+++Gsq+H++   +        s ++l++
++la+l++ ++itELDi     ++++++ le+q k+++e +
        k141_475762    3 KAKAGFLLEQVKRWVKNGIPIHCVGSQTHVEDTTtdkhfiGSPDSLRALAKELAK
LNIKLKITELDIGfkSGINVSQSDLERQGKTFREYL 93
                              4677778999********************98887777767889999999****
************954556799************** PP

  MSA_GH10_xylanases 291 kaclevkkcvgvtvWgvaDkdsWls…eespllfdenynpKpaynaivka 338
                              +++le ++  +  +Wgv+Dk sWl    +++ l++d+n+npKpa+++i+
        k141_475762   94 DIILEEPNADTYLIWGVSDKWSWLGglnRQKGLIYDDNLNPKPAFDSILVR 144
                              *******************985557777*************9865 PP


>> k141_4916380
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to    acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   82.5   0.1   6.8e-25   9.2e-25      46     191 ..     22     203 ..
4     206 .. 0.83


  Alignments for each domain:
  == domain 1  score: 82.5 bits;  conditional E-value: 6.8e-25
  MSA_GH10_xylanases  46 GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg…kfsFe
gadelvnfakkngkklRgHtlvWhs..QlPswvssi 125
```

```
                              G a    ++++++++++ ++f+slt  N+ K  ++ ++++         +
++++ad++ ++ak +g  +RgH lvW+   Q P +++++
          k141_4916380   22 GGAFGFWDMNNKTYMDFLGRHFNSLTCTNETKAYSLLDRNQcvrsedgmpRMNYA
NADRMIQWAKDHGIAVRGHVLVWDAvmQYPWFFHED 112
                              666666778899****************************999999*************
**********************9655999888877 PP


  MSA_GH10_xylanases 126 k…adketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…
…lres…vfyrvlgedyvkiafeaarea 191
                                 ++++ l + + + i++  +++ g +y WDVvNE++ + +s
+r+     f+  +g+dyv+ af +ar++
          k141_4916380 113 YdekkpfaspeVNRARLESYIDQVITHFEEKFPGVIYCWDVVNEAIGDSASdwra
ddprhiriVRDGgpnFFQAYVGDDYVEYAFLCARNT 203
                              79999997777777777777777777777889999***********999886555
5555655445433324788899*********999974 PP


>> k141_4333985
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   83.5   0.2   3.5e-25   4.8e-25      91     181 ..     10     113 ..
3     114 .] 0.90


  Alignments for each domain:
  == domain 1  score: 83.5 bits;  conditional E-value: 3.5e-25
  MSA_GH10_xylanases  91 egadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllevlkn
hiktvv…grYkgkvyaWDVvNEilnedgs.lr. 168
                             ++a  l  fa++n+ k+ gH lvWhsQ+P+ ++++        +++e +l
+l+n+i++v+     + Y g +++WDVvNE++++ ++ lr
          k141_4333985  10 SAATPLLRFAQRNNIKVHGHVLVWHSQTPEAFFHEGydtskpyVTREVMLGRLEN
YIREVLtrteEMYPGVIVSWDVVNEAIDDGTNwLRk 100
                             56677889*********************99998888999**9***********
******665566****************99998663 PP


  MSA_GH10_xylanases 169 esvfyrvlgedyv 181
                            s++y+v+ged++
          k141_4333985 101 TSNWYKVVGEDFL 113
                            799*********8 PP


>> k141_4570102
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   83.3   0.0   3.8e-25   5.2e-25      88     182 ..     26     133 ..
11     134 .] 0.91
```

```
  Alignments for each domain:
  == domain 1  score: 83.3 bits;  conditional E-value: 3.8e-25
  MSA_GH10_xylanases  88 fsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllev
lknhiktvv…grYkgkvyaWDVvNEilnedgs. 166
                         +F++a  l  fa++ g k+ gH lvWhsQ+P+ ++++        ++ke +l
+l+n+i++v+    + Y g +++WDVvNE++++ ++
        k141_4570102  26 VHFDAAKPLLRFAQSGGLKVHGHVLVWHSQTPEAFFHEGydsakplVSKEVMLGR
LENYIREVLtqteELYPGVIVSWDVVNEAIDDGTNw 116
                        6899**************************9999888899*************
********9666667****************99998 PP


  MSA_GH10_xylanases 167 lr.esvfyrvlgedyvk 182
                         lr  s++y+++ged+v+
        k141_4570102 117 LRtGSPWYKTIGEDFVN 133
                         77469**********96 PP


>> k141_3272949
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   83.2   0.0   4.1e-25   5.6e-25      24     112 ..      50     139 ..
28     140 .] 0.85


  Alignments for each domain:
  == domain 1  score: 83.2 bits;  conditional E-value: 4.1e-25
  MSA_GH10_xylanases  24 lesrqaaesldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsM
KweaiepsrgkfsFegadelvnfakkngkklRgHtl 112
                        +r+++e  d  lk a+k+yf  G av+++++++  + +++
++f+s+t+eN+MK++ +ep++g+f++e+ad+++nf++++g k+RgHtl
        k141_3272949  50 WGPRTIPEPTD-
GLKDAYKDYFkiGVAVNNRNVADPDQIKVVLREFNSITAENAMKPQPTEPRKGEFNWEDADKIANFCREHGIKMRGHTL
139
                        55666766666.799***************************************
*******************************9 PP


>> k141_1292909
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   82.5   0.0     7e-25   9.6e-25     169     290 ..       3     122 ..
1     135 [. 0.85


  Alignments for each domain:
  == domain 1  score: 82.5 bits;  conditional E-value: 7e-25
  MSA_GH10_xylanases 169 esvfyrvlgedyvkiafeaare.adpnakLyiNDYnlesasaklegmvklvkkll
eagvpidGiGsqsHlsagapsvaelkkalnalaslg 258
```

```
                               +s++y vlged++  af+aar+  +p   L++NDYn  ++ +k+++++
l+kkl+++++ +d +G+q+H+     ++  +++ a +a+a+lg
        k141_1292909    3 RSPWYAVLGEDFLPAAFRAARKgQAPGQTLCYNDYNAFDP-
VKRDAIIALLKKLQSENL-VDTMGMQGHYVQADMDIPACETAARAYAALG 91
                          69*******************889************99.*************9
9886.9*************9*************** PP


  MSA_GH10_xylanases 259 vevaitELDialeleateekleaqakdyvevv 290
                          + +++tELDi+ + +  e+  ++ a  y + +
        k141_1292909   92 LKLQVTELDIHCT-RGDEAGQRDLAVLYGNYF 122
                          **********933.322333334444444444 PP


>> k141_4512856
   #     score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   80.9   0.0   2.1e-24   2.9e-24     231     337 ..       1     123 [.
1     126 [. 0.94


  Alignments for each domain:
  == domain 1  score: 80.9 bits;  conditional E-value: 2.1e-24
  MSA_GH10_xylanases 231 iGsqsHlsagapsvaelkkalnalaslgvevaitELDialele…
..ateekleaqakdyvevvkaclevkkcv.gvtvWg 306
                          iG+q+H+++  p++++l+ka+n++++    ++itELD+++++e
++  +   q+++y++++k++++ k+++ +vt+W+
        k141_4512856    1 IGMQGHYNIYFPDEDQLEKAINRFSEIVKHIHITELDLRTNTEsggqlqfshgea
kpMAPYMQTLQTDQYARLFKVFRKHKDVIdNVTFWN 91
                          9****************************************887799********99
986677888999********************** PP


  MSA_GH10_xylanases 307 vaDkdsWls.eespllfdenynpKpaynaivk 337
                          + D+dsWl  ++ pl fdeny+pKp+y ai +
        k141_4512856   92 LGDRDSWLGvNNRPLPFDENYKPKPSYRAIRD 123
                          *******986889***************9976 PP


>> k141_1100704
   #     score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   80.8   0.0   2.2e-24     3e-24     185     309 ..       1     129 []
1     129 [] 0.86


  Alignments for each domain:
  == domain 1  score: 80.8 bits;  conditional E-value: 2.2e-24
  MSA_GH10_xylanases 185 feaare.adpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHls
agapsvaelkkalnalaslgvevaitELDialelea 274
```

```
                            fe+a++ ad+++ L++NDY + ++  k++ +++ + k l  +  +dG+G+qsHl
+ +p+ + +k al+++ +lg++++itELD++ + ++
        k141_1100704    1 FEFAKKyADSEVSLFYNDYETSEP-
WKRDFIIENILKPLIDKKLVDGMGLQSHLLMDHPDFEVYKTALEMYGALGIQIHITELDMH-NNDP 89
                         89999989**************99.99998877666666666789**********
****************************.6667 PP


  MSA_GH10_xylanases 275 teekleaqakdyvevvkaclevkk…cv.gvtvWgvaD 309
                         + e ++a a++y++ ++++ + kk    ++ +vt+W++ D
        k141_1100704   90 SGESMHALAQRYKQFFELYVDAKKtgkaNItSVTFWNIVD 129
                         78889999999999999988776542222788******987 PP


>> k141_9117506
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   80.5   0.0   2.9e-24   3.9e-24     100    260 ..     12    169 ..
2    171 .] 0.83


  Alignments for each domain:
  == domain 1  score: 80.5 bits;  conditional E-value: 2.9e-24
  MSA_GH10_xylanases 100 akkngkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvyaW
DVvNEilnedgs.lresvfyrvlge…dyvkiaf 185
                         +++g  l+gH l+Wh      w+ + + ++e + + l+  i+  v+ Ykg +
WDV+NE++      +  +r++ e      vk  f
        k141_9117506   12 LRERGVVLKGHPLCWHTACAPWLMQYS-NEEIMRRQLE-
RIHRDVSAYKGVIDLWDVINEVVIMPVFdKYDNAVTRICKEkgriRLVKEVF 100
                         578999*****************988.7777777775.699999**********
*****87654332445555555554222269***** PP


  MSA_GH10_xylanases 186
eaareadpnakLyiNDYnlesasaklegmvklvkkllleagvpidGiGsqsHlsagapsvaelkkalnalaslgve 260
                         aa+e dp+a L iND+n+  +        l++ lleagvpi  iG+qsH + g
+  ++l++ l+++++ g+
        k141_9117506 101 AAAKESDPDAVLLINDFNTSVS------
YEILLEGLLEAGVPISAIGIQSHQHQGYWGLEKLNDVLSRFSRFGLP 169
*******************977…4457899********************************99975 PP


>> k141_4280798
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   79.0   0.0   7.9e-24   1.1e-23     105    265 ..      2    159 ..
1    179 [. 0.83


  Alignments for each domain:
```

```
  == domain 1  score: 79.0 bits;  conditional E-value: 7.9e-24
  MSA_GH10_xylanases 105 kklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvyaWDVvNE
ilnedgs.lresvfyrvlge…dyvkiafeaare 190
                          ++gH l+Wh      w+ + + + e l + l+  i+  v+ ++g +
WDV+NE++          +  +r++ e     + vk  fe a++
        k141_4280798    2 VRVKGHPLCWHTACAPWLMNFS-NGEILRRQLE-
RIRRDVTAFRGVIDMWDVINEVVIMPVFdKYDNAITRICKEmgriKLVKAVFEEAKA 90
                          6799**************888.6666666665.699999**************
87543321333334444333222389********** PP


  MSA_GH10_xylanases 191
adpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitE 265
                          +p+a L iND+n+  +          l++ lleagvpi  iG+qsH + g +
+++l++ l+++++ g+ ++ tE
        k141_4280798   91 NNPDATLLINDFNTSAS------
YEILIEGLLEAGVPISAIGIQSHQHQGYWGEEKLRDVLERYSRFGLPIHFTE 159
**************9955…445799******************************************9 PP


>> k141_9056285
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   78.9   0.0   8.6e-24   1.2e-23     198     315 ..      1     121 [.
1     124 [. 0.88


  Alignments for each domain:
  == domain 1  score: 78.9 bits;  conditional E-value: 8.6e-24
  MSA_GH10_xylanases 198 yiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkaln
alaslgvevaitELDialeleateekleaqakdyve 288
                          ++NDY +     k++ +++ + k l ++  +dG+G+qsHl + +p+ + ++
aln++ +lg++++itELD++ + +++ + +++ a +y+e
        k141_9056285    1 FYNDYETALD-
WKRDLIIEKILKPLLEKKLVDGMGMQSHLLMDHPDPEVYSTALNMYGALGLQIHITELDMH-NADPSGDSMHRLAMRYQE
89
                          8*****9977.89998887666666667789***********************
****************.777888999999999999 PP


  MSA_GH10_xylanases 289 vvkaclevkk…cv.gvtvWgvaDkdsWls 315
                          +k++le kk    +v +vt+W+++D+dsWls
        k141_9056285   90 FFKIYLEAKKsgaaNVtSVTFWNLRDEDSWLS 121
                          99999988753333688************97 PP


>> k141_4506069
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
```

```
   1 !   78.2   0.2   1.4e-23   1.8e-23      89     192 ..       10     139 ..
6     149 .] 0.82


  Alignments for each domain:
  == domain 1  score: 78.2 bits;  conditional E-value: 1.4e-23
  MSA_GH10_xylanases  89 sFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllevl
knhiktvv…grYkgkvyaWDVvNEilnedgs.. 166
                         ++ +ad++ ++a+++g  +RgH lvW+  + sw++++         ad+et+
++l+++i++vv     +++ g vy WDVvNE++ +
         k141_4506069  10 NYVQADKMIAWAQEHGIRVRGHVLVWDAYMTSWFFHEDyddfkplADRETMRKRL
ESYIDQVVthfeEKFPGVVYCWDVVNEAIGDSDAec 100
                         899***********************************9999****************
********44444455679**********8754335 PP


  MSA_GH10_xylanases 167 …lres…vfyrvlgedyvkiafeaaread 192
                             lr +       +f + +gedyv+ +f +ar++
         k141_4506069 101 lagdarrLRTTrggqpnQFLESVGEDYVEYSFLCARNTV 139
                         555566655543333337****************9843 PP


>> k141_3574528
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------   ------- -------
------- -------    ----
   1 !   78.2   1.8   1.4e-23   1.9e-23     101     237 ..       1     144 [.
1     153 [. 0.80


  Alignments for each domain:
  == domain 1  score: 78.2 bits;  conditional E-value: 1.4e-23
  MSA_GH10_xylanases 101 kkngkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvyaWD
VvNEilnedgslresvf…yrvl…ge… 178
                         k+ng + ++H+lvW sQ P+w++  +   +  ++++ n+++ v ++Y + +
DVvNE+++  g++ + ++      +++   g
         k141_3574528   1 KQNGGHFKFHALVWGSQYPNWLNGLS--AADTKTAITNWMDAVKNHYPD-
LEMIDVVNEAIKSGGKYHS-NYgsqgnNNIIaalGGdngny 87
                         589999***************9877..66667899***********86.8899*
********999653.2222111233332333222333 PP


  MSA_GH10_xylanases 179
dyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHl 237
                         ++v+ af++are  p+a L +NDYn+ +    ++++ ++l++kl++a++p+d
G+q+H
         k141_3574528  88 EFVAEAFRMARERWPDAILIYNDYNTVQW--
QKNEGIDLIQKLKKANAPVDAYGLQAHD 144
7***********************9976..6667789******************4 PP


>> k141_8168242
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
```

```
envfrom   env to       acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   78.7   0.0   9.7e-24   1.3e-23     104     265 ..       1     159 [.
1     174 [. 0.87


  Alignments for each domain:
  == domain 1  score: 78.7 bits;  conditional E-value: 9.7e-24
  MSA_GH10_xylanases 104 gkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvyaWDVvN
Eilnedgslr.esvfyrvlged…yvkiafeaar 189
                           g +++gH l+Wh      w+ + + ++e + + l+  i+  v+ Y+g +
WDV+NE +     ++ +   +r++ e+     vk  f aa+
         k141_8168242   1 GVQVKGHPLCWHTVCAPWLMRYS-NEEIMRRQLE-
RIHRDVTAYRGVIDMWDVINEGVIMPVFYKyDNAITRICKEKgrirLVKEVFAAAK 89
                           5689**************998.7777777776.699999**************
*887777655366667777766433339********* PP


  MSA_GH10_xylanases 190
eadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitE 265
                           e +p+a L iND+n+  +         l++ lleagvpi  iG+qsH + g +
++l++ l+++++ g+ ++ tE
         k141_8168242  90 ESNPDATLLINDFNTSVS------
YEILLEGLLEAGVPISAIGIQSHQHQGYWGLDKLSDVLERFSRFGLPIHFTE 159
****************977…4457899*****************************************9 PP


>> k141_6221619
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom   env to       acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   78.1   0.1   1.5e-23     2e-23      58     143 ..       9     111 ..
1     113 [] 0.91


  Alignments for each domain:
  == domain 1  score: 78.1 bits;  conditional E-value: 1.5e-23
  MSA_GH10_xylanases  58 keeaiikkdfgsltpeNsMKweaiepsrg…kfsFe.gadelvnfak
kngkklRgHtlvWhsQlPswvssik…adket 131
                           + +++ikk+f+s+tpeN++K+++i +++         + +F  g+ +
f+++n   lRgHt+vW+sQ+P+w+++++      ++k+
         k141_6221619   9 SGADFIKKHFNSITPENELKPDSILNQQAcqsmgnnvntQVNFGsGTQATLRFCE
QNKIPLRGHTFVWYSQTPEWFFKENfgggnfVTKDV 99
                           46799*******************9**********999962567789****
******************************* PP


  MSA_GH10_xylanases 132 llevlknhiktv 143
                           + ++l+++ik+
         k141_6221619 100 MNKRLESFIKNT 111
                           *********986 PP


                              123
```

```
>> k141_7772334
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   77.3   0.0   2.7e-23   3.6e-23      78     242 ..      86     247 ..
83     254 .] 0.82


  Alignments for each domain:
  == domain 1  score: 77.3 bits;  conditional E-value: 2.7e-23
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEilnedgs.l 167
                           w   ep +g+  F ++ +++ + + +g +++gH l+Wh    +w+ + + ++e l
+ ++  i+  v  Ykg +  WDV+NE++
        k141_7772334   86 WGRYEPVEGQTAFPETMAAARWLRGQGVQVKGHPLCWHTVCADWLMQYS-
NEEILRRQIE-RIHREVAGYKGVIDLWDVINEVVIMPVFdK 174
                           677899*****************************************988.77777
77776.68888899**************875543213 PP


  MSA_GH10_xylanases 168
resvfyrvlge…dyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagap
242
                           +    +r++ +     + vk  f aa+e +p+a L iND+n+   +
l+++lleagvp+  iG+qsH + g +
        k141_7772334 175 YDNAVTRICKDkgrlQLVKEVFSAAKESNPEAILLINDFNTSAS------
YEMLLEELLEAGVPVSAIGIQSHQHQGYW 247
34444444433122389*********************9955…445899**************988765
PP


>> k141_7492124
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   76.8   0.1   3.6e-23   4.9e-23     200     297 ..       1     110 [.
1     111 [] 0.95


  Alignments for each domain:
  == domain 1  score: 76.8 bits;  conditional E-value: 3.6e-23
  MSA_GH10_xylanases 200 NDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnal
aslgvevaitELDialele…atee 277
                           NDYn  ++ +k++ ++++vkk+++agvpi+GiG+q+H+++  p+++++ +al+ +
+     +++tELDi+ ++e          +t++
        k141_7492124   1 NDYNECDP-VKSQRIYNMVKKMKDAGVPIHGIGMQGHYNIYGPKEEDIDEALSLY
KQVVSHIHVTELDIRANTEmggqlafsrdganVTDS 90
                           9*****99.*********************************************
***************777789*********988888 PP


                                       124
```

```
    MSA_GH10_xylanases 278 kleaqakdyvevvkaclevk 297
                           ++ a++y++v++++++ k
         k141_7492124  91 LKQHLADQYARVFRVFRKHK 110
                           889999********999876 PP


>> k141_2386947
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   75.4   0.2   9.9e-23   1.3e-22     121     218 ..       3     109 .]
1     109 [] 0.89


  Alignments for each domain:
  == domain 1  score: 75.4 bits;  conditional E-value: 9.9e-23
  MSA_GH10_xylanases 121 wvssik…adketllevlknhiktvvgrYkgkvyaWDVvNEilne…dgs.
.lresvfyrvlgedyvkiafeaareadpnakLyiND 201
                           w+ +++      ke++ + +k+hi+ +v +   vy W VvNE++ +    +g
lr+s  y++ ge+++ +a+e+a e dpna L++ND
         k141_2386947   3 WMYQDEkgnlLPKEEFYANMKHHIQAIVISFMYVVYCWEVVNEAVADcpvyQGRp
dLRNSAMYQIAGEEFIYTALEFALESDPNALLFYND 93
                           77777766677899999*****************************8844443335
6****************************** PP


  MSA_GH10_xylanases 202 Ynlesasaklegmvklv 218
                           Yn  ++ ak++ + +lv
         k141_2386947  94 YNDAEP-AKSQRIFNLV 109
                           **9999.9***999987 PP


>> k141_4192004
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   75.0   0.1   1.3e-22   1.8e-22      98     240 ..       6     145 ..
2     147 .. 0.82


  Alignments for each domain:
  == domain 1  score: 75.0 bits;  conditional E-value: 1.3e-22
  MSA_GH10_xylanases  98 nfakkngkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvy
aWDVvNEilnedgslr.esvfyrvlged…yvki 183
                           ++ +++g +++gH l+Wh    w+ + + ++e l + + + i+  v+ Ykg +
WDV+NE++     r +   +r++ e+    vk
         k141_4192004   6 KWLREKGVQVKGHPLCWHTACAPWLMRFS-NEEILRRQI-
ERIHRDVTAYKGVINLWDVINEVVIMPVFDRyDNAVTRICIEKgrvgLVKE 94
                           566899*******************988.666666666.5699999********
*******987665533244445555443233389** PP


                                   125
```

```
    MSA_GH10_xylanases 184
afeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsag 240
                          f aa+e +p+a L iND+n+ +a        ++l+++llea+vpi  iG+qsH +
g
        k141_4192004  95 VFAAAKESNPDAVLLINDFNTSEA------
YANLIEDLLEADVPIGAIGIQSHQHQG 145
********************965…99********************8765 PP


>> k141_7067511
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   74.9   0.0   1.4e-22   1.9e-22     232     336 ..      1     121 [.
1     124 [. 0.94


  Alignments for each domain:
  == domain 1  score: 74.9 bits;  conditional E-value: 1.4e-22
  MSA_GH10_xylanases 232 GsqsHlsagapsvaelkkalnalaslgvevaitELDialele…
.ateekleaqakdyvevvkaclevkkcv.gvtvWgv 307
                          G+q+H+++  p++++l+ka+n++++   ++itELD+++++e
+++ +   q+++y++++k++++ k+++ +vt+W++
        k141_7067511   1 GMQGHYNIYFPDEEKLEKAINRFSEIVNTIHITELDLRTNTEsggqlmfsrgeak
pQPAYMQTLQEDQYARLFKIFRKHKDVIkNVTFWNL 91
                          9*****************************************888799**********9
8888899999********************* PP


  MSA_GH10_xylanases 308 aDkdsWls.eespllfdenynpKpaynaiv 336
                          +DkdsWl  ++ pl fden+++K + + i
        k141_7067511  92 SDKDSWLGvNNHPLPFDENFKAKRSLQIIR 121
                          ******986899*************998775 PP


>> k141_6489240
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   74.8   2.3   1.5e-22   2.1e-22     127     211 ..      7      94 ..
2     103 .] 0.84


  Alignments for each domain:
  == domain 1  score: 74.8 bits;  conditional E-value: 1.5e-22
  MSA_GH10_xylanases 127 adketllevlknhiktvv…gr..YkgkvyaWDVvNEilnedgslresvfyrvl
gedyvkiafeaareadp.nakLyiNDYnlesasakl 211
                          +d+et+l++++ ik       +r  Y +  ya+DVvNE+ ne+g++res
+++++gedy+  af +a +++p ++ Ly+NDYn +++   +
        k141_6489240   7 VDRETMLSRMEAMIKGTFeelDRlgYLDLFYAYDVVNEAWNENGTMRESYWSQII
```

```
GEDYLWYAFYYADKYAPeSVALYYNDYNEQYK---A 94
                          799************988444225599*************************
***************6652689*******9865…3 PP


>> k141_6896667
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   74.4   0.1     2e-22   2.7e-22      85     164 ..      14     106 ..
7     111 .. 0.91


  Alignments for each domain:
  == domain 1  score: 74.4 bits;  conditional E-value: 2e-22
  MSA_GH10_xylanases  85 rgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adke
tllevlknhiktvv…grYkgkvyaWDVvNEiln 162
                           +   +F+ +d+l  fa+ +g ++R Htl Wh+Q+P w+++       a+ +
+l++l+n+i +v+    + + g vy+WDVvNE+++
        k141_6896667  14 HAAVDFTRVDALLSFARDHGISMRYHTLAWHNQTPVWFFKAGweddwnapsASGD
IMLARLENYILDVMhhvnTAFPGVVYTWDVVNEAIE 104
                           56779******************************999999999999999*
***************55555699**************9 PP


  MSA_GH10_xylanases 163 ed 164
                          d
        k141_6896667 105 PD 106
                         87 PP


>> k141_4196785
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   74.3   0.0   2.2e-22     3e-22     209     305 ..       5     115 .]
1     115 [] 0.95


  Alignments for each domain:
  == domain 1  score: 74.3 bits;  conditional E-value: 2.2e-22
  MSA_GH10_xylanases 209 aklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevai
tELDialele…ateekleaqakdy 286
                           +k++ ++++vkk+++agvpi+GiG+q+H+++  p+++++ ka +++++
+++tELD++ ++e          +t++  ++ a++y
        k141_4196785   5 VKSQRIYNMVKKMKDAGVPIHGIGMQGHYNIYGPKEEDIDKARSHYTQVVSHIHV
TELDLRANTEmggqlafsrdganVTDSLKQHLADQY 95
                           799**************************************************
******777789*********98888899999**** PP


  MSA_GH10_xylanases 287 vevvkaclevkkcv.gvtvW 305
```

```
                             ++v++++++ k+++ +vt+W
          k141_4196785   96 ARVFRVFRKHKDVIdCVTFW 115
                             ******************* PP


>> k141_2612004
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   73.9   0.0   2.7e-22   3.7e-22      78     232 ..      67     218 .]
32     218 .] 0.86


  Alignments for each domain:
  == domain 1  score: 73.9 bits;  conditional E-value: 2.7e-22
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEilnedgslr 168
                         w   ep++gk  F+++ +++++ ++ng +++gH l+Wh    w+ + + ++e l
+ l+  i+  v+ +kg +  WDV+NE++       r
        k141_2612004   67 WGRYEPEEGKTAFAETMAAAHWLRENGVQVKGHPLCWHTACAPWLLQYS-
NEEILRRQLE-RIHRDVNAFKGVINLWDVINEVVIMPVFDR 155
                         7788****************************************988.77777
77765.699999****************987665544 PP


  MSA_GH10_xylanases 169
.esvfyrv…lge.dyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiG 232
                         +    +r+   lg    vk  f aa+e dp+a L iND+n+ +a
++l+++llea+vpi  iG
        k141_2612004 156 yDNAITRIckdLGRvGLVKEVFAAAKECDPSATLLINDFNTSEA------
YAQLIEDLLEADVPISAIG 218
233333331114442589********************966…899**************99 PP


>> k141_3018142
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   73.8   0.0   3.1e-22   4.2e-22     142     334 ..       4     210 ..
1     214 [] 0.83


  Alignments for each domain:
  == domain 1  score: 73.8 bits;  conditional E-value: 3.1e-22
  MSA_GH10_xylanases 142 tvvgrYkgkvyaWDVvNEilnedgs..lre..svfyrvlge.dyvkiafeaarea
dpnakLyiNDYnlesasaklegmvklvkklleagvp 227
                         v+ +kg +  WDV+NE++         + + +   + lg    vk  f aa+e
dp+a L iND+n+ +a        +l+++llea+vp
        k141_3018142   4
RDVTAFKGVIDMWDVINEVVIMPVFdkYDNavTRICKDLGRiRLVKEVFAAAKESDPDAVLLINDFNTSKA------
YEHLIEELLEADVP 88
```

```
                               56789**************8754322113330033344554389**********
*************966…67889********* PP


  MSA_GH10_xylanases 228 idGiGsqsHlsagapsvaelkkalnalaslgvevaitELDia..lele…
…ateekleaqakdyvevvkaclevkkcv 300
                           i  iG+qsH + g +  ++l++ l+++++ g+ ++ tE  +
t e  e+qa++ +e+ +++    + +
         k141_3018142  89 IGAIGIQSHQHQGYWGLEKLNDVLERYSRFGLPIHFTENTLIsgDI-
MpghivdlndwqvnewpSTPEGEERQAREIAEMYSVLFAHPLVE 178
                           **********************************76552322.14778889
9999999988899999***********999999999 PP


  MSA_GH10_xylanases 301 gvtvWgvaDkdsWlseespllfdenynpKpayna 334
                           ++t+W++ D   Wl+  s +++++n   Kp+y+a
         k141_3018142 179 AITTWDFNDG-CWLKAPSGFVHEDNT-LKPSYHA 210
                           ********95.8*********99885.6888876 PP


>> k141_5942936
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   73.7   0.0   3.2e-22   4.4e-22     169     271 ..       9     110 ..
2     114 .] 0.93


  Alignments for each domain:
  == domain 1  score: 73.7 bits;  conditional E-value: 3.2e-22
  MSA_GH10_xylanases 169 esvfyrvlgedyvkiafeaare.adpnakLyiNDYnlesasaklegmvklvkkll
eagvpidGiGsqsHlsagapsvaelkkalnalaslg 258
                           +s+++   g+d++  af+aar+ a+p   L++NDYn  ++ +k+++++++k
l+++++ +d +G+q+H+    + + a+++ a +a+a+lg
         k141_5942936   9 RSPWFTAAGQDFLPAAFRAARRyAAPGQTLCYNDYNAFEP-
VKRDAILDVLKMLKAENL-VDTMGMQGHYLLPHLDIAACETAARAYAALG 97
                           79********************9899**************99.********999998
8775.9************************** PP

  MSA_GH10_xylanases 259 vevaitELDiale 271
                           + +++tELDi+ +
         k141_5942936  98 LKLQVTELDIHCN 110
                           **********943 PP


>> k141_4920788
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   72.5   0.0   7.3e-22   9.9e-22     108     236 ..       5     133 ..
2     137 .. 0.89
```

```
  Alignments for each domain:
  == domain 1  score: 72.5 bits;  conditional E-value: 7.3e-22
  MSA_GH10_xylanases 108 RgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvyaWDVvNEiln
edgs…lresvf.yrvlgedyvkiafeaareadp 193
                         ++H+lvW  Q P+w+ s +  k+ +++++ ++ + v ++Y  ++   DVvNE++
+    ++es      ++g d++ +afe+a+e  p
       k141_4920788    5 KFHALVWGAQYPGWLPSLS-PKDRFTAIV-SWFDAVKKKYP-
TMPMFDVVNEAVGTHQKdnpmIKESLGgGGKTGFDWLIKAFEMAYERWP 92
                         68**************999.899988776.68899****96.7899*******97
554444557888766789***************** PP


  MSA_GH10_xylanases 194 nakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsH 236
                         n  L +NDYn+ +     +++ ++lvk l++ag+pid  G qsH
       k141_4920788   93 NSILIYNDYNTFQW--NTNEFIELVKALRDAGAPIDAYGCQSH 133
                         **********9966..89*********************** PP


>> k141_5276643
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   72.5   0.0   7.4e-22     1e-21      40      143 ..       7      131 .]
2     131 .] 0.94


  Alignments for each domain:
  == domain 1  score: 72.5 bits;  conditional E-value: 7.4e-22
  MSA_GH10_xylanases  40 agkkyfGtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg…
…kfsFegadelvnfakkngkklRgHtlvWhs 116
                         +gk  fG+av q+ +++++ +a+++k+f  ltpeN++K++++ + +
+F++a  +  fak+ng k+ gH lvWhs
       k141_5276643    7 EGKFDFGAAVPQHAFMDANLKALMQKQFSILTPENELKPDSVLDVQAskslvrnt
gdetsvAVHFDAAKGVLSFAKANGLKVHGHVLVWHS 97
                         688899*****************************99998999*****
******************************** PP


  MSA_GH10_xylanases 117 QlPswvssik…adketllevlknhiktv 143
                         Q+P+ ++++        +++e +l +l+n+i++v
       k141_5276643   98 QTPEEFFHEGydrskpqVSREVMLGRLENYIREV 131
                         ***988877779999999************987 PP


>> k141_106785
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   72.3   0.0   8.5e-22   1.2e-21     144      337 ..       5      212 ..
1     215 [. 0.82
```

```
  Alignments for each domain:
  == domain 1  score: 72.3 bits;  conditional E-value: 8.5e-22
  MSA_GH10_xylanases 144 vgrYkgkvyaWDVvNEilnedgs..lresvf..yrvlge.dyvkiafeaareadp
nakLyiNDYnlesasaklegmvklvkklleagvpid 229
                             v+ +++ ++ WDV+NE++        + ++v    + lg    vk  f
aa+e+dp+a L iND+n+    +k e   +l++ llea+vpi
          k141_106785    5
VSAFRDVIRLWDVINEVVIMPEFdrYDNAVTriCKDLGRvGLVKEVFAAAKETDPDAVLLINDFNTS---PKYE---
QLIEALLEAEVPIS 89
                             7889************9765444113333322244455552589************
**********98…4555…567899******** PP


  MSA_GH10_xylanases 230 GiGsqsHlsagapsvaelkkalnalaslgvevaitELDia…lele…
…ateekleaqakdyvevvkaclevkkcvg 301
                             iG+qsH + g +  ++l++ l+++++ g+ ++ tE  +    l
e  e+qa++  e+  ++ + + + +
          k141_106785   90 AIGIQSHQHQGYWGLEKLNDVLERFSRFGLPIHFTENTLIsgeL--
Mapeivdlndwqvdewp SLPEYEERQAREISEMYTVLFSHPLVEA 178
                             ******************************88663322..256899999
**999997667788999999999999999999888* PP


  MSA_GH10_xylanases 302 vtvWgvaDkdsWlseespllfdenynpKpaynaivk 337
                             +t+W++ D   Wl+  s +++++n    Kp+y+a+ k
          k141_106785 179 ITTWDFNDG-CWLKAPSGFVHEDNS-EKPSYHALKK 212
                             *******95.8*********99885.6999998765 PP


>> k141_3963985
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   71.4   0.0   1.6e-21   2.2e-21      28     122 ..       9     113 .]
2     113 .] 0.84

  Alignments for each domain:
  == domain 1  score: 71.4 bits;  conditional E-value: 1.6e-21
  MSA_GH10_xylanases  28 qaaesldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKwea
iepsrg…kfsF.egadelvnfakkngk 105
                             ++a+s+d +lk+a k +f  Gt v+ +el+
++ikk+f+s+tpeN++K+++i ++++       + F +g+ +  +f+++ng
          k141_3963985   9 EVATSFD-TLKEAFKGKFriGTSVSPHELNG--
GGDFIKKHFNSITPENELKPDSIINQQQsqfqgnnvntQVVFgSGTSATLKFCESNGI 96
                             4556777.455555555555**********7..89*****************
*999999999999999777834567889******** PP


  MSA_GH10_xylanases 106 klRgHtlvWhsQlPswv 122
                             lRgHt+vW+sQ+P+w+
```

```
         k141_3963985   97 PLRGHTFVWYSQTPDWF 113
                           ***************6 PP


>> k141_6895992
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   71.4   0.0   1.6e-21   2.2e-21     185     295 ..       1     109 [.
1     112 [] 0.93


  Alignments for each domain:
  == domain 1  score: 71.4 bits;  conditional E-value: 1.6e-21
  MSA_GH10_xylanases 185 feaare.adpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHls
agapsvaelkkalnalaslgvevaitELDialelea 274
                           fe+ar+ a++ + Ly+NDYn+ ++ akl+g++kl+k+l+ +g  idG G+q H
++  ps ++++ a+++ a+lg+ + + ELD+     ++
        k141_6895992   1 FEFARKyAAEGVLLYYNDYNTAYT-AKLSGIIKLLKQLIPEG-
NIDGYGFQMHHGVAFPSIQQIRTAVETVAALGIRLRVSELDVG-VDNN 88
                           899**988899***********99.***************99.6**********
****************************.5567 PP


  MSA_GH10_xylanases 275 teekleaqakdyvevvkacle 295
                           +e+ +++qa+ y++v+k++
        k141_6895992  89 SESSFRRQAQYYADVMKILTA 109
                           7999***********998765 PP


>> k141_6566158
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   71.2   0.0   1.9e-21   2.6e-21     108     200 ..       1     116 []
1     116 [] 0.83


  Alignments for each domain:
  == domain 1  score: 71.2 bits;  conditional E-value: 1.9e-21
  MSA_GH10_xylanases 108 RgHtlvWhsQlPswvssik…adketllevlknhiktvv…grYkg.k
vyaWDVvNEilnedgs.lr…esvfyrvlg 177
                           RgHt+vW+sQ+P+w+++++      ++k+ + ++l++ ik+       ++Y +
+vya+DV+NE +++dg  +r        s + ++ g
        k141_6566158   1 RGHTFVWYSQTPDWFFRENfsnngayVSKDIMNKRLESMIKNTFealkTQYPNlD
VYAYDVCNELFKNDGGgMRpagnagsgGSTWVQIYG 91
                           9***************************8899999998888888744446775558
************999876633333333589****** PP


  MSA_GH10_xylanases 178 ed.yvkiafeaareadpn.akLyiN 200
                           +d +v  af++ar+++p   kLy+N
```

```
        k141_6566158   92 DDsFVVNAFKYARQYAPAgCKLYLN 116
                          877***********887538***99 PP


>> k141_5813762
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   71.0   0.2   2.1e-21   2.9e-21      35     163 ..      24     148 ..
18     152 .. 0.88


  Alignments for each domain:
  == domain 1  score: 71.0 bits;  conditional E-value: 2.1e-21
  MSA_GH10_xylanases  35 allkaagkkyfGtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfs
FegadelvnfakkngkklRgHtlvWhsQlPswvssi 125
                         a+l+++   k +G+++++ ++e     +    + ++++t eN+ Kw ++e
+rg+f++ g d++ n+ak+++ + ++H+lvW  Q Psw+++
       k141_5813762  24
AQLSSNPYKFLGNITTRGNVEAGGGVPSYYTLWNQITCENESKWSSVEGTRGSFNW-
GCDKAFNYAKQHNFTYKFHALVWGAQYPSWLEKL 113
                         55666666778999999999998888888999*********************
*.69****************************88 PP


  MSA_GH10_xylanases 126 kadketllevlknhiktvvgrYkgkvyaWDVvNEilne 163
                          +    ++  +++ n+ ++v ++Yk +     DVvNE++
       k141_5813762 114 S--AKERFAAITNWYNKVKTKYKT-LPLIDVVNEAVGT 148
                          7..455567899**********95.7889*****9965 PP


>> k141_4289006
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   71.0   0.2   2.2e-21     3e-21      44     195 ..       5     157 .]
2     157 .] 0.87


  Alignments for each domain:
  == domain 1  score: 71.0 bits;  conditional E-value: 2.2e-21
  MSA_GH10_xylanases  44 yfGtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelvn
fakkngkklRgHtlvWhsQlPswvssikadketlle 134
                          +G++++++++     +a   + ++++tpeN+ Kw ++e +r+++++ g d+
n+a +++   ++H+lvW  Q P+w+s+ +  ke  ++
       k141_4289006   5 FLGNITTRYNVDAGGGVAPYWQLWNQITPENESKWGSVEGTRNSYNW-
GCDRPFNYAIQHNFPYKFHALVWGAQYPNWLSNLS-IKERYQS 93
                          56899999999888888888999***********************.69*****
************************998.6666666 PP


  MSA_GH10_xylanases 135
```

```
vlknhiktvvgrYkgkvyaWDVvNEil..nedgs..lresvf.yrvlgedyvkiafeaareadpna 195
                          ++ ++ + v ++Y  ++   DVvNE++  +++g+  ++es     ++g d++
+afe+a+e  pna
         k141_4289006  94 IV-KWFNAVKNKYA-
TLPLIDVVNEAVgmHQNGNpmMKESLGgGGKTGYDWLIKAFEMAYERWPNA 157
55.57899*****7.68899******73356666878888876789***************988775 PP


>> k141_8764640
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !   70.5   0.0     3e-21   4.1e-21     229     338 ..     31     142 ..
23     144 .. 0.80


  Alignments for each domain:
  == domain 1  score: 70.5 bits;  conditional E-value: 3e-21
  MSA_GH10_xylanases 229 dGiGsqsHlsagapsvaelkkalnalaslgvevaitELDia.leleateeklea.
.qakdyvevvkaclevkkcvgvtvWgvaDkdsWlse 316
                           GiG+q+H+s ++ + +e+  al+ +a+   ev+itELD++ +  ++++e  +a
+++ ++++v    ++  +  +vt+Wg++D++sW+++
         k141_8764640   31 GGIGMQGHISDNN-
DLDEYITALRDYAAFAPEVHITELDVKcTCANVNREYYQAvfYKELFRRLVAERKNGVNLTSVTLWGLTDDNSWIRG
120
                          69********999.799999*****************************43344555544431
13445555555555555566**************** PP

  MSA_GH10_xylanases 317 espllfdenynpKpaynaivka 338
                         pl+f +++ +K++y+a+v a
       k141_8764640 121 ADPLVFRKDLSKKKSYDALVYA 142
                         *****************99876 PP


>> k141_5216115
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !   69.7   0.0   5.3e-21   7.3e-21     121     265 ..      4     145 ..
2     149 .. 0.85


  Alignments for each domain:
  == domain 1  score: 69.7 bits;  conditional E-value: 5.3e-21
  MSA_GH10_xylanases 121 wvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs.lresvfyr
vlge…dyvkiafeaareadpnakLyiNDYnles 206
                          w+ + +  +e++l++  + i+  ++ +kg +  WDV+NE++        +
+r++g+      vk  f aa+e+dp+a L iND+n+ +
       k141_5216115   4 WLMQYS--NEEILRRQLDRIRRDMSAFKGVIGLWDVINEVVIMPVFdKYDNAITR
ICGDlgrvGIVKEVFAAAKETDPDAVLLINDFNTSK 92
```

```
                             555554..45555555578999****************9876554277888899
98874433589*********************96 PP


  MSA_GH10_xylanases 207
asaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitE 265
                             a        +l+++ll+agvpi  iG+qsH + g +  ++l++ l+++++ g+
++ tE
        k141_5216115  93 A------
YEHLIEDLLQAGVPISTIGIQSHQHQGYWGLEKLNDVLERFSRFGLPIHFTE 145
6…67889****************************************9 PP


>> k141_2255399
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   68.3   0.1   1.4e-20     2e-20     126     235 ..       6     152 ..
1     153 [] 0.70


  Alignments for each domain:
  == domain 1  score: 68.3 bits;  conditional E-value: 1.4e-20
  MSA_GH10_xylanases 126 k…adketllevlknhiktvv…grYkgkvyaWDVvNEilnedgs…
…lr…esvfyrvlgedyvkiafeaare 190
                             +        ad+et+ ++lk++i++v+     +++ g +y WDVvNE++ +++
lr      + vf + +gedyv+ af +ar+
        k141_2255399    6 EydekkplADRETMRARLKSYIEQVIthfeEKFPGVIYCWDVVNEAIGDNSAewr
agdprhLRtkrsgsSNVFLDQVGEDYVEYAFLCARD 96
                             4555566689****************44444455679**********99876555
55566633222332459****************98 PP


  MSA_GH10_xylanases 191
…adpnakLyiNDYnlesasaklegmvklvkkll…eagv…pidGiGsqs 235
                               ++ +++L++NDYn+   +  k+++++ l+++++     g+
dGiG+q+
        k141_2255399  97 tvekLGADIRLFYNDYNMFIS-
EKRTAALALLQSVNtyaTDGTgeyrkLADGIGMQG 152
77778999**********9977.66665555555444111444322222578999886 PP


>> k141_2593531
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   69.8   0.0   5.1e-21     7e-21     209     303 ..       4     114 .]
1     114 [] 0.94


  Alignments for each domain:
  == domain 1  score: 69.8 bits;  conditional E-value: 5.1e-21
```

```
  MSA_GH10_xylanases 209 aklegmvklvkklleagvpidGiGsqsHlsaga.psvaelkkalnalaslgveva
itELDialele…ateekleaqak 284
                            ak++ ++++vkkl+++g+pi GiG+q+H+++   p+ ++ + a++++ +l
+++itE+Di+++ e                tee  ++q+k
          k141_2593531    4 AKRTYIYNMVKKLQAEGAPITGIGMQGHYNIFDnPTLEDFETAIKMYLELVDDIQ
ITEFDIRIHEEaggglqfsrgegqvYTEEIQQQQEK 94
                            8999************************987799*******************
*******666689***********9899999999** PP


  MSA_GH10_xylanases 285 dyvevvkaclevkkcv.gvt 303
                            +y++++++++++k+++ +vt
          k141_2593531  95 KYKDLFEIMRKYKDNIsCVT 114
                            ****************7876 PP


>> k141_1956985
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   69.4   0.0   6.8e-21   9.3e-21      40     140 ..      11     132 .]
3     132 .] 0.92


  Alignments for each domain:
  == domain 1  score: 69.4 bits;  conditional E-value: 6.8e-21
  MSA_GH10_xylanases  40 agkkyfGtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg…
…kfsFegadelvnfakkngkklRgHtlvWhs 116
                            +gk  fG+av q+ +++sk +a++ k+f  ltpeN++K++++ + +
+F++a  +  fak+ng k+ gH lvWhs
        k141_1956985  11 EGKFDFGAAVPQHAFMDSKLKALMLKQFSILTPENELKPDSVLDIQAskslvynt
gdetavVVHFDAAKGVLSFAKANGLKVHGHVLVWHS 101
                            577788******************************************999888899*****
******9**************************** PP


  MSA_GH10_xylanases 117 QlPswvssik…adketllevlknhi 140
                            Q+P+ +++++      a++e +l +l+n+i
        k141_1956985 102 QTPEDFFHESydkskplASREIMLGRLENYI 132
                            ***99998887888888889999999987 PP


>> k141_7099078
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   67.5   0.5   2.6e-20   3.5e-20     103     169 ..      17      97 ..
5     101 .. 0.89


  Alignments for each domain:
  == domain 1  score: 67.5 bits;  conditional E-value: 2.6e-20
```

```
   MSA_GH10_xylanases 103 ngkklRgHtlvWhsQlPswvssik…adketllevlknhiktvv…
.grYkgkvyaWDVvNEilnedgslre 169
                             ++ k+RgH lvWhsQ+P+w++++        ++ e + ++l+ +i+tv+
++Yk+  y WDVvNE++++ +   +
         k141_7099078  17 REIKVRGHVLVWHSQTPEWFFHEDydkskpyVSAELMDKRLEWYIRTVLtrytge
dSKYKDLFYGWDVVNEAISDATATYR 97
                             6789***************99999999999999***************888888
7789999***********99887544 PP


>> k141_8196762
    #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
    1 !   67.4   0.3   2.7e-20   3.7e-20     183     316 ..       1     126 [.
1     133 [. 0.91


  Alignments for each domain:
  == domain 1  score: 67.4 bits;  conditional E-value: 2.7e-20
  MSA_GH10_xylanases 183 iafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHl
sagapsvaelkkalnalaslgv.evaitELDialel 272
                             +afe+a+e  pna L +ND+n+ +     +++ ++lv++l++ag+pid  G qsH
+   s ++ k+++n+l ++     + itE Di  +
         k141_8196762    1 KAFELAYERWPNAILIYNDFNTFQW--
NTDQYIELVQTLRDAGAPIDAYGCQSHDLTDC-SLNTFKNSMNKLQNALKiPMYITEYDIG-TY 87
                             59******************9966..899**********************8
8877.89**********987555**********.33 PP


  MSA_GH10_xylanases 273 eateekleaqakdyvevvkaclevkkcvgvtvWgvaDkdsWlse 316
                             +      + q+++y+e + ++ e + c gvt+Wg     +W ++
         k141_8196762   88 D-----DNYQKQRYQEQFPVMWEADYCAGVTLWGHYYGCTWTEN 126
                             3…378999*****************999999876 PP


>> k141_7521840
    #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
    1 !   66.9   0.0   3.7e-20   5.1e-20     242     337 ..       3     113 ..
1     115 [. 0.92


  Alignments for each domain:
  == domain 1  score: 66.9 bits;  conditional E-value: 3.7e-20
  MSA_GH10_xylanases 242 psvaelkkalnalaslgvevaitELDialele…ateekleaqa
kdyvevvkaclevkkcv.gvtvWgvaDkdsWls.ee 317
                             p+++++ kal+ + +     +++tELDi+ ++e           +t++  ++
a++y++v++++++ k+++ +vt+W+++D+dsWl  ++
         k141_7521840    3 PKEEDVDKALELYKKVVSHIHVTELDIRANQEmggqlafsrdgasVTDSLKQHLA
```

```
DQYARVFRVFRKHKDVIdCVTFWNLSDRDSWLGqNN 93
                        567899*********************766689*********99889999999*
***************************96378 PP


  MSA_GH10_xylanases 318 spllfdenynpKpaynaivk 337
                        +pl fd +y+pK ay+ i +
        k141_7521840  94 YPLPFDVDYKPKMAYEYIRD 113
                        9*************99865 PP



>> k141_2114742
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !   66.8   0.2   4.1e-20   5.6e-20     176     324 ..      12     152 ..
9     161 .. 0.84


  Alignments for each domain:
  == domain 1  score: 66.8 bits;  conditional E-value: 4.1e-20
  MSA_GH10_xylanases 176 lgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidG
iGsqsHlsagapsvaelkka.lnalaslgvevaitE 265
                        +g d++ +af +a e  p+a L +NDYn+ +    +++ ++lv++l++ag+pid
G qsH +    s ++ k+a  +  ++l + +   tE
        k141_2114742  12 TGYDWLIKAFDMAGERWPDAILIYNDYNTFQW--
NTDEYIDLVRTLRDAGAPIDAYGCQSHDLTDC-SFTNFKNAeTKIQTALKMPMYSTE 99
                        799************************9966..899*****************
******87777.45555554144446677899**** PP


  MSA_GH10_xylanases 266
LDialeleateekleaqakdyvevvkaclevkkcvgvtvWgvaDkdsWlseespllfde 324
                         Di     ++++    q ++y+e +  + e++ c g+t+Wg    ++W ++ ++
l+ +
        k141_2114742 100 YDIG----TADD--
ALQLQRYQEQIPYMWEKPYCAGITLWGYVYGKTWTTDGNSGLYKN 152
****…3333..457789****************************99888877754 PP


>> k141_7473579
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !   66.7   0.0   4.4e-20     6e-20     114     265 ..       1     149 []
1     149 [] 0.82


  Alignments for each domain:
  == domain 1  score: 66.7 bits;  conditional E-value: 4.4e-20
  MSA_GH10_xylanases 114 WhsQlPswvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs.l
resvf…yrvlge.dyvkiafeaareadpnakLyi 199
```

```
                                      Wh         w+ + +  ++++ ++   + i+   ++ +k+ +   WDV+NE++
+         + +g      v+   f aa+e+dp+a L i
            k141_7473579    1 WHTACAPWLMQYS--
NQEIFRRQLERIHRDISAFKDVIGLWDVINEVVIMPVFdKYDNAItriCKEMGRvPLVRAVFAAAKETDPDAVLLI 89
                               9999999999887..555555555679999****************975443213
34444011444454258999*************** PP


  MSA_GH10_xylanases 200
NDYnlesasaklegmvklvkkllleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitE 265
                               ND+n+ ++           +l+++llea+vpi  iG+qsH + g +  ++l +
l+++++ g+ ++ tE
          k141_7473579   90 NDFNTSKS------
YEQLIESLLEADVPISAIGIQSHQHQGYWGLEKLYDVLERYSRFGLPIHFTE 149
                               *****965…678999*************************************99 PP


>> k141_722048
   #     score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   65.8   0.2    8e-20   1.1e-19     161     257 ..      13     111 ..
10      117 .] 0.89


  Alignments for each domain:
  == domain 1  score: 65.8 bits;  conditional E-value: 8e-20
  MSA_GH10_xylanases 161 lnedgslresvfyrvlg.edyvkiafeaareadp.nakLyiNDYnlesasakleg
mvklvkklle.agvpidGiGsqsHlsagapsvaelk 248
                               l++d++  +s + +v g ++++  af++a++++p +  Ly+NDYn  +a  k+
g+++l+++++ +g++i G G+q+H+s++apsv++++
          k141_722048   13 LSDDTHSSKSSWWKVYGsNEFIINAFKFANKYAPaSLELYYNDYNECDA-
KKRGGIIQLINDVKAaEGTRITGFGMQGHYSVNAPSVTQIE 102
                               78899999999999999458**********7773689*******9999.9****
*******986379********************** PP


  MSA_GH10_xylanases 249 kalnalasl 257
                               +a++ +a+
          k141_722048 103 EAVRDYAKV 111
                               ******986 PP


>> k141_381101
   #     score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   65.7   0.1   8.7e-20   1.2e-19     247     338 ..       2      99 ..
1      101 [. 0.86


  Alignments for each domain:
```

```
  == domain 1  score: 65.7 bits;  conditional E-value: 8.7e-20
  MSA_GH10_xylanases 247 lkkalnalaslgv.evaitELDia.lele…ateekleaqakdyvevvkaclev
kkcv.gvtvWgvaDkdsWlseespllfdenynpKpa 331
                         ++k+l+++ + +   v + ELD++ + +        e+  +qa
y++++++++e+++ +  vt+Wg  D++sW++e++pllf +n++pK+a
           k141_381101    2 VRKSLDMFRKIDGiKVSVSELDVQiNGISngkYDGEQEMTQAIFYARLFNLYKEN
ADLIeRVTFWGYKDNTSWRAESAPLLFKSNLEPKEA 92
                         67899999997555**********53333555555666778999**********
******************************* PP


  MSA_GH10_xylanases 332 ynaivka 338
                         y+a++++
         k141_381101   93 YYAVLNT 99
                         ****986 PP


>> k141_1792251
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   65.1   0.0   1.3e-19   1.8e-19     128     234 ..       3     106 .]
1     106 [] 0.92

  Alignments for each domain:
  == domain 1  score: 65.1 bits;  conditional E-value: 1.3e-19
  MSA_GH10_xylanases 128 dketllevlknhiktvvgrYkgkvyaWDVvNEilnedgslresvfyrvlgedyvk
iafeaareadpnakLyiNDYnlesas.akle..gmv 215
                         +++ l+++++n ++++++rYkgk +++DV NE+l+       s ++++lg+d  +
f++ +++dp+a L++NDY +e+ + ++++  + +
         k141_1792251    3 SNNDLMTAVQNRMNDLLTRYKGKFKHYDVNNEMLH------
GSFYQDKLGKDIRANMFKTSHQLDPDALLFVNDYHIEDGNdTRSTpeKYI 87
                         57889999***********************987…58899*********
***********************997665445999 PP


  MSA_GH10_xylanases 216 klvkklleagvpidGiGsq 234
                         + + +l+e+g+p+ GiG+q
       k141_1792251   88 EQILDLQEQGAPVGGIGIQ 106
                         9999*************98 PP


>> k141_6451618
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   65.1   0.6   1.3e-19   1.8e-19     127     207 ..      26     116 ..
5     120 .. 0.85


  Alignments for each domain:
```

```
  == domain 1  score: 65.1 bits;  conditional E-value: 1.3e-19
  MSA_GH10_xylanases 127 adketllevlknhiktvv…grYkgkvyaWDVvNEilnedgs…lresvf
yrvlgedyvkiafeaare.adpnakLyiNDYnlesa 207
                           +d++t+l++l+++i++++    + Y +++yaWDVvNE+++   +    lr+s
+y+v+g+d++  af++a++ +++  k y    Y ++ +
         k141_6451618   26 VDRDTMLKRLESYIHSMLdylykNGYAEQIYAWDVVNEAIELADKtetgLRNSYW
YQVIGDDFIYWAFRFANDaVADYSKQYAKEYGIDAS 116
                           79**************998888888***************9843322467******
****************98688999*******99976 PP


>> k141_1055552
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   64.8   0.1   1.6e-19   2.2e-19      43     161 ..       6     122 ..
1     123 [] 0.90


  Alignments for each domain:
  == domain 1  score: 64.8 bits;  conditional E-value: 1.6e-19
  MSA_GH10_xylanases  43 kyfGtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsFegadelv
nfakkngkklRgHtlvWhsQlPswvssikadketll 133
                          k +G++++ +++      ++   + ++++tpeN+ Kw ++e +rg+f++ g+d+
n+ak+ng + ++H+lvW  Q P+  ++++    +
         k141_1055552   6 KFLGNITTGYRMDPGGISEKYYQLWNQVTPENESKWGSVEGNRGNFNW-
GSDTPFNYAKQNGFTYKFHALVWGAQYPDRWFNENLPLPERF 95
                          556999999999888888888999***********************.68****
*******************87777887999999 PP


  MSA_GH10_xylanases 134 evlknhiktvvgrYkgkvyaWDVvNEil 161
                          ++++n+ ++v ++Y   ++   DVvNE++
         k141_1055552  96 NAIENWFNKVKSHYP-TLPMIDVVNEAV 122
                          9*************7.68899*****97 PP


>> k141_5292368
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   64.6   0.0   1.9e-19   2.7e-19      98     233 ..      11     143 .]
5     143 .] 0.80


  Alignments for each domain:
  == domain 1  score: 64.6 bits;  conditional E-value: 1.9e-19
  MSA_GH10_xylanases  98 nfakkngkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvy
aWDVvNEilnedgs.lresvfyrvlge…dyvki 183
                          ++ +++g  ++gH l+Wh    sw+ +   +ke l + l+  i+   v+ Y+g +
WDV+NE++        +   +r++ e      + vk
```

```
         k141_5292368  11 KWLRERGVAVKGHPLCWHTACASWLMQFD-NKEILRRQLE-
RIHRDVTAYRGVIDMWDVINEVVIMPVFnKYDNAITRICREkgriKLVKE 99
                            566789*******************888.7888887776.6999999*******
*******865443213344445555444222279*** PP


  MSA_GH10_xylanases 184 afeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGs 233
                          f aare +p+a L iND+n+  a         l++ lleagvp+  iG+
        k141_5292368 100 VFAAARESNPDAVLLINDFNTSAA------YEILLEGLLEAGVPVSAIGI 143
                          *******************966…44578899999**9999995 PP


>> k141_6278524
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   64.7   0.2   1.7e-19   2.4e-19      92     175 ..      18     117 ..
7     119 .] 0.82


  Alignments for each domain:
  == domain 1  score: 64.7 bits;  conditional E-value: 1.7e-19
  MSA_GH10_xylanases  92 gadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllevlknh
iktvv…grY.kgkvyaWDVvNEilnedgs.lr. 168
                         g+ +  +f++ ng +lRgHt+vW+ Q+P+w+++++       ++k+ +
++l+++ik+      + Y + +vya+DV+NE + ++g  lr
        k141_6278524  18 GTRATLKFCEYNGISLRGHTFVWYAQTPDWFFRENfqnngnyVNKNVMNQRLESF
IKNTFallkSDYpRLNVYAYDVCNELFVNNGGgLRp 108
                         4556789*****************************************************
***9944444442347*********99777665775 PP


  MSA_GH10_xylanases 169 ..esvfyrv 175
                           +s+++++
        k141_6278524 109 asNSKWMQI 117
                          557888876 PP


>> k141_7545186
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   64.7   0.8   1.8e-19   2.5e-19     105     165 ..      33     107 ..
10     108 .] 0.91


  Alignments for each domain:
  == domain 1  score: 64.7 bits;  conditional E-value: 1.8e-19
  MSA_GH10_xylanases 105
kklRgHtlvWhsQlPswvssik…adketllevlknhiktvv…grYkgkvyaWDVvNEilnedg 165
                          k+RgH lvWhsQ+P+w++++          ++k+++ ++l+ +i++++
++Yk+  y WDVvNE++++++
```

```
        k141_7545186  33
IKVRGHVLVWHSQTPEWFFHEDydaskdyVSKDEMNKRLEWYISSMLtyytgadSKYKDLFYGWDVVNEAISDNT 107
68*****************999999***9*****************9999999999****************9987 PP


>> k141_6791180
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   64.5   0.0     2e-19   2.7e-19      91     169 ..      21     112 ..
6     118 .] 0.84


  Alignments for each domain:
  == domain 1  score: 64.5 bits;  conditional E-value: 2e-19
  MSA_GH10_xylanases  91 egadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllevlkn
hiktvv…grY.kgkvyaWDVvNEilnedgs.lr 168
                         +g+ +  +f++ ng  lRgHt+vW+sQ+P+w+++++       ++k+ +
++l+++ik+         Y k +vya+DV NE + +dg  +r
        k141_6791180  21 SGTQTTLKFCEDNGIPLRGHTFVWYSQTPDWFFKENfnsggnyVSKDIMDQRLES
FIKNTFdllaRSYpKLEVYAYDVANELFLNDGGgMR 111
                         4677889****************************************9**********
***98766656675789*********9877765477 PP


  MSA_GH10_xylanases 169 e 169


        k141_6791180 112 P 112
                         5 PP


>> k141_715426
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   64.4   0.0   2.2e-19     3e-19     131     258 ..       5     131 ..
1     133 [] 0.80


  Alignments for each domain:
  == domain 1  score: 64.4 bits;  conditional E-value: 2.2e-19
  MSA_GH10_xylanases 131 tllevlknhiktvvgrYkgkvyaWDVvNEilnedgs.lresvfyrvlge…dy
vkiafeaareadpnakLyiNDYnlesasaklegmvk 216
                         +++++ + i+  v+ Ykg +  WDV+NE++       +   +r++ e
vk  f aa+e +p+a+L iND+n+        + +
        k141_715426   5 EIMRRQLERIHREVTAYKGVINLWDVINEVVIRPVFdKYDYAVTRICKEkgrvRL
VKEVFTAAKECNPEARLLINDFNTSA------DYEN 89
                         4444445679999***************9865432133333344444111358
9*********************984…5789 PP


  MSA_GH10_xylanases 217 lvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslg 258
```

```
                              l+++llea+vpi  +G+qsH + g + +++l++ l+++++ g
           k141_715426   90 LLEELLEADVPISAVGIQSHQHQGYWGGEKLEDVLERFSRFG 131
                              9************************************9987 PP


>> k141_7712328
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !   63.8   0.0   3.4e-19   4.6e-19     243     337 ..       3     113 ..
1     116 [. 0.92


  Alignments for each domain:
  == domain 1  score: 63.8 bits;  conditional E-value: 3.4e-19
  MSA_GH10_xylanases 243 svaelkkalnalaslgvevaitELDialele…ateekleaqa
kdyvevvkaclevkkcv.gvtvWgvaDkdsWls.ee 317
                            +++++ +a++++++l    +++tELDi++++e            ++   +
+++y++++k++++ k+++ +vt+W++ D+dsWl   ++
        k141_7712328    3 TEEDIDAAITKYSQLVKHIHVTELDIRMNTEmggqlrfsrgeakpVAPYMNTLLT
DQYNRIFKIFRKHKDVIdCVTFWNLGDRDSWLGvNN 93
                            678999*******************998899********99986677778889
9****************************98689 PP


  MSA_GH10_xylanases 318 spllfdenynpKpaynaivk 337
                            pl fdeny++Kpay ai +
        k141_7712328   94 HPLPFDENYKKKPAYFAIRD 113
                            9**************99976 PP


>> k141_6844872
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !   63.7   0.0   3.7e-19      5e-19     121     265 ..       4     145 .]
2     145 .] 0.79


  Alignments for each domain:
  == domain 1  score: 63.7 bits;  conditional E-value: 3.7e-19
  MSA_GH10_xylanases 121 wvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs.lresvfyr
v…lge.dyvkiafeaareadpnakLyiNDYnles 206
                            w+ + +  +e++ +   + i+  v+ Ykg +  WDV+NE++   +     +
+r+   +g  + k  fe a++ +pna L iND+n+
        k141_6844872    4 WLMQYS--NEEIFRLQLERIRREVSAYKGIIDIWDVINEVVIMPNFnKYDNAITR
IcrdMGRfKLAKAVFEEAKACNPNAVLLINDFNTSV 92
                            655544..444555555679999****************9765443144444444
41115552455666*****************98 PP


  MSA_GH10_xylanases 207
```

```
asaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitE 265
                        a        l++ ll+agvpi  iG+qsH + g +   ++l++ l+++++ g+
++ tE
         k141_6844872  93 A------
YEILLEGLLDAGVPIGAIGIQSHQHQGFWGPEKLHEVLERFSRFGLPIHFTE 145
7…4457899*****************************************99 PP
```

>> k141_1144944

```
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to      acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   63.8   0.0   3.4e-19   4.7e-19      236      337 ..       1      111 [.
1      113 [] 0.87
```

```
  Alignments for each domain:
  == domain 1  score: 63.8 bits;  conditional E-value: 3.4e-19
  MSA_GH10_xylanases 236 HlsagapsvaelkkalnalaslgvevaitELDialeleateekleaqakdyvevv
kaclevkk…cv.gvtvWgvaDkdsWls.e 316
                         Hl + +p+ ++++ al+++ +lg+ ++itELD++ + ++ ee  +a a++y+
++++l+ kk       + +vt+W++ D++sWl+       +
         k141_1144944    1 HLLMDHPDLDNYRTALEMYGALGLKINITELDMH-
NNDPGEESQKALAERYAAFFRIYLDAKKsgkaDItSVTFWNLLDENSWLTgfrreT 90
                         88999999***********************.66666788888899999999
888887652222577***************9999889 PP
```

```
  MSA_GH10_xylanases 317 espllfdenynpKpaynaivk 337
                         ++pllf  + ++K+ay+a+++
         k141_1144944  91 SYPLLFRGKCEAKEAYYAVLR 111
                         99***************986 PP
```

>> k141_3956792

```
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to      acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   63.6   0.1   3.9e-19   5.3e-19       36      163 ..      13      136 ..
4      148 .. 0.86
```

```
  Alignments for each domain:
  == domain 1  score: 63.6 bits;  conditional E-value: 3.9e-19
  MSA_GH10_xylanases  36 llkaagkkyfGtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrgkfsF
egadelvnfakkngkklRgHtlvWhsQlPswvssik 126
                         +l+++  k +G++++ +++          k ++++tpeN+ Kw +++ +r++f++
g d+  n+akkng + ++H+++W  Q Psw++s +
         k141_3956792  13
QLSTNPDKFLGNITTGYQMDAGGGIPQYYKLWNQVTPENESKWSSVQGNRNSFNW-
GCDTPFNYAKKNGFTYKFHAFLWGAQYPSWLESLS 102
```

```
                              5666677888999999999997777777899***********************
.68***************************998 PP

  MSA_GH10_xylanases 127 adketllevlknhiktvvgrYkgkvyaWDVvNEilne 163
                          k+   ++++++ + + ++Y  ++   DVvNE++
        k141_3956792 103 -IKDR-FDAVETWFDAIKSHYS-TLPLIDVVNEAVGM 136
                          .5555.5678***********6.78999*****9854 PP


>> k141_9442212
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   63.5   0.0    4e-19   5.4e-19     254      337 ..      4     102 ..
1     105 [. 0.89


  Alignments for each domain:
  == domain 1  score: 63.5 bits;  conditional E-value: 4e-19
  MSA_GH10_xylanases 254 laslgvevaitELDialele…ateekleaqakdyvevvkacle
vkkcv.gvtvWgvaDkdsWls.eespllfdenynpK 329
                          + +    +++tELDi+ ++e            +t++  +  a++y++v++++++
k+++ +vt+W+++D+dsWl  +++pl fd +y+pK
        k141_9442212   4 YKKVVSHIHVTELDIRANQEmggqlafsrdgaaVTDSLTQFLADQYARVFRVFRK
HKDVIdCVTFWNLSDRDSWLGqNNYPLPFDVDYKPK 94
                          55555699********766689**********9899999999*************
*******************963789*********** PP


  MSA_GH10_xylanases 330 paynaivk 337
                          ay+ i +
        k141_9442212  95 MAYEYIRD 102
                          ***99976 PP


>> k141_3380878
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   61.2   1.7    2e-18   2.8e-18     127      217 ..     10     122 ..
4     124 .] 0.77


  Alignments for each domain:
  == domain 1  score: 61.2 bits;  conditional E-value: 2e-18
  MSA_GH10_xylanases 127 adketllevlknhiktvv…grYkgkvyaWDVvNEilnedgs…
.lr…esvfyrvlgedyvkiafeaare…adpn 194
                          ad++t+ e+++++i++v+    +++ g +y WDVvNE++ +++s
+r   + vf + +g+dyv+ af +ar+    ++ +
        k141_3380878  10 ADQKTMRERVRSYIDQVMthfeEKFPGVIYCWDVVNEAIGDNASewdakdarhlr
tIRsgaSNVFLDRVGDDYVEYAFLCARDtvekLGAD 100
```

146

```
                              799**************44444455679**********9999866655655533
32233235899***************9877778999 PP


  MSA_GH10_xylanases 195 akLyiNDYnlesasaklegmvkl 217
                         + L++NDYn+ ++  k+++++ l
       k141_3380878 101 IHLFYNDYNMFMK-EKRTAALAL 122
                         **********988.677666655 PP


>> k141_5451066
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   63.3   0.1   4.8e-19   6.5e-19      88     170 ..      10     103 ..
6     111 .. 0.89


  Alignments for each domain:
  == domain 1  score: 63.3 bits;  conditional E-value: 4.8e-19
  MSA_GH10_xylanases  88 fsFegadelvnfakkngkklRgHtlvWhsQlPswvssik…adketllev
lknhiktvv…grYkgkvyaWDVvNEilnedgsl 167
                         ++++ad++ ++a+++g  +RgH lvW+  +  w++++        ad et+
++l  +i+ v+    +++ g +y WDVvNE++ + +
       k141_5451066   10 MNYSQADKMIAWAQERGIGVRGHVLVWDAYMTPWFFHEGydeknpiADPETMRAR
LACYIERVIthfeKKFPGVIYCWDVVNEAIGDSAAE 100
                         589***************************9999998889999*99********
**********4444455678***********998877 PP


  MSA_GH10_xylanases 168 res 170
                         +++
       k141_5451066 101 WNA 103
                         665 PP


>> k141_8646947
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   63.2   0.2   5.2e-19   7.1e-19      87     170 ..      23     118 ..
5     126 .. 0.86


  Alignments for each domain:
  == domain 1  score: 63.2 bits;  conditional E-value: 5.2e-19
  MSA_GH10_xylanases  87 kfsFegadelvnfakkngkklRgHtlvWhs..QlPswvssik…adk
etllevlknhiktvvgrYkgkvyaWDVvNEilnedg 165
                         + ++++ad++ ++++++gk +RgH lvW+   Q P +++++
+++e l + + + i++  +++ g +y WDVvNE++ + +
       k141_8646947   23 RMNYTNADKMIAWCQEHGKAVRGHVLVWDAvmQYPWFFHEDYdekkpfadpeVNR
ERLASYIDQVISHFEEKFPGVIYCWDVVNEAIGDSA 113


                                     147
```

```
                         789************************96559998888777999***8888888
8888888888888888999999*************999 PP

  MSA_GH10_xylanases 166 slres 170
                         s ++s
       k141_8646947 114 SDWRS 118
                         87766 PP


>> k141_5523933
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   63.0   0.0   5.9e-19      8e-19     247     338 ..       7     107 ..
2     109 .. 0.89


  Alignments for each domain:
  == domain 1  score: 63.0 bits;  conditional E-value: 5.9e-19
  MSA_GH10_xylanases 247 lkkalnalaslgvevaitELDialeleateekleaqakdyvevvkaclevkk…
.cv.gvtvWgvaDkdsWls…eespllfdenyn 327
                         ++ al+++ +lg++++itELD++ + ++++e ++a a +y++ +k++l+ k+
+ +vt+W+++D+dsWls     +++pllf    +
        k141_5523933   7 YRTALEMYGALGIQIHITELDMH-
NADPSDESMHALALRYQDFFKIYLDAKRsgkaDItSVTFWNLTDEDSWLSgfrreTSYPLLFKGRCE 96
                         5789*****************.8888999**************9999864222
2577**************999998999********* PP


  MSA_GH10_xylanases 328 pKpaynaivka 338
                         +K+ay+++++a
       k141_5523933  97 AKEAYYSVLEA 107
                         *******986 PP


>> k141_2683772
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   62.7   0.0   7.3e-19      1e-18     139     265 ..       8     133 ..
1     156 [. 0.83


  Alignments for each domain:
  == domain 1  score: 62.7 bits;  conditional E-value: 7.3e-19
  MSA_GH10_xylanases 139 hiktvvgrYkgkvyaWDVvNEilnedgslr.e…svfyrvlg.edyvkiafeaa
readpnakLyiNDYnlesasaklegmvklvkkllea 224
                         i+  v+ Y+g + WDV+NE++      r +  +  + lg   vk f
aa+e dp+a L iND+n+  a         l++ llea
        k141_2683772   8
RIHRDVTAYRGVIDMWDVINEVVIMPVFDRyDnaiTRICKQLGrIRLVKEVFAAAKESDPDAVLLINDFNTSVA------


                               148
```

```
YEILLEGLLEA 92
                             57778999**************9765444331300133344442589********
****************987…4457899**** PP


  MSA_GH10_xylanases 225 gvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitE 265
                         gvpi  iG+qsH + g +  ++l++ l+++++ g+ ++ tE
        k141_2683772   93 GVPISAIGIQSHQHQGYWGLDKLNDVLTRFSRFGLPIHFTE 133
                         ****************************************9 PP


>> k141_8386520
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   62.2   0.0     1e-18   1.4e-18     140     265 ..       6     130 ..
3     143 .. 0.84


  Alignments for each domain:
  == domain 1  score: 62.2 bits;  conditional E-value: 1e-18
  MSA_GH10_xylanases 140 iktvvgrYkgkvyaWDVvNEilne.dgslresvfyrvl…ge.dyvkiafeaar
eadpnakLyiNDYnlesasaklegmvklvkklleag 225
                         i+  v+ ++g++  WDV+NE++   d + +   +r++    g    vk  f
aa++a+p+a L iND+nl +     + ++l+++ l+ag
        k141_8386520    6
IHRDVSAFRGTIDIWDVINEVVIMpDFDRYDNAVTRICrryGRvPLVKEVFAAAKAANPEALLLINDFNLSE------
KYADLIRECLDAG 90
                         6667899*************8754144444444444443111442479********
****************94…58999********* PP


  MSA_GH10_xylanases 226 vpidGiGsqsHlsagapsvaelkkalnalaslgvevaitE 265
                         vp+   iG+q+H + g + v++l++ l+++   g+ ++ tE
        k141_8386520   91 VPVGAIGLQTHQHQGYMGVEKLNDILKRFETIGLPLHFTE 130
                         ***********************************99 PP


>> k141_6460686
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   62.1   0.7   1.1e-18   1.5e-18      89     169 ..       1      93 [.
1     102 [. 0.85


  Alignments for each domain:
  == domain 1  score: 62.1 bits;  conditional E-value: 1.1e-18
  MSA_GH10_xylanases  89 sFegadelvnfakkngkklRgHtlvWhs..QlPswvssik…adket
llevlknhiktvvgrYkgkvyaWDVvNEilnedgsl 167
                         ++++ad++ ++++++gk++RgH lvW+   Q P +++++          +++e
l + + + i++  +++ g +y WDVvNE++ + +s
```

```
        k141_6460686    1 NYTQADQMLKWCQAHGKQVRGHVLVWDAvmQYPWFFHEDYdaskpfasqeVNRER
LASYIDQVITHFEEKFPGVIYCWDVVNEAIGDSASD 91
                          699*********************9655999888877799****777777778
8888888888888999999***********999884 PP


  MSA_GH10_xylanases 168 re 169
                          ++
        k141_6460686  92 WR 93
                          43 PP



>> k141_5470296
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   61.9   0.8   1.3e-18   1.8e-18      64     163 ..      19     116 ..
1     123 [. 0.82


  Alignments for each domain:
  == domain 1  score: 61.9 bits;  conditional E-value: 1.3e-18
  MSA_GH10_xylanases  64 kkdfgsltpeNsMKweaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQl
Ps.wvssikadketllevlknhiktvvgrYkgkvya 153
                          + ++++tpeN+ Kw ++e +r++++++ +d+  n+ak+++ + ++H+lvW sQ
P+ w++   ++   ++   +++ ++ ++v  +Y   ++
        k141_5470296  19 YTLWNQITPENESKWGSVEGNRNNYNWA-
SDTPFNYAKNHNFTYKFHALVWGSQYPDrWFN-SSMPVDERYKAMVKWFDEVKRHYP-ELPM 106
                          5668*********************7.7*********************
*73555.555888889999999999999996.6888 PP


  MSA_GH10_xylanases 154 WDVvNEilne 163
                          DVvNE++
        k141_5470296 107 IDVVNEAVGM 116
                          9*****9864 PP



>> k141_2343559
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   61.7   0.0   1.5e-18     2e-18     202     309 ..       1     105 []
1     105 [] 0.96


  Alignments for each domain:
  == domain 1  score: 61.7 bits;  conditional E-value: 1.5e-18
  MSA_GH10_xylanases 202 YnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalas
lgvevaitELDialeleateekleaqakdyvevvka 292
                          Yn+  + akl g++kl+k+l+e+g  idG G+q H+s + ps
a++++a++++a+lg+ + + ELDi    ++e+ l +q+++++e++++
```

```
        k141_2343559    1 YNTPVP-AKLAGITKLLKQLMEEG-
NIDGYGFQMHYSNNDPSIAQITNAVDQIAALGLKLRVSELDIG--ASMSESGLMQQKARFKEIMQL 87
                          899988.***************99.6*****************************
**************..6778899************** PP

  MSA_GH10_xylanases 293 clevkkcv.gvtvWgvaD 309
                         +l+++++   +v vWg++D
        k141_2343559  88 MLQYADQTeAVQVWGLTD 105
                         *******99*******98 PP


>> k141_2370290
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   60.9   0.0   2.6e-18   3.5e-18     140     309 ..       6     191 ..
3     194 .] 0.83


  Alignments for each domain:
  == domain 1  score: 60.9 bits;  conditional E-value: 2.6e-18
  MSA_GH10_xylanases 140 iktvvgrYkgkvyaWDVvNEilnedgs.lresvfyrvlged…yvkiafeaar
eadpnakLyiNDYnlesasaklegmvklvkklleag 225
                         i+   v+ +k+ + WDV+NE++        +   +r++ ++     +k+ f
a+e +p+a L +ND+n+   +        l+   l+ag
        k141_2370290   6
IDREVTGFKEVIDMWDVINEVVIMPIFdKYDNAITRICKDKgrvgLIKTVFDKAHECNPDATLLLNDFNTSIN------
YEILIDGCLNAG 90
                         7888999**************86543321344444444433222239*********
***************966…44578999**** PP

  MSA_GH10_xylanases 226 vpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDia..lele…
…ateekleaqakdyvevvkaclevkkc 299
                         vpi  iG+qsH + g + +++l++ l++++  g+ ++ tE  +      ++
t e  ++qa++ +e+ +++ e + +
        k141_2370290  91 VPISAIGIQSHQHQGYWGKEKLNEVLDRFSTFGLPIHFTENTLIsgEIMPayied
lndwqvdewpSTPEGEKRQADQIEEMYRILFEHPLV 181
                         *****************************876634333389999
********9988899999**************9999 PP

  MSA_GH10_xylanases 300 vgvtvWgvaD 309
                          ++t+W+ +D
        k141_2370290 182 EAITTWDYRD 191
                         9******999 PP


>> k141_1425005
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
```

151

```
    ------- -------     ----
   1 !   60.6   0.0   3.1e-18   4.2e-18      60      146 ..       6      111 ..
2     122 .] 0.89


  Alignments for each domain:
  == domain 1  score: 60.6 bits;  conditional E-value: 3.1e-18
  MSA_GH10_xylanases  60 eaiikkdfgsltpeNsMKweaiepsrg…kfsFegadelvnfakk
ngkklRgHtlvWhsQlPswvssik…adket 131
                         +++ik +   ltpeN++K++++ +            F++a  l
fa++ng k+ gH l+WhsQ+P+ ++++      +++e
        k141_1425005   6 MQLIKDQCSILTPENELKPDSVLDVSAsrklaqedetavAVRFDAAKPLLRFAQA
NGIKVHGHVLIWHSQTPEAFFHEGydpqkpiVSREV 96
                        789*****************988777788*********9**************
****************999988889********** PP


  MSA_GH10_xylanases 132 llevlknhiktvvgr 146
                         +l++++n+i++v+++
        k141_1425005  97 MLARMENYIREVLTQ 111
                         ************954 PP



>> k141_4636443
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   60.2   0.0   4.1e-18   5.6e-18     232      323 ..       2      128 .]
1     128 [] 0.93


  Alignments for each domain:
  == domain 1  score: 60.2 bits;  conditional E-value: 4.1e-18
  MSA_GH10_xylanases 232 GsqsHlsagapsvaelkkalnalaslgvevaitELDia.lele…
…ateekleaqakdyvevvkaclevkk 298
                         G+q H  a+   + +e+k++++a+a+lg+ +++tELDi+ + +
+t e+l+a ++ yv+++ +++++++
        k141_4636443   2 GMQQHHFAKP-
DLDEIKRSIEAYAALGLRLHVTELDISlMAVMnqtdrrlkpgdpgfdeyikevtkPTPENLGAISDMYVKLFAIYRSYSD
91
                        9999988776.8*****************************733335889********
*********99999********************* PP


  MSA_GH10_xylanases 299 cv.gvtvWgvaDkdsWls…eespllfd 323
                         ++ +vt+WgvaD+++Wl+          +++pllf+
        k141_4636443  92 VIdCVTTWGVADDNTWLDffglapgipkiKQYPLLFN 128
                         *****************9999999999999996 PP



>> k141_8841745
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
```

```
   ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !   60.0   0.0   4.8e-18   6.6e-18     261     337 ..       3      94 ..
1      97 [. 0.89


  Alignments for each domain:
  == domain 1  score: 60.0 bits;  conditional E-value: 4.8e-18
  MSA_GH10_xylanases 261 vaitELDialele…ateekleaqakdyvevvkaclevkkcv.g
vtvWgvaDkdsWls.eespllfdenynpKpaynaiv 336
                         +++tELDi+ ++e            ++++   +  a++y++v++++++ k+++
+vt+W+++D+dsWl  +++pl fd +y+pK ay+ i
        k141_8841745   3 IHVTELDIRANQEmggqlafsrdgaaVNDSLKQYLADQYARVFRVFRKHKDVIdC
VTFWNLSDRDSWLGqNNYPLPFDVDYKPKMAYEYIR 93
                         89*******766689*********9766777777899******************
***********963789**************9987 PP


  MSA_GH10_xylanases 337 k 337
                         +
        k141_8841745  94 D 94
                         6 PP


>> k141_8150841
   #     score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
  ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !   59.7   0.0   5.8e-18   7.9e-18     243     329 ..       2     103 .]
1     103 [] 0.92


  Alignments for each domain:
  == domain 1  score: 59.7 bits;  conditional E-value: 5.8e-18
  MSA_GH10_xylanases 243 svaelkkalnalaslgvevaitELDialele…ateekleaqak
dyvevvkaclevkkcv.gvtvWgvaDkdsWls.ees 318
                         +++++ kal+ + +     +++tELDi+ ++e           +t++   +
a++y++v++++++ k+++ +vt+W+++D+dsWl  +++
        k141_8150841   2 KEEDVDKALELYKQVVNHIHVTELDIRANTEmggqlafsrdgavVTDSLKQFLAD
QYARVFRVFRKHKDVIdCVTFWNLSDRDSWLGqNNY 92
                         568999**********99**********777789**********8888888889**
***************************963789 PP


  MSA_GH10_xylanases 319 pllfdenynpK 329
                         pl fd +y+pK
        k141_8150841  93 PLPFDVDYKPK 103
                         **********9 PP


>> k141_4955497
   #     score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
```

```
   ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !   59.6   0.0   6.4e-18   8.8e-18     140     269 ..       7     135 ..
4     188 .] 0.73

  Alignments for each domain:
  == domain 1  score: 59.6 bits;  conditional E-value: 6.4e-18
  MSA_GH10_xylanases 140 iktvvgrYkgkvyaWDVvNEilnedgslr.esvfyrvl…ge.dyvkiafeaar
eadpnakLyiNDYnlesasaklegmvklvkklleag 225
                           i+  v+ + g v  WDV+NE++       r +   +r++  g    vk
feaa++a+p+a L iND+nl +       ++l+++ l+ag
        k141_4955497   7
IQRDVSAFAGVVDIWDVINEVVIMPEFDRyDNAITRICkryGRvPLVKEVFEAAKAANPKALLLINDFNLSDR------
YADLIRDCLDAG 91
                             66678899************9876555441444444441113324799*******
***************976…8999********* PP

  MSA_GH10_xylanases 226 vpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDia 269
                           vpi  iG+q+H + g +  ++l++ l+++   g+ ++ tE  +
        k141_4955497  92 VPIGAIGLQTHQHQGYMGAEKLNEVLRRFEVFGLPLHFTENTLV 135
                           ***********************************96655 PP


>> k141_83729
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------    ----
   1 !   59.5   0.0   6.8e-18   9.2e-18     129     258 ..       5     133 ..
1     135 [] 0.79


  Alignments for each domain:
  == domain 1  score: 59.5 bits;  conditional E-value: 6.8e-18
  MSA_GH10_xylanases 129 ketllevlknhiktvvgrYkgkvyaWDVvNEilnedgslr.esvfyrvlge…
dyvkiafeaareadpnakLyiNDYnlesasaklegm 214
                           +t+l+     i+  v+ + g +  WDV+NE++       r +   +r++ e
vk+ f aa+e+dp+a L iND+n+    +k e
           k141_83729   5 DKTILDKQLARIHRDVTAFAGVIDVWDVINEVVIMPVFDRyDNAITRICKElgrv
GLVKKVFDAAKETDPDAVLLINDFNTS---PKYE-- 90
                             44444444467899999*************98765543324444444332223
59*********************98…4555.. PP

  MSA_GH10_xylanases 215 vklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslg 258
                           +l+  ll+a+vpi  iG+qsH + g +  ++l++ l+++++ g
           k141_83729  91 -ELIAALLDADVPISAIGIQSHQHQGYWGAEKLNDVLERFSRFG 133
                           .567899************************************9987 PP


>> k141_7140457
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
```

```
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   59.0   0.0   9.3e-18   1.3e-17     229     322 ..      26     121 ..
19     122 .] 0.79


  Alignments for each domain:
  == domain 1  score: 59.0 bits;  conditional E-value: 9.3e-18
  MSA_GH10_xylanases 229 dGiGsqsHlsagapsvaelkkalnalaslgvevaitELDia.leleateeklea.
.qakdyvevvkaclevkkcvgvtvWgvaDkdsWlse 316
                           GiG+q+H+s ++ + +e+  al+ +a+   ev+itELD++ +  ++++e  +a
+++ +++++   ++  +  +vt+Wg++D++sW+++
        k141_7140457  26 GGIGMQGHISDNN-
DIDEYITALRDYAAFAPEVHITELDVKcTCSNVNREYYQAvfYKELFERLIAERRNGVNLTSVTLWGLTDDNSWIRG
115
                           69********999.899**********************43334444444431
14455566666666666667*************** PP


  MSA_GH10_xylanases 317 espllf 322
                           pl+f
        k141_7140457 116 ADPLVF 121
                           *****9 PP


>> k141_3315131
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   58.8   0.3   1.1e-17   1.5e-17      87     169 ..       9     103 ..
2     115 .. 0.82


  Alignments for each domain:
  == domain 1  score: 58.8 bits;  conditional E-value: 1.1e-17
  MSA_GH10_xylanases  87 kfsFegadelvnfakkngkklRgHtlvWhs..QlPswvssik…adketll
evlknhiktvv…grYkgkvyaWDVvNEilnedg 165
                           + ++++ad++ ++a++ +  +RgH lvW+   Q P +++++         ad et
++l ++i++v+    +++ g vy WDVvNE++ +
        k141_3315131   9 RMNYTNADKMIQWAQSGNIGVRGHVLVWDAvmQYPWFFHEDYdekkpfADAETNR
ARLASYIDQVIthfeEKFPGVVYCWDVVNEAIGDSP 99
                           679***********************96559998888777999***7777777
777777777733336666789**********9988 PP


  MSA_GH10_xylanases 166 slre 169
                           s ++
        k141_3315131 100 SDWR 103
                           7554 PP


>> k141_2330025


                           155
```

```
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   57.7   0.0   2.4e-17   3.3e-17     240     336 ..       4     116 ..
1     119 [. 0.89


  Alignments for each domain:
  == domain 1  score: 57.7 bits;  conditional E-value: 2.4e-17
  MSA_GH10_xylanases 240 gapsvaelkkalnalaslgvevaitELDialele…ateekle
aqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls 315
                         p++++l+ka+n++ +     ++itELD+++++e              ++
q+++y++++k++++ k+++ +vt+W+++DkdsWl
        k141_2330025   4 YFPEEDQLEKAINRFKEIVNIIHITELDLRTNTEtggqlrfsrgeakpQAPYIGT
LQEDQYARLFKIFRKHKDVIkNVTFWNLSDKDSWLG 94
                         567899************99**********777789********99754445557
79999*************************98 PP


  MSA_GH10_xylanases 316 .eespllfdenynpKpaynaiv 336
                          ++ pl fden+++K + + i
        k141_2330025  95 vNNHPLPFDENFKAKRSLQIIR 116
                         6899***********998775 PP


>> k141_7170802
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   57.5   0.0   2.8e-17   3.8e-17     248     336 ..       3     107 ..
1     111 [. 0.93


  Alignments for each domain:
  == domain 1  score: 57.5 bits;  conditional E-value: 2.8e-17
  MSA_GH10_xylanases 248 kkalnalaslgvevaitELDialele…ateekleaqakdyve
vvkaclevkkcv.gvtvWgvaDkdsWls.eespllf 322
                         a++++a+l    ++itELD+++++e              +++   +
q+++y+++++++++ k+++ +vt+W+++D+dsWl   ++ pl f
        k141_7170802   3 DTAISRFAELVKHIHITELDLRTNTEsggqlmfargevvpQPSYIATIQEDQYAR
IFRVFRKHKDVIdNVTFWNLSDRDSWLGvNNHPLPF 93
                         5799*****************888799**********9888899999*******
************************986899**** PP


  MSA_GH10_xylanases 323 denynpKpaynaiv 336
                         d+n+++K + + i
        k141_7170802  94 DQNFKAKRSLQIIR 107
                         *******998876 PP


>> k141_4678575
```

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```
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   57.3   0.0   3.1e-17   4.3e-17     246     337 ..       2     109 ..
1     112 [. 0.89


  Alignments for each domain:
  == domain 1  score: 57.3 bits;  conditional E-value: 3.1e-17
  MSA_GH10_xylanases 246 elkkalnalaslgvevaitELDialele…ateekleaqakdy
vevvkaclevkkcv.gvtvWgvaDkdsWls.eespl 320
                         +l+ka+n++++    ++itELD+++++e            ++      q+++y
+++k++++ k+++ +vt+W++ D+dsWl   ++ pl
        k141_4678575    2 QLEKAINRFSEIVNIIHITELDLRTNTEqggqlmfsrgeakpQAGYIGTLQEDQY
SRIFKIFRKHKDVIdNVTFWNLGDRDSWLGvNNHPL 92
                         7899********99************777789********9874333445679999*
***************************986899** PP


  MSA_GH10_xylanases 321 lfdenynpKpaynaivk 337
                         fdeny+pK +++ i +
        k141_4678575  93 PFDENYRPKRSFYIIKN 109
                         ************98876 PP


>> k141_446825
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   57.1   0.0   3.6e-17   4.9e-17     181     338 ..      15     181 ..
7     183 .. 0.87


  Alignments for each domain:
  == domain 1  score: 57.1 bits;  conditional E-value: 3.6e-17
  MSA_GH10_xylanases 181 vkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqs
HlsagapsvaelkkalnalaslgvevaitELDia.. 269
                         v+  f aare +p+a L iND+n+ +a        +l+++lleagvpi
iG+qsH + g +  ++l++ l+++++ g+ ++ tE  +
        k141_446825  15 VTEVFAAARESNPDAVLLINDFNTSKA------
YEHLIEDLLEAGVPIGTIGIQSHQHQGYWGLEKLNDVLERFSRFGLPIHFTENTLIsg 99
                         7788*****************966…67889*****************
****************************765423 PP


  MSA_GH10_xylanases 270 lele…ateekleaqakdyvevvkaclevkkcvgvtvWgva
DkdsWlseespllfdenynpKpaynaivka 338
                                                 t e  e+qa++  e+  ++ + + + ++t+W++
D   Wl+  s ++ ++n   Kp y+a+++
        k141_446825 100 DI-
MpahivdlndwqvdewpSTPEGEERQAREISEMYTVLFSHPLVEAITTWDFNDG-CWLKAPSGVVREDN-
```

SEKPVYHALMNL 181
```
                              22.146778899999**9998899999***********999999999********
95.8**99999887766.568999988875 PP
```

>> k141_5811690

```
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   57.3   0.0   3.2e-17   4.4e-17      39     123 ..      45     143 ..
14     145 .] 0.89
```

  Alignments for each domain:
  == domain 1 score: 57.3 bits; conditional E-value: 3.2e-17
  MSA_GH10_xylanases 39 aagkkyfGtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg…
…kfsFegadelvnfakkngkklRgHtlvWh 115
```
                              ag+  fG+a+ q  + + k ++++ ++f  ltpeN++K++a+ +  g
F++a+ l  fa++ng k+ gHtl+Wh
```
        k141_5811690 45 YAGRFDFGAAAPQMAFLDPKWTKLMSEQFSILTPENELKPDAVLDVAGsqklvre
tgdetsvAVRFDAANGLLRFAANNGLKVHGHTLLWH 135
```
                              3466677*******************************99999999****
*******9*************************** PP
```

  MSA_GH10_xylanases 116 sQlPswvs 123
```
                              +Q+P+ ++
```
        k141_5811690 136 NQTPATFF 143
```
                              ****8765 PP
```

>> k141_3933205

```
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   56.9   0.2   4.2e-17   5.8e-17     117     185 ..      47     120 ..
42     121 .] 0.88
```

  Alignments for each domain:
  == domain 1 score: 56.9 bits; conditional E-value: 4.2e-17
  MSA_GH10_xylanases 117
QlPswvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgs…lresvfyrvlgedyvkiaf
185
```
                              +P++v +   +ke++ + lk hi+tvv+rYk+ +y WDVvNE++++ ++
+r+s+ y+++g++++k af
```
       k141_3933205 47 KVPKYVPA---
TKEEFYDSLKVHINTVVNRYKDVIYCWDVVNEAMSDANNpdasyedsFRKSQAYQLCGDEFIKNAF 120
```
57888884…569***************************9876555667777*****************9 PP
```

>> k141_3884755

```
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   55.7   0.6   9.4e-17   1.3e-16     127     230 ..       5     128 .]
1     128 [] 0.76


  Alignments for each domain:
  == domain 1  score: 55.7 bits;  conditional E-value: 9.4e-17
  MSA_GH10_xylanases 127 adketllevlknhiktvvgrYkgk…vyaWDVvNEilnedgs…lr…
…esvfyrvlge.dyvkiafeaareadpn.ak 196
                         ++ +t+ ++++++ik++   Yk +      +ya+DV+NE++n+ +      lr
+s + rv g+  +v++af +ar+++p+  +
        k141_3884755   5 VNSATMDKRMESYIKNMFAAYKTQypqlnLYAYDVCNEVINDGTAnqggLRptng
tngqngSSAWVRVYGNnSFVEKAFTYARQYAPEgCQ 95
                         57899**************999986444448**********85444444443322
222233699*****9636**********777648* PP


  MSA_GH10_xylanases 197 LyiNDYnlesasaklegmvklvkklleagvpidG 230
                         L++NDYn   a+ k++ +++++ k l+a+  idG
        k141_3884755  96 LFYNDYNEF-ANDKQNCIINTILKPLQAKGLIDG 128
                         *******87.66999999988777666666776 PP


>> k141_173967
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   56.7   0.2   4.9e-17   6.7e-17     121     240 ..       3     119 ..
1     121 [] 0.78


  Alignments for each domain:
  == domain 1  score: 56.7 bits;  conditional E-value: 4.9e-17
  MSA_GH10_xylanases 121 wvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgslr.esvfyr
vlge…dyvkiafeaareadpnakLyiNDYnles 206
                         w+ +   d++t+l+   n i+  v  +kg +  WDV+NE++      r +
+r++ e    + vk  f aa++a+p+a L iND+nl +
        k141_173967   3 WLLKY--DNKTILDKQLNRIHRDVIAFKGVINMWDVINEVVIMPVFDRyDNAITR
ICREygqvNLVKEVFDAAKSANPDAVLLINDFNLSD 91
                         66644..4556666666789999999*************9876655442444444
44332223689*****************96 PP


  MSA_GH10_xylanases 207 asaklegmvklvkklleagvpidGiGsqsHlsag 240
                         +         ++l+ k leagvpi  iG+q+H + g
        k141_173967  92 K------YAELIDKCLEAGVPIGAIGLQTHQHQG 119
                         5…8899****************8776 PP


>> k141_4004474
```

```
    #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   56.6   0.2   5.3e-17   7.3e-17     101     206 ..       3     111 ..
1     116 [. 0.80


  Alignments for each domain:
  == domain 1  score: 56.6 bits;  conditional E-value: 5.3e-17
  MSA_GH10_xylanases 101 kkngkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvyaWD
VvNEilnedgslr.esvfyrvl…ge.dyvkiafe 186
                         +++g k++gH l+Wh    +w+ +    ++t+l+   + i+  v+ +kg +
+WDV+NE++     r +  +r++   g + vk  f
        k141_4004474   3 RSHGVKVKGHPLCWHTVCADWLMKYD--
NATILQKQLDRINRDVSAFKGVIDYWDVINEVVIMPVYDRyDNAITRICkdlGRiKLVKEVFD 91
                         689*****************9665..66666666678****************
****99776664424444444311143379****** PP


  MSA_GH10_xylanases 187 aareadpnakLyiNDYnles 206
                         aa++a+p+  L iND+nl +
        k141_4004474  92 AAKAANPDSVLLINDFNLSE 111
                         *****************975 PP


>> k141_1992987
    #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   56.5   0.4   5.7e-17   7.7e-17     200     316 ..       1     109 [.
1     113 [. 0.89


  Alignments for each domain:
  == domain 1  score: 56.5 bits;  conditional E-value: 5.7e-17
  MSA_GH10_xylanases 200 NDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnal
aslgv.evaitELDialeleateekleaqakdyvev 289
                         NDYn +    l++ + lv++l++ag+pid  G qsH  +   sv+++++al++
++    + itELDi +     +  ++q+k+y+++
        k141_1992987   1 NDYNSFTW--DLDNYITLVRTLRDAGAPIDAYGNQSHDVTDI-
SVSNMENALKKQQDALQmPMFITELDIDI------ASDDQQKKQYENI 82
                         99*98855..999*********************87777.9********998
876544**********3…33468999***** PP


  MSA_GH10_xylanases 290 vkaclevkkcvgvtvWgvaDkdsWlse 316
                         + ++ e + c gvt+Wg      +W+++
        k141_1992987  83 FPLMWEADYCAGVTLWGYVLGATWVTN 109
                         **********************976 PP


>> k141_3542429


160
```

```
    #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom   ali to
 envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------   ------- -------
------- -------    ----
   1 !   56.1   0.0   7.1e-17   9.7e-17     140      265 ..       6      130 .]
 2     130 .] 0.84


  Alignments for each domain:
  == domain 1  score: 56.1 bits;  conditional E-value: 7.1e-17
  MSA_GH10_xylanases 140 iktvvgrYkgkvyaWDVvNEilnedgs.lresvfyrvlge…dyvkiafeaar
eadpnakLyiNDYnlesasaklegmvklvkklleag 225
                           i+  v Y+g +  WDV+NE++         +   +r++ e      vk  f
aa+e +p a L iND+n+  +        l++ lleag
          k141_3542429    6
IHRDVAAYRGVISLWDVINEVVIMPVFdKYDNAITRICREkgriRLVKEVFAAAKESNPGAVLLINDFNVSVS------
YEILLEGLLEAG 90
                          6667889************8755433244555556555 4222269*********
***************977…4457899***** PP


  MSA_GH10_xylanases 226 vpidGiGsqsHlsagapsvaelkkalnalaslgvevaitE 265
                           vpi  iG+qsH + g +  ++l++ l+++++ g+ ++ tE
          k141_3542429   91 VPISAIGIQSHQGYWGLEKLNDVLERFSRFGLPLHFTE 130
                           ***********************************99998 PP


>> k141_961282
    #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom   ali to
 envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------   ------- -------
------- -------    ----
   1 !   56.1   0.1   7.2e-17   9.8e-17     176      269 ..       5       96 ..
 3     102 .] 0.90


  Alignments for each domain:
  == domain 1  score: 56.1 bits;  conditional E-value: 7.2e-17
  MSA_GH10_xylanases 176 lgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidG
iGsqsHlsagapsvaelkkalnalaslgv.evaitE 265
                           +g d++ +afe+a+e  p+a L +NDYn  +      ++ + lv++l++ag+pid
G qsH +   s++elk+al++  ++     + itE
          k141_961282    5 TGYDWLIKAFELAYERWPDAILIYNDYNSIRW--
DIDAYITLVQTLRDAGAPIDAYGNQSHDVTDI-SQSELKSALKKQQDALKmPMYITE 92
                           799***********************9865..899***************
******87777.9********999876555****** PP


  MSA_GH10_xylanases 266 LDia 269
                           LDi
          k141_961282   93 LDID 96
                           ***8 PP
```

```
>> k141_1952417
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   55.4   0.0   1.2e-16   1.6e-16     130     258 ..     12     139 .]
2     139 .] 0.77


  Alignments for each domain:
  == domain 1  score: 55.4 bits;  conditional E-value: 1.2e-16
  MSA_GH10_xylanases 130 etllevlknhiktvvgrYkgkvyaWDVvNEilnedg.slresvfyrvlge…d
yvkiafeaareadpnakLyiNDYnlesasaklegmv 215
                         e +le   + i+  v+ +kg + +WDV+NE++    + +   +r++ +
v+  feaa+e +p    L iND+n+++a
        k141_1952417  12 EVILEKQLQRIRRDVKAFKGVIDKWDVINEVVIMPEfDKYDNAITRICKQygrfG
LVSRVFEAAKEENPGSELLINDFNTTNA------YE 96
                         33444445799999**************97543313444444444443311124
799********************966…56 PP


  MSA_GH10_xylanases 216 klvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslg 258
                          lv+ ll+ gvpi  iG+qsH + g +  ++l+  l+++++ g
        k141_1952417  97 ILVEGLLDMGVPITTIGIQSHQHQGYWGLEKLHTVLERFSQFG 139
                         689********************************9865 PP


>> k141_3526777
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   55.1   0.0   1.5e-16     2e-16      78     204 ..     76     205 .]
73     205 .] 0.82


  Alignments for each domain:
  == domain 1  score: 55.1 bits;  conditional E-value: 1.5e-16
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEilnedgs.l 167
                         w   ep++gk  F + + +++ +++g +++gH l+Wh     w+ + + ++e l
+ l+  i+  v+ +kg v  WDV+NE++
        k141_3526777  76 WGRYEPEEGKTAFVPTMAGAQWLRERGVQVKGHPLCWHTVCAPWLMQYS-
NEEILRRQLE-RIRRDVTAFKGVVDLWDVINEVVIMPVFdK 164
                         77789*******************************************988.77777
77775.699999***************875433213 PP


  MSA_GH10_xylanases 168 resvf…yrvlge.dyvkiafeaareadpnakLyiNDYnl 204
                         +       r +g   vk  f aa+e +p a L iND+n+
        k141_3526777 165 YDNAItriCREMGRiRLVKEVFAAAKESNPGATLLINDFNT 205
                         33333011344443379*********************6 PP
```

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```
>> k141_3369516
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !   55.3   0.1   1.2e-16   1.7e-16     176     274 ..      19     115 ..
6     121 .] 0.87


  Alignments for each domain:
  == domain 1  score: 55.3 bits;  conditional E-value: 1.2e-16
  MSA_GH10_xylanases 176 lgedyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidG
iGsqsHlsagapsvaelkkalnalas.lgvevaitE 265
                        +g d++  afe+a+e  p+a L +NDYn+ +    +++ ++lv++l++ g+pid
G+qs   +++ +sv++lk+++++l + l + + itE
       k141_3369516  19 TGYDWLIRAFEMAYERYPDAILIYNDYNTFQH--
DTNNYLELVRTLRDFGAPIDAYGHQSQ-DVHDISVDKLKSSMKTLNDgLKMPMYITE 106
                        799************************976..99******************
*****7.566669***********9735669***** PP


  MSA_GH10_xylanases 266 LDialelea 274
                        LDi +  ++
       k141_3369516 107 LDIDVADDN 115
                        ***933332 PP


>> k141_1939943
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !   55.0   0.0   1.6e-16   2.2e-16     180     337 ..      22     188 ..
12     191 .. 0.89


  Alignments for each domain:
  == domain 1  score: 55.0 bits;  conditional E-value: 1.6e-16
  MSA_GH10_xylanases 180 yvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsq
sHlsagapsvaelkkalnalaslgvevaitELDia. 269
                         vk  f aa+e +p+a L iND+n+ +a       l++ lleagvpi
iG+qsH + g +  ++l++ l ++++ g+ ++ tE +
       k141_1939943  22 LVKEVFAAAKESNPDAVLLINDFNTSQA------
YEILIEGLLEAGVPISAIGIQSHQHQGYWGLEKLRDVLGRFSRFGLPIHFTENTLIs 106
                        68999*****************966…556899***************
****************************87663 PP


  MSA_GH10_xylanases 270 .lele…ateekleaqakdyvevvkaclevkkcvgvtvWgva
DkdsWlseespllfdenynpKpaynaivk 337
                         ++                t e  e+qa++  e+ +++   + + ++t+W++
D   Wl+  s l+ ++n   Kp+y a+++
       k141_1939943 107
```

```
gEIMPahivdlndwqvdswpSTPEGEERQAREISEMYSVLFAHPLVEAITTWDFNDG-CWLKAPSGLVREDN-
SEKPSYLALQN 188
                              4333389999********998899999**********9999999999********
95.8****999998777.57999988776 PP


>> k141_2689211
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   54.9   0.0   1.6e-16   2.3e-16     180      335 ..      21     185 ..
14      190 .. 0.87


  Alignments for each domain:
  == domain 1  score: 54.9 bits;  conditional E-value: 1.6e-16
  MSA_GH10_xylanases 180 yvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsq
sHlsagapsvaelkkalnalaslgvevaitELDia. 269
                           vk  f aare +p+a L iND+n+   +         l++ lleagvpid
iG+qsH + g +  ++l++ l+++++ g+ ++ tE +
        k141_2689211   21 LVKEVFDAARESNPDAVLLINDFNTSVS------
YEILLEGLLEAGVPIDAIGIQSHQHQGYWGLEKLNDVLERFSRFGLPIHFTENTLIs 105
                           58899*****************977…4457899**************
*****************************87663 PP


  MSA_GH10_xylanases 270 .lele…ateekleaqakdyvevvkaclevkkcvgvtvWgva
DkdsWlseespllfdenynpKpaynai 335
                           ++               t e  e+qa++  e+  ++   + + ++t+W++
D   Wl+  s ++ ++n   Kp+y a+
        k141_2689211 106
gEIMPahivdlndwqvdswpSTPEGEERQAREISEMYTTLFRHPLVEAITTWDFNDG-CWLHAPSGFVREDN-
SEKPSYFAL 185
                           4333389999********998889999999999999999999999988*******9
95.89999999887766.467888765 PP


>> k141_6113822
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   54.9   0.0   1.7e-16   2.3e-16      78      204 ..      43     172 .]
40      172 .] 0.82


  Alignments for each domain:
  == domain 1  score: 54.9 bits;  conditional E-value: 1.7e-16
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEilnedgslr 168
                           w   ep +g+  + ++ +++++ +++g +++gH l+Wh    w+   + ++e l
+ +   i+  v+ Ykg +  WDV+NE++       r
```

```
          k141_6113822   43 WGRYEPVEGQTAYPETFAAAKWLREKGVQVKGHPLCWHTACAPWLLPFS-
NEEILRRQI-GRIHRDVTAYKGVIGLWDVINEVVIMPVFDR 131
                           67789999**********************************9877.55555
5555.6799999***************987665533 PP


  MSA_GH10_xylanases 169 .esvfyrvlged…yvkiafeaareadpnakLyiNDYnl 204
                          +    +r++ e+      v+   f aa+e+dp+a L iND+n+
          k141_6113822 132 yDNAVTRICIEKgrvgLVREVFAAAKETDPDAALLINDFNT 172
                           244445555443233389*****************6 PP


>> k141_7536866
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   54.4   0.3   2.4e-16   3.3e-16     140     257 ..     16     134 ..
3     143 .] 0.81


  Alignments for each domain:
  == domain 1  score: 54.4 bits;  conditional E-value: 2.4e-16
  MSA_GH10_xylanases 140 iktvvgrYkgkvyaWDVvNEilnedgs…lresvf.yrvlgedyvkiafeaar
eadpnakLyiNDYnlesasaklegmvklvkklleag 225
                          + v  +Yk ++   DVvNE++    +     ++e+     ++g d++
+afe+a+e  p+a L +ND+n+ +     +++ ++lv++l++ag
          k141_7536866  16 YDAVKRKYK-
TLPMIDVVNEAVGTHQKgnpmMKETMGgGGKTGYDWLIKAFEMAYERWPDAILIYNDFNTFQW--
NTNEYIDLVRYLRDAG 103
                           456777777.57788******96554434867777766789**************
***************9966..89************** PP


  MSA_GH10_xylanases 226 vpidGiGsqsHlsagapsvaelkkalnalasl 257
                          +p+d  G q+H       +v++ k+a++++ ++
          k141_7536866 104 APVDAYGCQAHDLDDI-NVTNFKNAMKKIQDA 134
                           ***********66555.689999999888765 PP


>> k141_971700
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   53.9   0.0   3.4e-16   4.6e-16      36     120 ..    109     209 ..
81     210 .] 0.91


  Alignments for each domain:
  == domain 1  score: 53.9 bits;  conditional E-value: 3.4e-16
  MSA_GH10_xylanases  36 llkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg..
…kfsFegadelvnfakkngkklRgH 110
                          +lk+ ++++f  G a+ q+ + ++k +++i k++  +tpeN++K++++ + +g
```

```
+ ++a   l +fak+ng k+ gH
          k141_971700 109 SLKEIYADKFdfGVAAPQQAFYNNKLTDMILKQYSIVTPENELKPDSVLDVNGsi
klvnqtgdetqvAVHLDAAKPLLDFAKANGLKVHGH 199
                         566777776666**********************************
**********99999******************** PP

  MSA_GH10_xylanases 111 tlvWhsQlPs 120
                         l+WhsQ+P+
          k141_971700 200 VLIWHSQTPE 209
                         *********6 PP


>> k141_6202951
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   54.0   0.0   3.1e-16   4.2e-16     256     338 ..      2      93 ..
1      95 [. 0.89

  Alignments for each domain:
  == domain 1  score: 54.0 bits;  conditional E-value: 3.1e-16
  MSA_GH10_xylanases 256 slgvevaitELDialeleateekleaqakdyvevvkaclevkk…cv.gvtvW
gvaDkdsWls…eespllfdenynpKpaynaiv 336
                         +lg+++++tELDi+ + +++e+ +++ a +y++ ++++l+ kk     ++
+vt+W++ D++sWl+      +++pllf  + ++K+ay++++
          k141_6202951   2 ELGLQIHVTELDIH-
NADPSESSMHDLALRYRKFFEIYLDAKKsgkaNItSVTFWNLLDENSWLTgfrreTSYPLLFRGKCEAKEAYYEVL 91
                         689***********.888889999************99987653333688*****
**********999988999****************9 PP

  MSA_GH10_xylanases 337 ka 338
                         ka
          k141_6202951  92 KA 93
                         87 PP


>> k141_3569566
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   53.8   0.0   3.7e-16     5e-16     248     336 ..      2     106 ..
1     109 [. 0.92

  Alignments for each domain:
  == domain 1  score: 53.8 bits;  conditional E-value: 3.7e-16
  MSA_GH10_xylanases 248 kkalnalaslgvevaitELDialele…ateekleaqakdyve
vvkaclevkkcv.gvtvWgvaDkdsWls.eespllf 322
                         +ka+n++ +     ++itELD+++++e             ++    +
```

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```
q+++y++++k++++ ++++ +vt+W+++DkdsWl  ++ pl f
        k141_3569566    2 EKAINRFKEIVNIIHITELDLRTNTEsggqlmfargeakpQAPYIATLQEDQYAR
LFKIFRKHADVIkNVTFWNLSDKDSWLGvNNHPLPF 92
                          789******999**********888799*********98766778999*******
*************************986899**** PP


  MSA_GH10_xylanases 323 denynpKpaynaiv 336
                         den+++K + + i
       k141_3569566   93 DENFKAKRSLQIIR 106
                         *******998775 PP


>> k141_6860267
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   53.7   0.0   3.8e-16   5.2e-16     147     265 ..       3     120 ..
1     125 [. 0.82


  Alignments for each domain:
  == domain 1  score: 53.7 bits;  conditional E-value: 3.8e-16
  MSA_GH10_xylanases 147 YkgkvyaWDVvNEil…nedgslresvfyrvlgedyvkiafeaareadpnak
LyiNDYnlesasaklegmvklvkklleagvpidGiG 232
                         +kg + WDV+NE++     ++ +       r    + vk  f aa++a+p+
iND+n++    +k     +l+++ l+agv i  iG
        k141_6860267    3
FKGVIDIWDVINEVVimpifDKYDNAVTRLCKRYGRVELVKEVFAAAKAANPDGMFLINDFNTT---PKY---
EQLIEECLDAGVEISAIG 87
                         9************86222113333333333344444689***************
*******98…355…5678899*********** PP


  MSA_GH10_xylanases 233 sqsHlsagapsvaelkkalnalaslgvevaitE 265
                         +qsH + g + +++l + l+++++ g+ ++ tE
        k141_6860267   88 IQSHQHQGYWGTEKLYDVLKRFSRFGLPIHFTE 120
                         *****************************9 PP


>> k141_8414726
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   53.5   0.0   4.6e-16   6.3e-16     121     241 ..       7     124 ..
1     132 [] 0.76


  Alignments for each domain:
  == domain 1  score: 53.5 bits;  conditional E-value: 4.6e-16
  MSA_GH10_xylanases 121 wvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilnedgslr.esvfyr
vlge…dyvkiafeaareadpnakLyiNDYnles 206
```

```
                                w+ + + ++e l  +   + i+  v+ Ykg v  WDV+NE++      r +
+r++ e      vk  f aa+e +p+a L iND+n+
        k141_8414726    7 WLLQFS-NEEILR-
RQLERIHRDVTAYKGVVDMWDVINEVVIMPVFDRyDNAITRICKEmgrvGLVKEVFAAAKESNPDAVLLINDFNTSP 95
                          555444.444454.5556799999***************9876655332555555
5544222258*********************995 PP


  MSA_GH10_xylanases 207 asaklegmvklvkklleagvpidGiGsqsHlsaga 241
                         a          l+++ll+agvpi  iG+qsH + g
        k141_8414726   96 A------YETLLEDLLSAGVPIGAIGIQSHQHQGY 124
                         5…667899****************98876 PP


>> k141_5586099
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   53.1   0.0   6.1e-16   8.3e-16     155     270 ..       7     125 ..
2     138 .] 0.79


  Alignments for each domain:
  == domain 1  score: 53.1 bits;  conditional E-value: 6.1e-16
  MSA_GH10_xylanases 155 DVvNEilnedgs…lresvf.yrvlgedyvkiafeaareadpnakLyiNDYnl
esasaklegmvklvkklleagvpidGiGsqsHlsag 240
                         DVvNE++          ++es     ++g d++ +afe+a+e  pn  L +NDYn+
+     +++ ++lv++l+++g+pid  G qsH  +
        k141_5586099    7
DVVNEAVGTHQAgnplMKESLGgGGKTGYDWLIKAFELAYERFPNSILIYNDYNTFQW--
NTDEYIDLVRYLRDSGAPIDAYGCQSHDLTD 95
                         9*****9765444878888876789*****************************9
966..899*********************8777 PP


  MSA_GH10_xylanases 241 apsvaelkkalnal.aslgvevaitELDial 270
                           s ++ k a +++ ++l + +  tE Di +
        k141_5586099   96 C-SLSNFKTAEQKIqTALKMPMYSTEYDIGT 125
                         7.455555554444155667899999999982 PP


>> k141_2372622
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   52.9   0.0   7.1e-16   9.7e-16     186     336 ..       1     160 [.
1     164 [. 0.88


  Alignments for each domain:
  == domain 1  score: 52.9 bits;  conditional E-value: 7.1e-16
  MSA_GH10_xylanases 186 eaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsag
```

```
apsvaelkkalnalaslgvevaitELDia..lele. 273
                         eaa+e dp+a L iND+n+  +          l++ lleagvpi  iG+qsH + g
+  ++l++ l ++++ g+ ++ tE  +       ++
         k141_2372622    1 EAAKECDPDATLLINDFNTSVS------
YEILLEGLLEAGVPISAIGIQSHQHQGYWGLEKLNDVLARFSRFGLPIHFTENTLIsgEIMPa 85
                         689***************977…4457899*********************
***********************87663433338 PP


  MSA_GH10_xylanases 274
…ateekleaqakdyvevvkaclevkkcvgvtvWgvaDkdsWlseespllfdenynpKpaynaiv
336
                                   t +  e+qa++   e+ +++ + + + ++t+W++ D
Wl+   s +++++n   Kp+y+a+
         k141_2372622   86 hivdlndwqvdewpSTPAGEERQAREISEMYSVLFSHPLVEAITTWDFNDG-
CWLKAPSGFVHEDNS-EKPSYYALK 160
9999*******99877788899999999999999999988********95.8*********99885.699999875 PP


>> k141_5259053
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   51.6   0.1   1.7e-15   2.3e-15      283      337 ..      24       80 ..
11       82 .. 0.91


  Alignments for each domain:
  == domain 1  score: 51.6 bits;  conditional E-value: 1.7e-15
  MSA_GH10_xylanases 283
akdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                          +++y ++++++++ k+ + +vt+W+++D+dsWl  +++pllfd+ny+pK+ayna+
+
         k141_5259053   24
TDQYSRIFRVLRKHKDDIeCVTFWNLSDRDSWLGaNNYPLLFDANYRPKQAYNAVKN 80
579*****************************964889**************976 PP


>> k141_3370902
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   51.2   0.0   2.3e-15   3.2e-15      180      313 ..      18      161 ..
11      169 .. 0.90


  Alignments for each domain:
  == domain 1  score: 51.2 bits;  conditional E-value: 2.3e-15
  MSA_GH10_xylanases 180 yvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsq
sHlsagapsvaelkkalnalaslgvevaitELDia. 269
                          vk  feaa++a+p+a L iND+nl ++           l+   l+agvpi
```
169

```
                    iG+q+H + g +  ++l++ l++++  g+ ++ tE  +
        k141_3370902  18 LVKDVFEAAKAANPEATLLINDFNLSES------
YRILIDGCLNAGVPISAIGIQTHQHQGYMGLEKLQDILDRFSVFGLPLHFTENTLVs 102
                         58889*******************966…5568999**************
****************************98874 PP


  MSA_GH10_xylanases 270
.lele…ateekleaqakdyvevvkaclevkkcvgvtvWgvaDkdsW 313
                         ++                 +t e  e+q+++++e+++++ + + + +vt
W++aD  +W
        k141_3370902 103
gHIMPpeivdlndyqipewpTTPEGEERQKNEWAEMMSVLFDHPMVEAVTGWDFADG-AW 161
4334489999*********99889999*******************999********95.45 PP


>> k141_322990
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   51.3   0.0   2.2e-15   2.9e-15     152     265 ..      2     114 ..
1     123 [. 0.86


  Alignments for each domain:
  == domain 1  score: 51.3 bits;  conditional E-value: 2.2e-15
  MSA_GH10_xylanases 152 yaWDVvNEilnedgslr.esvfyrvlged…yvkiafeaareadpnakLyiND
YnlesasaklegmvklvkklleagvpidGiGsqsHl 237
                         +WDV+NE++        r +   +r+++e       +k  f +a++a+p+a+L
iND+nl ++         +++ + leag+pi+ iG+q+H
        k141_322990   2
DKWDVINETVIMPVFDRyDNAITRICNEYgripLIKEVFTTAHDANPDAQLLINDFNLSDQ------
YREVISDSLEAGAPINAIGIQTHQ 86
                         68******998777655266667777663333337999*****************
***977…6788999***************** PP


  MSA_GH10_xylanases 238 sagapsvaelkkalnalaslgvevaitE 265
                         + g + +a l + l++++  ++ ++ tE
        k141_322990  87 HQGYKGMAWLDDVLKRFSVFNLPLHFTE 114
                         ******************999999998 PP


>> k141_2025155
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   50.9   0.0   2.8e-15   3.8e-15     260     337 ..      3      96 ..
1      98 [. 0.92


  Alignments for each domain:
```

```
   == domain 1  score: 50.9 bits;  conditional E-value: 2.8e-15
  MSA_GH10_xylanases 260 evaitELDialele…ateekleaqakdyvevvkaclevkkcv
.gvtvWgvaDkdsWls.eespllfdenynpKpayna 334
                            ++itELD++++ e            ++   +   q+++y++++k++++ ++++
+vt+W++ DkdsWl  ++ pl fdeny+pK+ y a
       k141_2025155    3 HIHITELDLRMNNEsggqlmfsrgeakpMPGYMGTLQTDQYARLFKVFRKHADVI
dNVTFWNLGDKDSWLGvNNHPLPFDENYRPKACYRA 93
                            589*******888799********999877888899*******************
**************986899***************9 PP


  MSA_GH10_xylanases 335 ivk 337
                            i +
       k141_2025155  94 IRD 96
                            975 PP


>> k141_8794455
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   50.5   0.2   3.7e-15   5.1e-15     196     270 ..      1      85 [.
1     104 [. 0.82


  Alignments for each domain:
  == domain 1  score: 50.5 bits;  conditional E-value: 3.7e-15
  MSA_GH10_xylanases 196 kLyiNDYnlesa…saklegmvklvkklleagv.pidGiGsqsHlsaga…
.psvaelkkalnalaslgvevaitELDial 270
                            kL++NDYnles    + k++ mvk ++k+++ gv +idGiG+q H+s  +
+++++ k ++ +a++g  v + ELD+ +
       k141_8794455    1 KLFVNDYNLESDwddNGKVKSMVKWIEKWEADGVtKIDGIGTQMHISCYEnanlq
kSAEDHIVKMFQIMANSGKLVRVSELDMGY 85
                            9********97533259****************857**********988777776
66678899999****************983 PP


>> k141_8083224
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   49.9   0.0   5.8e-15   7.9e-15     179     313 ..     18     162 ..
11     175 .. 0.87


  Alignments for each domain:
  == domain 1  score: 49.9 bits;  conditional E-value: 5.8e-15
  MSA_GH10_xylanases 179 dyvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGs
qsHlsagapsvaelkkalnalaslgvevaitELDia 269
                            + +k+ f  ar+++pna L +ND+n+    +k e    +l++  l+agv i
iG+qsH + g + ++++ + l+++++ g+ ++ tE
```

171

```
        k141_8083224   18 ELIKTVFDEARKMNPNATLLLNDFNTS---PKYE---
ELIEGCLDAGVSISAIGIQSHQHQGYWGKDKVLDVLERFSRFGLPIHFTENTFV 102
                           57999*******************98…4555…567899************
****************************8655 PP


  MSA_GH10_xylanases 270
..lele…ateekleaqakdyvevvkaclevkkcvgvtvWgvaDkdsW 313
                                      +t e   +qa++ +e+ +++ e++ +
++t+W+  D  +W
        k141_8083224 103 sgD--
LmpahivdlndwqvpewpTTPEGEARQAQNVEEMYRLLFENPLVQAITTWDYKDG-AW 162
332..1357888999999999987888889999999********99999*******995.45 PP


>> k141_3361406
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   49.9   0.1   5.8e-15   7.9e-15      78     198 ..      61     184 ..
59     185 .] 0.78


  Alignments for each domain:
  == domain 1  score: 49.9 bits;  conditional E-value: 5.8e-15
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEilnedgs.. 166
                          w   ep +g+  F+++ +++++ +++g +++gH l+Wh     w+ + + ++e l
+ l+  i+  v+ Ykg +   WDV+NE++
        k141_3361406   61 WGRYEPVEGRPAFTETMKAAKWMREQGVQVKGHPLCWHTACAPWLMQYS-
NEEILRRQLE-RIHRDVTAYKGVIDMWDVINEVVIMPVFdk 149
                          6778999**************************************988.77777
77775.699999***************875432211 PP


  MSA_GH10_xylanases 167 lre..svfyrvlge.dyvkiafeaareadpnakLy 198
                          + +  +   + lg    vk  f aare +p+a L
        k141_3361406 150 YDNavTRICKDLGRiRLVKEVFAAARESNPDAVLL 184
                          22200233444432788999999999999998876 PP


>> k141_3206100
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   49.6   0.0   7.1e-15   9.7e-15     180     334 ..      27     190 ..
20     196 .. 0.86


  Alignments for each domain:
  == domain 1  score: 49.6 bits;  conditional E-value: 7.1e-15
  MSA_GH10_xylanases 180 yvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsq
```

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```
sHlsagapsvaelkkalnalaslgvevaitELDia. 269
                         vk  f aa+e  p+a L iND+n+   +         l+++ll agvp+
iG+qsH + g +  ++l++ l+++++ g+ ++ tE  +
         k141_3206100   27 LVKEVFTAAKESSPDAILLINDFNTSAS------
YEMLLEELLGAGVPVSAIGIQSHQHQGYWGLEKLEDVLERFSRFGLPIHFTENTLIs 111
                         68999*****************9955…445799***************
****************************87653 PP


   MSA_GH10_xylanases 270 .lele…ateekleaqakdyvevvkaclevkkcvgvtvWgv
aDkdsWlseespllfdenynpKpayna 334
                                      t e  e+qa + +e+ + +   + + ++t+W++
D   Wl+  s ++ ++n   Kp+y a
         k141_3206100 112 gDL-
MpayivdlndwqveswpSTPEGEERQAGEITEMYSFLFAHPLVEAITTWDFNDG-CWLKAPSGFVREDNS-EKPSYFA
190
                         322.25888999999999988889999999999999999988888*******
995.899999988877664.5777765 PP


>> k141_4598294
    #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
  ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
    1 !   49.7   0.2   6.5e-15   8.9e-15     102     203 ..       2     105 ..
1     106 [] 0.86


   Alignments for each domain:
   == domain 1  score: 49.7 bits;  conditional E-value: 6.5e-15
   MSA_GH10_xylanases 102 kngkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvyaWDV
vNEilnedgs…lresvf.yrvlgedyvkiafea 187
                         +++ + ++H+lvW  Q P+w++s +  ++    +++ n+ ++  ++Y +++
DVvNE++ +       ++es      ++g d++ +afe+
         k141_4598294    2 QHDFTYKFHALVWGAQYPGWLESLS-ARDR-FNAITNWFDHAKDQY-
DTLPMIDVVNEAIGNHQAgnpmMKESLGgGGKTGYDWLIKAFEM 89
                         6778889**************998.5555.578999999999999.689999**
*****7654444768888876789*********** PP


   MSA_GH10_xylanases 188 areadpnakLyiNDYn 203
                         a+e  p+a L +NDYn
         k141_4598294   90 AYERWPDAILIYNDYN 105
                         ***************9 PP


>> k141_8171587
    #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
  ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
    1 !   43.3   1.3   5.5e-13   7.6e-13     156     254 ..       1     130 [.
```

```
1      133 [. 0.77

  Alignments for each domain:
  == domain 1  score: 43.3 bits;  conditional E-value: 5.5e-13
  MSA_GH10_xylanases 156 VvNEilnedgs…lresvfyrvlgedyvkiafeaare…
.adpna…kLyiNDYnlesasaklegmvklvk 219
                          VvNE+++   +    lr+s +yr++g+d++  af+aa++
d++a       L++NDYn  +++ k+  ++ l +
        k141_8171587    1 VVNEAIEPADKqetgLRNSYWYRIIGDDFMYFAFKAAHDavtelsvkyagkygid
aSDEKAlsairpLLFYNDYNEWQKEKKSYIIAALNR 91
                          8****9843333446*********************9999*********9999
75555533333369********99888888888888 PP


  MSA_GH10_xylanases 220 klleagvp…idGiGsqsHlsagapsvaelkkalnal 254
                          + + +g        idGiG+q+Hls ++ +v e+ +al ++
        k141_8171587   92 EGHGHGSIigeglIDGIGMQGHLSDNN-DVGEYLEALYEY 130
                          87777764222238*********9988.555666666555 PP


>> k141_8363470
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   48.5   0.3   1.5e-14   2.1e-14     283     337 ..      7      63 ..
2      65 .. 0.92

  Alignments for each domain:
  == domain 1  score: 48.5 bits;  conditional E-value: 1.5e-14
  MSA_GH10_xylanases 283
akdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                          +++yv+++k +++ k++v  vt+W+++D+dsW+
+++pllfd+++n+K+ayna++k
        k141_8363470    7
TDQYVQLFKCLRKHKDVVdVVTFWNLSDRDSWVGtSNYPLLFDKDLNKKEAYNAVLK 63
689***************99***********974889****************98 PP


>> k141_3005971
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   48.4   0.0   1.6e-14   2.2e-14      29     115 ..     34     135 .]
11     135 .] 0.87


  Alignments for each domain:
  == domain 1  score: 48.4 bits;  conditional E-value: 1.6e-14
  MSA_GH10_xylanases  29 aaesldallkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweai
epsrg…kfsFegadelvnfakkn 103
```

```
                        ae++  +lk+ ++++f  G+a+ q+ +++ k   ++k++f  ltpeN+MK++++
+ +                 +F++a  l  fa++n
        k141_3005971  34 EAENIP-SLKEIYANQFdfGSAAPQNVFRDPKWLTLMKEQFSILTPENEMKPDSV
LDVSKsrqllkdtgdetavAVHFDAARPLLRFAQSN 123
                        334444.788899998888***************************98
77666677********************** PP


  MSA_GH10_xylanases 104 gkklRgHtlvWh 115
                        g k+ gH l+Wh
        k141_3005971 124 GIKVHGHVLIWH 135
                        ***********9 PP


>> k141_5950360
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   48.1   0.2   1.9e-14   2.7e-14      78     161 ..      48     129 ..
45     151 .. 0.93


  Alignments for each domain:
  == domain 1  score: 48.1 bits;  conditional E-value: 1.9e-14
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEil 161
                        w   ep++gk  F+++ +++++ +++g  ++gH l+Wh     w+ + + ++e
+++ l   i+  v+ Ykg +  WDV+NE++
        k141_5950360  48 WGRYEPEEGKTAFSETMAAAQWLQEKGVRVKGHPLCWHTVCAPWLMQYS-
NEEIMQKQLA-RIHRDVTAYKGVIDMWDVINEVV 129
                        77889****************************************999.88888
88886.6999999**************97 PP


>> k141_677431
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   47.6   0.0   2.8e-14   3.8e-14      62     154 ..       2     138 .]
1     138 [] 0.87


  Alignments for each domain:
  == domain 1  score: 47.6 bits;  conditional E-value: 2.8e-14
  MSA_GH10_xylanases  62 iikkdfgsltpeNsMK…weaiepsrgkfsF…egadelvnfakkngkkl
RgHtlvWhsQlPswvssik… 126
                        +i+++f s+t  N+MK      w++ e +++   +    +a ++
++a+++g+k+R H +vWhsQ P   + +
        k141_677431   2 LIAREFSSMTCANEMKpaynmgWDSPEAQEDYLPYvinPNAKRMLDWAREHGMKM
RAHVMVWHSQCPREAFCKGykpvtiptdpeklkenp 92
                        7899**********9966666667777777766653335899*************
```

```
*************866655556*************** PP

  MSA_GH10_xylanases 127 …adketllevlknhiktvv…grYkgkvyaW 154
                                   +d++t+l++l+++i++++    + Y +++yaW
        k141_677431  93 rlkfferldpvcfVDRDTMLKRLESYIHSMLdylykNGYAETIYAW 138
                        ****************************998888788999****9 PP


>> k141_5494989
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   46.8   0.1     5e-14   6.9e-14     280      336 ..      26      84 ..
15      87 .. 0.90


  Alignments for each domain:
  == domain 1  score: 46.8 bits;  conditional E-value: 5e-14
  MSA_GH10_xylanases 280
eaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaiv 336
                              q+++y++v+k+++++++++ +vt+W+++D+dsWl  ++ pllfdeny+pK
y+ +
        k141_5494989  26
ILQQDQYNRVFKVLRKYHDVIdNVTFWNLSDQDSWLGvNNHPLLFDENYKPKTVYKIVR 84
5699****************************986899**************9775 PP


>> k141_6758321
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   46.7   0.0   5.3e-14   7.3e-14     210      297 ..       7      97 ..
1     100 [. 0.79


  Alignments for each domain:
  == domain 1  score: 46.7 bits;  conditional E-value: 5.3e-14
  MSA_GH10_xylanases 210 klegmvk.lvkklleagvpidGiGsqsHlsaga…psvaelkkalnalaslg
vevaitELDialeleateeekleaqakdyvevvkacl 294
                          k++ +++ ++k l+e+g  idG+G+qsH+sa +       + ++ +a++ +
slg++v++tELDi+  +e  + l++qa++y+ +++ +
        k141_6758321   7 KKRCIINtILKPLMEKG-
LIDGMGMQSHVSAASgqydwGGTPSYLAAMDDYLSLGLDVQVTELDIS--TEGGKYSLQQQAEKYKAIFQHAV 94
                          44444440556666666.6**********9987776545668899*********
***********..888899*************99887 PP


  MSA_GH10_xylanases 295 evk 297
                          e +
        k141_6758321  95 EAN 97
                          765 PP


                                   176
```

```
>> k141_2001968
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   46.3   0.1   6.9e-14   9.4e-14     276      337 ..      9      72 ..
3      75 .. 0.88

  Alignments for each domain:
  == domain 1  score: 46.3 bits;  conditional E-value: 6.9e-14
  MSA_GH10_xylanases 276
eekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                        ++   ++ a++y++v+++++ k+++ +vt+W+++D+dsWl  +++pl fd
+y+pK ay+ i +
        k141_2001968    9
DSLKQHLADQYARVFRVFRKHKDVIdCVTFWNLSDRDSWLGqNNYPLPFDVDYKPKMAYEYIRD 72
455577799*****************************963789***************99876 PP


>> k141_7179537
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   46.5   0.0     6e-14   8.2e-14      40      126 ..      5     110 ..
1     115 [. 0.90

  Alignments for each domain:
  == domain 1  score: 46.5 bits;  conditional E-value: 6e-14
  MSA_GH10_xylanases  40 agkkyfGtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg…
…kfsFegadelvnfakkngkklRgHtlvW.. 114
                        agk  fG av  + + ++k +++i +++  +tpeN+MK++a+ +
+ ++a  l nfak+ng k+ gHtl+W
        k141_7179537    5 AGKFDFGVAVPGHAFGQAKLKEMILQQYSIMTPENEMKPDAVLDVAAskklaees
gddtsaAVHLDAAKPLLNFAKENGLKVHGHTLLWgk 95
                        689999*****************************998877788*****
*****999********************66 PP

  MSA_GH10_xylanases 115 …hsQlPswvssik 126
                          sQ+P+ ++++
        k141_7179537  96 nppESQTPKAFFHEG 110
                          666689998777665 PP


>> k141_9339147
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
```

```
   1 !   46.2   0.1   7.5e-14     1e-13      78     161 ..      63     144 ..
30     147 .. 0.92

  Alignments for each domain:
  == domain 1  score: 46.2 bits;  conditional E-value: 7.5e-14
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEil 161
                          w   ep++gk + ++ +++++ + ng +++gH l+Wh      w+ + + ++e l
+ l+  i+  vg Ykg +  WDV+NE++
        k141_9339147  63 WGRYEPEEGKTAYPETMAAAKWLRDNGVQVKGHPLCWHTACAPWLLKYS-
NEEILRRQLE-RIHRDVGAYKGVINLWDVINEVV 144
                         77889*****************************************888.67777
66665.69999***************97 PP


>> k141_4818106
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   46.1   0.1      8e-14   1.1e-13      78     161 ..      21     102 ..
19     139 .. 0.91

  Alignments for each domain:
  == domain 1  score: 46.1 bits;  conditional E-value: 8e-14
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEil 161
                          w   ep++gk + ++ +++++ +++g +++gH l+Wh      w+ + + ++e l
+ l+  i+  v+ Ykg +  WDV+NE++
        k141_4818106  21 WGRYEPEEGKTAYPETMAAAKWLREKGVQVKGHPLCWHTACAPWLMKYS-
NEEILRRQLE-RIHRDVTAYKGVIDLWDVINEVV 102
                         77789*****************************************888.77777
77665.699999**************97 PP


>> k141_8171708
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   45.8   0.0   9.7e-14   1.3e-13     180     265 ..      19      98 ..
11     118 .. 0.91

  Alignments for each domain:
  == domain 1  score: 45.8 bits;  conditional E-value: 9.7e-14
  MSA_GH10_xylanases 180 yvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsq
sHlsagapsvaelkkalnalaslgvevaitE 265
                          vk  f aa+e++p+a L iND+n+  +         l++ lleagvpi
iG+qsH + g +  ++l++ l+++++ g+ ++ tE
        k141_8171708  19 LVKEVFAAAKETNPDATLLINDFNTSVS------
```

178

```
YEILLEGLLEAGVPISAIGIQSHQHQGYWGLEKLNNVLERFSRFGLPIHFTE 98
                         68999*****************977…4457899**************
***************************9 PP


>> k141_9141803
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   45.3   0.1   1.4e-13   1.9e-13      86     164 ..       8      83 ..
2     100 .. 0.90


  Alignments for each domain:
  == domain 1  score: 45.3 bits;  conditional E-value: 1.4e-13
  MSA_GH10_xylanases  86
gkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketllevlknhiktvvgrYkgkvyaWDVvNEilned
164
                          +k++++ +d++ +++k+ng + ++H lvW sQ P+ ++   +   ++l++ +
+++ v+ +Y + +   DVvNE+++
        k141_9141803    8 QKWNWRSSDAHYKWCKENGVLFKFHCLVWTSQFPTCLNGVT--
GNELKQQVGYWMDAVAMKYPD-LAVIDVVNEAIKGH 83
79********************************9777..99*****************87.6778******9865
PP


>> k141_8971703
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   45.0   0.0   1.7e-13   2.3e-13     181     321 ..      24     174 ..
16     191 .. 0.84


  Alignments for each domain:
  == domain 1  score: 45.0 bits;  conditional E-value: 1.7e-13
  MSA_GH10_xylanases 181 vkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqs
HlsagapsvaelkkalnalaslgvevaitELDia.. 269
                          +k  f  a++ +p+a L +ND+n+  +         l+   l+agvpi
iG+qsH + g +  ++l++ l+++++ g+ ++ tE +
        k141_8971703   24 IKEVFDRAHADNPDAVLLLNDFNTSIN------
YEILIDGCLNAGVPISAIGIQSHQHQGYWGLEKLEEVLERFSHFGLPIHFTENTLIsg 108
                          7889*****************966…44578999**************
****************************755423 PP


  MSA_GH10_xylanases 270
lele…ateekleaqakdyvevvkaclevkkcvgvtvWgvaDkdsWlseespll 321
                                     t e  e+qa++ +e+ +++   + + ++t+W+
+D  +Wl+  s +
        k141_8971703 109 DI-
```

```
MpkhivdlndwqvdewpSTPEGEERQAREIEEMYRTLFAHPLVEAITTWDYRDG-AWLKAPSGYI 174
22.136678899999**9998899999***************9999999********96.6887665544 PP


>> k141_6494427
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   43.7   0.0   4.2e-13   5.7e-13     180     265 ..      25     104 ..
13     115 .. 0.92


  Alignments for each domain:
  == domain 1  score: 43.7 bits;  conditional E-value: 4.2e-13
  MSA_GH10_xylanases 180 yvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsq
sHlsagapsvaelkkalnalaslgvevaitE 265
                         vk  f aar+a+p+   iND+n+  +        kl+++ll+agv i
iG+qsH + g + +a+l++ l+++++ g+ ++ tE
        k141_6494427   25 LVKEVFAAARAANPDGTFLINDFNTSPQ------
YEKLIEELLDAGVEISAIGIQSHQHQGYWGEAKLRDVLKRFSRFGLPIHFTE 104
                         68999******************9944…668999***************
***************************9 PP


>> k141_5928501
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   44.4   0.0   2.7e-13   3.7e-13     193     318 ..       1     136 [.
1     148 [] 0.85


  Alignments for each domain:
  == domain 1  score: 44.4 bits;  conditional E-value: 2.7e-13
  MSA_GH10_xylanases 193 pnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvael
kkalnalaslgvevaitELDia..lele… 273
                         p+a  iND+n+ ++        kl+++ leagv+i  iG+qsH + g +  ++l
+ l+++++ g+ ++ tE +
        k141_5928501   1 PDATFLINDFNTSEK------
YEKLIEDCLEAGVKISTIGIQSHQHQGYWGDEKLYDVLKRFSRFGLPIHFTENTLIsgDI-Mpahiidln 84
                         678889*****9844…667899***************************
*****************76542322.146788899 PP


  MSA_GH10_xylanases 274 …ateekleaqakdyvevvkaclevkkcvgvtvWgvaDkdsWlsees
318
                             +t e  e+qa++++++++++ + +++ +vt W+++D  +Wl+  s
      k141_5928501   85 dwqvdewpTTPEGEERQANEWENMMRILFNDPNVEAVTGWDFTDG-AWLKAPS
136
                         999**999899999****************99999********96.6887655
PP
```

180

```
>> k141_1962241
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   44.4   0.0   2.7e-13   3.6e-13     181     265 ..       3      81 ..
1     102 [. 0.92

  Alignments for each domain:
  == domain 1  score: 44.4 bits;  conditional E-value: 2.7e-13
  MSA_GH10_xylanases 181 vkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqs
HlsagapsvaelkkalnalaslgvevaitE 265
                         vk  f aa+e +p+a L iND+n+  +         l++ lleagvpi
iG+qsH + g +  ++l++ l+++++ g+ ++ tE
        k141_1962241   3 VKEVFAAAKESNPDAVLLINDFNVSVS------
YEILLEGLLEAGVPISAIGIQSHQHQGFWGLDKLNDVLERFSRFGLPIHFTE 81
                         7889*******************977…4457899**************
***************************9 PP


>> k141_3029768
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   43.6   0.1   4.5e-13   6.1e-13     278     337 ..       7      68 ..
1      71 [. 0.90

  Alignments for each domain:
  == domain 1  score: 43.6 bits;  conditional E-value: 4.5e-13
  MSA_GH10_xylanases 278
kleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                          +   q+++y+++++++++ k+++ +vt+W+++D+dsWl  ++ pl
fdeny++K++++ i +
        k141_3029768   7
IATIQEDQYARIFRVFRKHKEVIdNVTFWNLSDRDSWLGvNNHPLPFDENYKAKSSFTVIRD 68
5677999***************************986899***************99976 PP


>> k141_3877129
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   43.4   0.0   5.3e-13   7.3e-13     181     265 ..      29     107 ..
19     112 .. 0.94

  Alignments for each domain:
  == domain 1  score: 43.4 bits;  conditional E-value: 5.3e-13
```

```
   MSA_GH10_xylanases 181 vkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqs
HlsagapsvaelkkalnalaslgvevaitE 265
                           vk  fe a++ +p+a L +ND+n+  a        +l+ + l+agvpi
iG+qsH + g +  ++l + l+++++ g+ ++ tE
         k141_3877129   29 VKAVFERAKANNPEATLLLNDFNTSAA------
YEELISDCLDAGVPISAIGIQSHQHQGYWGLEKLYDVLERFSKFGLPIHFTE 107
                           8899*******************966…678899***************
**************************9 PP


>> k141_4517395
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   43.3   0.0   5.8e-13      8e-13     278      337 ..      8      69 ..
1      71 [. 0.90


  Alignments for each domain:
  == domain 1  score: 43.3 bits;  conditional E-value: 5.8e-13
  MSA_GH10_xylanases 278
kleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                           +   q+++y++++k++++ ++++ +vt+W++ DkdsWl  ++ pl fdeny+pK+
+ ai +
         k141_4517395    8
MGTLQTDQYARLFKVFRKHADVIdNVTFWNLGDKDSWLGvNNHPLPFDENYRPKACFRAIRD 69
5567899************************986899**************9975 PP


>> k141_1043855
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   43.1   0.0   6.7e-13    9.1e-13     180      265 ..     12      91 ..
7     106 .. 0.93


  Alignments for each domain:
  == domain 1  score: 43.1 bits;  conditional E-value: 6.7e-13
  MSA_GH10_xylanases 180 yvkiafeaareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsq
sHlsagapsvaelkkalnalaslgvevaitE 265
                           vk  f aare +p+a L iND+n+  a        l++ lle+gv+i
iG+qsH + g +  ++l++ l+++++ g+ ++ tE
         k141_1043855   12 LVKEVFAAARESNPDAVLLINDFNTSVA------
YEILLEGLLESGVQICAIGIQSHQHQGYWGLEKLRDVLERFSRFGLPIHFTE 91
                           58999*******************987…4457899************
**************************9 PP


>> k141_1958016
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
```

```
envfrom  env to      acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   43.0   0.0   7.1e-13   9.7e-13      78     160 ..      31     111 .]
29     111 .] 0.94


  Alignments for each domain:
  == domain 1  score: 43.0 bits;  conditional E-value: 7.1e-13
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEi 160
                          w  ep++gk  Fe+  +++ f + +g  l+gH l+Wh    +w+ +   dk+ l
+ l+  i+  v+ + g +  WDV+NE+
        k141_1958016  31 WGRYEPEEGKPAFENRMNAARFLTGRGVRLKGHPLCWHTVCADWLMQYD-
DKTILDKQLER-IHRDVTAFAGVIDIWDVINEV 111
                         77789**********************************999.99999
999975.899999**************6 PP


>> k141_8028958
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   42.6   0.0   9.2e-13   1.3e-12     274     337 ..       6      71 ..
2      73 .. 0.90


  Alignments for each domain:
  == domain 1  score: 42.6 bits;  conditional E-value: 9.2e-13
  MSA_GH10_xylanases 274
ateekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                          +++ +   q+++y +++k++++ ++++ +vt+W++ D+dsWl  ++ pl
fdeny+pK+ + ai +
        k141_8028958   6
QPAYMQTLQTDQYSRLFKIFRKHADVIdNVTFWNLGDRDSWLGvNNHPLPFDENYRPKQCFRAIRD 71
5566777899********************************986899**************9975 PP


>> k141_2084643
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   42.5   0.1   9.8e-13   1.3e-12      78     161 ..      38     119 ..
35     157 .. 0.89


  Alignments for each domain:
  == domain 1  score: 42.5 bits;  conditional E-value: 9.8e-13
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEil 161
                          w  ep +g+  + ++ +++++ k++g  ++gH l+Wh     w+ + + ++e l
```

```
             + l+  i+  v+ Y+g +  WDV+NE++
         k141_2084643   38 WGRYEPVEGQTAYPETMAAAQWLKEQGVRVKGHPLCWHTACAPWLMQYS-
NEEILRRQLE-RIHRDVTAYRGVIDLWDVINEVV 119
                           6778999**********************************988.77777
77775.699999***************97 PP


>> k141_740240
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   41.8   0.0   1.7e-12   2.3e-12     274     337 ..     20      85 ..
12      87 .. 0.90


  Alignments for each domain:
  == domain 1  score: 41.8 bits;  conditional E-value: 1.7e-12
  MSA_GH10_xylanases 274
ateeekleaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                       +++ +   q+++y +++k++++ ++++ +vt+W++ DkdsWl  ++ pl
fdeny+pK+ + ai +
         k141_740240   20
QPAYMQTLQTDQYSRLFKIFRKHADVIdNVTFWNLGDKDSWLGvNNHPLPFDENYRPKQCFRAIRD 85
5566778899**************************986899***************9975 PP


>> k141_9468170
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   41.4   0.1   2.2e-12     3e-12     279     336 ..     22      81 ..
11      84 .. 0.89


  Alignments for each domain:
  == domain 1  score: 41.4 bits;  conditional E-value: 2.2e-12
  MSA_GH10_xylanases 279
leaqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaiv 336
                       +   q+++y++++k++++ k+++ +vt+W+++DkdsWl  ++ pl fden+++K +
i
       k141_9468170   22
ATIQEDQYNRIFKVFRKHKDVIkNVTFWNLSDKDSWLGvNNHPLPFDENFKAKRSLAVIR 81
567899**************************986899************998875 PP


>> k141_4903408
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   41.3   0.1   2.3e-12   3.1e-12     282     337 ..     24      81 ..
```

```
11       84 ..  0.91

  Alignments for each domain:
  == domain 1  score: 41.3 bits;  conditional E-value: 2.3e-12
  MSA_GH10_xylanases 282
qakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                         +++++ +++k+++  k+++ +vt+W+v+D+dsW+  +++pl+fd++++
K+ay+a+ +
        k141_4903408  24
HTNQFSQLFKVLRRHKDVIdNVTCWNVSDRDSWVGvNNYPLMFDKDLKRKQAYYAVRD 81
578999*********************986899***************9976 PP


>> k141_5131461
   #     score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   41.3   0.0   2.3e-12   3.1e-12      41     121 ..      13     102 .]
5      102 .] 0.91

  Alignments for each domain:
  == domain 1  score: 41.3 bits;  conditional E-value: 2.3e-12
  MSA_GH10_xylanases  41 gkkyfGtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg…
kfsFegadelvnfakkngkklRgHtlvWhsQlPsw 121
                         +   fG a + ++++++    +++++f+slt  N+ K  ++ +++
+ s++ ad++  +a++n+  +RgH lvW+  + +w
        k141_5131461  13 YGFMFGGAFSFSDMNNKAFIGFLARHFNSLTCCNETKAYSLLDEQRsrtsgdgmp
RMSYSRADAMISWAQRNNIRVRGHVLVWDAYMTQW 102
                         5556899999999999999999**************9999998889*******
****************************999888 PP


>> k141_5153724
   #     score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   40.8   0.0   3.3e-12   4.6e-12      78     161 ..      35     116 ..
33     120 .. 0.91

  Alignments for each domain:
  == domain 1  score: 40.8 bits;  conditional E-value: 3.3e-12
  MSA_GH10_xylanases  78 weaiepsrgkfsFegadelvnfakkngkklRgHtlvWhsQlPswvssikadketl
levlknhiktvvgrYkgkvyaWDVvNEil 161
                         w   ep +g+  + ++ +++ + +++g +++gH l+Wh     w+ + + ++e l
+ l+  i+  v+ Y+g +  WDV+NE++
        k141_5153724  35 WGRYEPAEGQTAYPETIAAARWLREKGVQVKGHPLCWHTACAPWLLKYS-
NEEILRRQLE-RIHRDVTAYRGVIGLWDVINEVV 116
                         67789*****************************************888.77777
```

```
77665.699999**************97 PP


>> k141_1750054
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   39.5   0.2   8.4e-12   1.1e-11     299       337 ..       3        43 ..
1       45 [. 0.88


  Alignments for each domain:
  == domain 1  score: 39.5 bits;  conditional E-value: 8.4e-12
  MSA_GH10_xylanases 299 cv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                         ++ +vt+W+v+D+dsWl    ++pllfdeny+pK+ay a+ +
        k141_1750054   3 VIdCVTFWNVSDRDSWLGaANYPLLFDENYKPKQAYLAVKN 43
                         5679*************964789**************99976 PP


>> k141_2589822
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   39.2   0.0     1e-11   1.4e-11     281       336 ..      13        70 ..
4       73 .. 0.91


  Alignments for each domain:
  == domain 1  score: 39.2 bits;  conditional E-value: 1e-11
  MSA_GH10_xylanases 281
aqakdyvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaiv 336
                         q+++y++++k++++ k+++ +vt+W+++DkdsWl  ++ pl fden+++K + +
i
        k141_2589822  13
LQEDQYARLFKIFRKHKDVIkNVTFWNLSDKDSWLGvNNHPLPFDENFKAKRSLQIIR 70
57899***************************986899*************998775 PP


>> k141_7756742
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   38.0   0.0   2.4e-11   3.3e-11      58       120 ..       6        77 ..
1      126 [] 0.70


  Alignments for each domain:
  == domain 1  score: 38.0 bits;  conditional E-value: 2.4e-11
  MSA_GH10_xylanases  58
keeaiikkdfgsltpeNsMK…weaiepsrgkfsF…egadelvnfakkngkklRgHtlvWhsQlPs 120
                         +e+++ ++f+s+t  N++K      w++ e +++   F    ++a ++ +f+kkn
```

```
                          +k+RgH lvWhsQ  +
        k141_7756742   6
AKEDLMLREFNSMTFANELKpaynmgWDSPEAREDYLPFvinDNAKTMLDFCKKNKMKVRGHVLVWHSQCAK 77
56778888999999888755444444999999999999993334666789********************854 PP


>> k141_9128397
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   36.4   0.0   7.2e-11   9.8e-11     197     333 ..       2     147 .]
1     147 [] 0.85


  Alignments for each domain:
  == domain 1  score: 36.4 bits;  conditional E-value: 7.2e-11
  MSA_GH10_xylanases 197 LyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkal
nalaslgvevaitELDia..lele… 273
                           L iND+n+  +        l+   leagvpi  iG+qsH + g +  +++ +
l+++ + g+ ++ tE  +
        k141_9128397   2 LLINDFNTSVS------
YEILIDGCLEAGVPISAIGIQSHQHQGYWGADKVYEVLERYEHFGLPIHFTENTLIsgDI-Mpayiedlndwqv 85
                          78999999976…44578999*****************************
**************75442222.136677999**** PP


  MSA_GH10_xylanases 274
…ateekleaqakdyvevvkaclevkkcvgvtvWgvaDkdsWlseespllfdenynpKpayn 333
                          +t e   e+qa++ +e+ +++ + + + ++t+W+ +D  +Wl   s  +
+  pKpayn
        k141_9128397  86 pewpTTPEGEERQAREIEEMYRILFSHPLVQAITTWDYRDG-AWLGAPSGYIRK-
DNSPKPAYN 147
**99889999******************9999********96.799888877754.457888886 PP


>> k141_7094414
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   36.2   0.0   8.4e-11   1.1e-10     217     321 ..      12     132 ..
1     150 [. 0.83


  Alignments for each domain:
  == domain 1  score: 36.2 bits;  conditional E-value: 8.4e-11
  MSA_GH10_xylanases 217 lvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDia..
lele…ateekleaqakdyvevv 290
                          l+   l+agvpi  iG+qsH + g + ++++++ l++++s g+ ++ tE  +
++              t e  e+qa++ +e+
        k141_7094414  12 LIDGCLNAGVPISAIGIQSHQHQGYWGRQKVEEVLERFSSFGLPIHFTENTLIsg
EIMPayiedlndwqvdewpSTPEGEERQAREVEEMY 102
```

```
                             4567789********************************************886634
333389999********99889999*********** PP


  MSA_GH10_xylanases 291 kaclevkkcvgvtvWgvaDkdsWlseespll 321
                         +++ e + + ++t+W+++D  +Wl+  s ++
        k141_7094414 103 RLLFEHPLVEAITTWDFRDG-AWLKAPSGFV 132
                         *****99999********96.6988766655 PP


>> k141_5469463
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   35.3   0.0   1.6e-10   2.2e-10      37     110 ..      34     123 .]
12     123 .] 0.89


  Alignments for each domain:
  == domain 1  score: 35.3 bits;  conditional E-value: 1.6e-10
  MSA_GH10_xylanases  37 lkaagkkyf..GtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg…
…kfsFegadelvnfakkngkklRgH 110
                         lk+ ++++f  Gtav q  ++  + ++ii  +f+ ltpeN+MK++++ +
++a  l nfak+ng k+ gH
        k141_5469463  34 LKEIYADKFnfGTAVPQFAFMMPQLKQIILDQFNILTPENEMKPNSVLDVDAsrk
lvkdsgdetqaAVRLNDAKPLLNFAKENGLKVHGH 123
                         56667666666********************************9988777778
*********9999999*****************9 PP


>> k141_8982903
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   34.7   0.1   2.4e-10   3.3e-10     286     336 ..       1      53 [.
1      56 [. 0.93


  Alignments for each domain:
  == domain 1  score: 34.7 bits;  conditional E-value: 2.4e-10
  MSA_GH10_xylanases 286 yvevvkaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaiv
336
                         y+++++++++ k+++ +vt+W+++DkdsWl  ++ pl fden+++K + + i
        k141_8982903   1 YNRIFRIFRKHKDVIkNVTFWNLSDKDSWLGvNNHPLPFDENFKAKRSLQVIR
53
                         8999************************986899************99886
PP


>> k141_8992782
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
```

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```
   ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   34.2   0.0   3.3e-10   4.5e-10     291     337 ..       2      50 ..
1      53 [. 0.90

  Alignments for each domain:
  == domain 1  score: 34.2 bits;  conditional E-value: 3.3e-10
  MSA_GH10_xylanases 291 kaclevkkcv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                         +a+++ k+++ +vt+W++ D+dsWl   ++pl fd++y+pK ay+ i +
        k141_8992782   2 RAFRKHKDVIdCVTFWNLGDRDSWLGaANYPLPFDSEYKPKMAYEFIKD 50
                         689999****************964789**************98866 PP


>> k141_4516513
   #     score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
   ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   34.0   0.1   3.9e-10   5.3e-10     299     337 ..       3      43 ..
1      45 [. 0.90

  Alignments for each domain:
  == domain 1  score: 34.0 bits;  conditional E-value: 3.9e-10
  MSA_GH10_xylanases 299 cv.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                         ++ +vt+W++ D+dsWl  ++ pl fdeny+pK+ay+ai +
        k141_4516513   3 VIdCVTFWNLGDRDSWLGvNNHPLPFDENYKPKQAYYAIKN 43
                         5679***********986899**************976 PP


>> k141_2612768
   #     score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
   ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   33.9   0.0   4.1e-10   5.6e-10     197     309 ..       2     125 ..
1     126 [] 0.87

  Alignments for each domain:
  == domain 1  score: 33.9 bits;  conditional E-value: 4.1e-10
  MSA_GH10_xylanases 197 LyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkal
nalaslgvevaitELDia..lele… 273
                         L iND+n+ ++          +l++ llea+vpi  iG+qsH + g +  ++l++
l+++++ g+ ++ tE  +      ++
        k141_2612768   2 LLINDFNTGRS------
YENLIEGLLEADVPIGAIGIQSHQHQGYWGLEKLNDVLERFSRFGLPIHFTENTLIsgEIMPahivdlndwqvd 86
                         789****9966…77999********************************
**************8766333333889999999999 PP


  MSA_GH10_xylanases 274 …ateekleaqakdyvevvkaclevkkcvgvtvWgvaD 309
                         t e  ++qa++  e+ +++   + + +++t+W++ D
```

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```
          k141_2612768  87 swpSTPEGEDRQAREISEMYSVLFAHPLVEAITTWDFND 125
                           99877888889999999999998888888999999988 PP


>> k141_1708990
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   33.4   0.1   5.9e-10     8e-10     300     337 ..       3      42 ..
1       44 [. 0.90


  Alignments for each domain:
  == domain 1  score: 33.4 bits;  conditional E-value: 5.9e-10
  MSA_GH10_xylanases 300 v.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                         + +vt+W++ D+dsWl  ++ pl fdeny+pK+ay+ai +
        k141_1708990   3 IdCVTFWNLGDRDSWLGvNNHPLPFDENYKPKQAYYAIKN 42
                         569************986899***************976 PP


>> k141_1112321
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   33.2   0.1   6.6e-10     9e-10     274     338 ..      23      97 ..
15       99 .. 0.83


  Alignments for each domain:
  == domain 1  score: 33.2 bits;  conditional E-value: 6.6e-10
  MSA_GH10_xylanases 274
ateekleaqakdyvevvkaclevkk…cv.gvtvWgvaDkdsWls…eespllfdenynpKpaynaivka 338
                         ++++ +++ a +y+e +k++le kk    ++ +vt+W++ D++sWls
+++pl+f  + ++K+ay+a+++a
        k141_1112321  23
IPKRFIDKVAMRYQEFFKIYLEAKKsgkaNItSVTFWNLLDENSWLSgfrreTSYPLVFRGKCEAKEAYYAVLEA 97
5667778888999999998887754222278**************999998999***************986 PP


>> k141_2597435
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   33.0   0.1   7.6e-10     1e-09     187     272 ..       1      98 [.
1      108 [] 0.77


  Alignments for each domain:
  == domain 1  score: 33.0 bits;  conditional E-value: 7.6e-10
  MSA_GH10_xylanases 187 aareadpnakLyiNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsaga
…psvaelkkalnalaslgv.evai 263
```

```
                              +are  p+a L +NDYn+ +   ++++ ++l++kl++ag+p+d  G+q+H    +
+ ++lk++++++ +      + i
        k141_2597435    1 MARERWPDAILIYNDYNTVQW--
QKNEGIDLINKLKKAGAPVDAYGLQAHDMQVSggqaggqggggscLNINTLKSTIEEIWNKTQiPLFI 89
                         699999**********9976..6667789********************55444
4667888888887778888888877655444888 PP


  MSA_GH10_xylanases 264 tELDialel 272
                         E Dia +
        k141_2597435   90 SEYDIASND 98
                         999998333 PP


>> k141_7688599
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to   alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------   ------- -------
------- -------    ----
   1 !   32.9   0.0   8.2e-10   1.1e-09     176     260 ..       1     104 []
1     104 [] 0.67


  Alignments for each domain:
  == domain 1  score: 32.9 bits;  conditional E-value: 8.2e-10
  MSA_GH10_xylanases 176 lgedyvkiafeaare…adpnakLyiNDYnlesasakle..gmvklvkkll..
…eagvpidGiGsqsHlsaga…psvael 247
                         +g+dyv+ +f +ar+    ++ +++L++NDYn+ +++ ++   ++++ +++
++   idGiG+q+ l+           +++
        k141_7688599    1 VGDDYVEYSFLCARDtvekLGVDIRLFYNDYNMFMSEKRTAglALADSINHYAkd
esgNYRKLIDGIGMQGYLGGYGtqsgclspSLISDV 91
                         699**********9876668889*********9987544442223333333211
11134567*********9865545566664456777 PP


  MSA_GH10_xylanases 248 kkalnalaslgve 260
                         + +++++a+ g+e
        k141_7688599   92 RTSIRTYAANGLE 104
                         7788888877765 PP


>> k141_367108
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to   alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------   ------- -------
------- -------    ----
   1 !   32.3   0.1   1.3e-09   1.7e-09     300     337 ..       2      41 ..
1      43 [. 0.90


  Alignments for each domain:
  == domain 1  score: 32.3 bits;  conditional E-value: 1.3e-09
  MSA_GH10_xylanases 300 v.gvtvWgvaDkdsWls.eespllfdenynpKpaynaivk 337
                         + +vt+W++ D+dsWl  ++ pl fdeny+pK+ay ai +
```

```
        k141_367108    2 IdCVTFWNLGDRDSWLGvNNHPLPFDENYKPKQAYFAIKN 41
                         459*************986899***************99976 PP


>> k141_748038
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   32.6   0.0     1e-09   1.4e-09      38     113 ..      23     107 .]
2     107 .] 0.84


  Alignments for each domain:
  == domain 1  score: 32.6 bits;  conditional E-value: 1e-09
  MSA_GH10_xylanases  38 kaagkkyfGtavdqkelekskeeaiikkdfgsltpeNsMKweaiepsrg…
…kfsFegadelvnfakkngkklRgHtlv 113
                         + +    +G a    +++ +++ ++++  +f+slt  N+ K   ++ +++
+ ++++ad++ ++++++gk++RgH lv
        k141_748038   23 AEPYGFRLGGAFGIYDMFNANFMDFLDDHFNSLTCTNETKAYSLLDQNAsrrsed
gmpRMNYTNADRMIAWCQAHGKHVRGHVLV 107
                         444445567777777778899****************999998888999**
*************************998 PP


>> k141_1465015
   #     score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   31.9   0.0   1.7e-09   2.3e-09     200     309 ..       1     121 [.
1     122 [] 0.83


  Alignments for each domain:
  == domain 1  score: 31.9 bits;  conditional E-value: 1.7e-09
  MSA_GH10_xylanases 200 NDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnal
aslgvevaitELDia..lele… 273
                         ND+n+ +a         +l+++llea+vpi  iG+qsH + g +  ++l++
l+++++ g+ ++ tE  +
        k141_1465015   1 NDFNTSKA------
YEHLIEDLLEADVPISAIGIQSHQHQGYWGLEKLNDVLERYSRFGLPIHFTENTLIsgDI-Mpahivdlndwqvdew 84
                         66666644…667899*********************************
***********75542222.1366778889999999 PP


  MSA_GH10_xylanases 274 .ateekleaqakdyvevvkaclevkkcvgvtvWgvaD 309
                          t e  ++qa++  e+  ++ + + + ++t+W++ D
        k141_1465015  85 pSTPEGEDRQAREISEMYTILFSHPLVEAITTWDFND 121
                         87788888999999999999988888899999988 PP


>> k141_9484671
   #     score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
```

```
envfrom   env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   31.4   0.0   2.3e-09   3.2e-09     217     309 ..      2     111 .]
1     111 [] 0.91

  Alignments for each domain:
  == domain 1  score: 31.4 bits;  conditional E-value: 2.3e-09
  MSA_GH10_xylanases 217 lvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDia..
lele…ateekleaqakdyve 288
                        l+++ l+agvpi  iG+q+H + g +  ++l++ l+++   g+ ++ tE +
+t e  +qa++++e
       k141_9484671   2
LIRDCLDAGVPIGAIGLQTHQHQGYMGAEKLHEILKRFETIGLPLHFTENTLLsgH--
LmppdivdlndyqipewpTTPEGEARQAREWKE 90
                        678999****************************************888743
3..235899999999999999888888999****** PP


  MSA_GH10_xylanases 289 vvkaclevkkcvgvtvWgvaD 309
                        +++++ e +++ +vt W+++D
       k141_9484671  91 MLEILFEHPQVQAVTGWDFTD 111
                        ******************998 PP


>> k141_3608109
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom   env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   30.8   0.0   3.5e-09   4.8e-09     219     334 ..      2     132 ..
1     138 [. 0.86

  Alignments for each domain:
  == domain 1  score: 30.8 bits;  conditional E-value: 3.5e-09
  MSA_GH10_xylanases 219 kklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDia..le
le…ateekleaqakdyvevvk 291
                        ++ll+a+v+i  iG+qsH + g +  ++l+k l+++++ g+ ++ tE +
t +  e+qa++ +e+
       k141_3608109   2
EDLLAADVKISVIGIQSHQHQGYWGLEKLEKVLERFSRFGLPIHFTENTLIsgEL-
MppeiddlndwqvdnwpSTPAGEERQAREVTEMYT 91
                        57899****************************************88663433
.258999********998777888999999999999 PP


  MSA_GH10_xylanases 292 aclevkkcvgvtvWgvaDkdsWlseespllfdenynpKpayna 334
                        a+   + + ++t W+++D+  Wl+ + +l  ++   Kp+y+
       k141_3608109  92 ALFRHPLVQAITSWDFTDR-CWLNAPAGFL-RRDGTEKPSYQV 132
                        999999999*********7.7999888877.466777888876 PP
```

```
>> k141_8781529
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   30.5   0.0   4.4e-09      6e-09     218     309 ..      11     119 ..
5     123 .] 0.87


  Alignments for each domain:
  == domain 1  score: 30.5 bits;  conditional E-value: 4.4e-09
  MSA_GH10_xylanases 218 vkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitELDia..l
ele…ateekleaqakdyvevv 290
                         ++ lleagvpi  iG+qsH + g +  ++l++ l+++++ g+ ++ tE  +
t e  ++qa++  e+
        k141_8781529  11
LEGLLEAGVPISAIGIQSHQHQGYWGLEKLQDVLERYSRFGLPIHFTENTLIsgEL-
MpphivdlndwqvdewpSTPEGEDRQAREISEMY 100
                         56799*****************************************8766343
3.258999999999999888888899999999999 PP


  MSA_GH10_xylanases 291 kaclevkkcvgvtvWgvaD 309
                         +++ + + + ++t+W++ D
        k141_8781529 101 SVLFSHPLVEAITTWDFND 119
                         9999999888*****9998 PP


>> k141_6150587
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   29.5   0.0   9.1e-09   1.2e-08     199     265 ..       2      62 ..
1     103 [. 0.89


  Alignments for each domain:
  == domain 1  score: 29.5 bits;  conditional E-value: 9.1e-09
  MSA_GH10_xylanases 199
iNDYnlesasaklegmvklvkklleagvpidGiGsqsHlsagapsvaelkkalnalaslgvevaitE 265
                         iND+n+ +            l++ lleagvpi  iG+qsH + g +  ++l++
l+++++ g+ ++ tE
        k141_6150587   2 INDFNTSVS------
YEILLEGLLEAGVPISAIGIQSHQHQGYWGLEKLNNVLERFSRFGLPIHFTE 62
788888866…3446889****************************************9 PP


>> k141_8997217
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
```

```
   1 !   28.9   0.0   1.3e-08   1.8e-08     125     163 ..       60       98 ..
36      101 .. 0.90


   Alignments for each domain:
   == domain 1  score: 28.9 bits;  conditional E-value: 1.3e-08
   MSA_GH10_xylanases 125 ikadketllevlknhiktvvgrYkgkvyaWDVvNEilne 163
                          ++++k+tl+ +l+n+i+ +++   +gkv+aWDVvNE +++
        k141_8997217   60 EEVKKDTLTWALNNFISGMMKACNGKVKAWDVVNEPMSD 98
                          4579**************************9876 PP


>> k141_3860753
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   28.7   0.0   1.6e-08   2.2e-08     241     312 ..      11       93 ..
1     124 [] 0.74


   Alignments for each domain:
   == domain 1  score: 28.7 bits;  conditional E-value: 1.6e-08
   MSA_GH10_xylanases 241 a…psvaelkkalnalaslgvevaitELDia.leleateekleaqakdy
vevvkaclevkkcv..gvtvWgvaDkds 312
                                       + +k++++ ++s+g+ev++tE+ ++ +++ +++e++e +a+
++ev+  + + ++    +v +Wg+ D+d
        k141_3860753   11 GtqegcleeSLITGVKESIELFSSMGLEVQLTEMAVRnFDQSKAAEHAEFYARLF
TEVFMKANSEDSHPltAVCIWGLVDADP 93
IOPub message rate exceeded.
The notebook server will temporarily stop sending output
to the client in order to avoid crashing it.
To change this limit, set the config variable
`--NotebookApp.iopub_msg_rate_limit`.

Current values:
NotebookApp.iopub_msg_rate_limit=1000.0 (msgs/sec)
NotebookApp.rate_limit_window=3.0 (secs)
```

[30]:
```
%use bash
head -n 20 GH10_results.txt
```

```
#                                                        --- full
sequence ---- --- best 1 domain ---- --- domain number estimation ----
# target name         accession  query name              accession   E-value  score
bias   E-value   score  bias   exp reg clu  ov env dom rep inc description of
target
#------------------- ---------- -------------------- ---------- --------- ------
----- --------- ------ -----    --- --- --- --- --- --- --- ---
```

```
--------------------
k141_4174516          -          MSA_GH10_xylanases    -          1.9e-105  347.8
0.1  2.4e-105  347.5   0.1   1.0   1   0   0   1   1   1   1 -
k141_8751303          -          MSA_GH10_xylanases    -          6.4e-104  342.8
0.1    9e-104  342.3   0.1   1.1   1   0   0   1   1   1   1 -
k141_2596728          -          MSA_GH10_xylanases    -          5.1e-100  329.9
3.0  5.7e-100  329.8   3.0   1.0   1   0   0   1   1   1   1 -
k141_8352380          -          MSA_GH10_xylanases    -          6.2e-100  329.7
2.8  7.8e-100  329.3   2.8   1.1   1   0   0   1   1   1   1 -
k141_7876638          -          MSA_GH10_xylanases    -           1.5e-99  328.4
1.2   2.7e-99  327.6   1.2   1.3   1   1   0   1   1   1   1 -
k141_7518864          -          MSA_GH10_xylanases    -           1.9e-98  324.8
0.5   2.2e-98  324.6   0.5   1.0   1   0   0   1   1   1   1 -
k141_3207327          -          MSA_GH10_xylanases    -           2.2e-98  324.6
0.3   2.4e-98  324.4   0.3   1.0   1   0   0   1   1   1   1 -
k141_8446463          -          MSA_GH10_xylanases    -           3.9e-98  323.8
3.5   4.7e-98  323.5   3.5   1.0   1   0   0   1   1   1   1 -
k141_3648730          -          MSA_GH10_xylanases    -           2.5e-96  317.8
2.9   2.8e-96  317.7   2.9   1.0   1   0   0   1   1   1   1 -
k141_382248           -          MSA_GH10_xylanases    -           7.2e-96  316.3
0.0   1.1e-95  315.7   0.0   1.2   1   0   0   1   1   1   1 -
k141_7690424          -          MSA_GH10_xylanases    -           1.3e-94  312.2
3.2   1.5e-94  312.0   3.2   1.0   1   0   0   1   1   1   1 -
k141_2078416          -          MSA_GH10_xylanases    -           5.1e-91  300.4
2.1   5.7e-91  300.2   2.1   1.0   1   0   0   1   1   1   1 -
k141_5777399          -          MSA_GH10_xylanases    -           1.1e-89  296.0
0.4   1.3e-89  295.7   0.4   1.0   1   0   0   1   1   1   1 -
k141_6414633          -          MSA_GH10_xylanases    -           1.4e-89  295.6
1.2   1.8e-89  295.3   1.2   1.0   1   0   0   1   1   1   1 -
k141_1984896          -          MSA_GH10_xylanases    -           1.2e-87  289.3
1.8   1.5e-87  289.0   1.8   1.0   1   0   0   1   1   1   1 -
k141_3321694          -          MSA_GH10_xylanases    -           3.2e-87  287.9
1.6   3.6e-87  287.7   1.6   1.0   1   0   0   1   1   1   1 -
k141_1057675          -          MSA_GH10_xylanases    -           2.4e-85  281.7
1.6   2.7e-85  281.6   1.6   1.0   1   0   0   1   1   1   1 -
```

This file contains the most likely contigs to be xylanase proteins. We will use the top three of them for the next structural analysis.

[31]:
```
%use bash
cd ../
```

Let's do the same for GH11 subfamily

[32]:
```
%use bash
cd GH11/
```

```
[33]: %use bash
      cd Sequences/
```

```
[34]: %use bash
      ls
```

```
A6YAP7.fasta.txt   P0CT48.fasta.txt
P55330.fasta.txt   Q4P0L3.fasta.txt
B3VSG7.fasta.txt   P18429.fasta.txt
P55331.fasta.txt   Q4WG11.fasta.txt
G0RUP7.fasta.txt   P26220.fasta.txt
P55332.fasta.txt   Q9HFA4.fasta.txt
I1RII8.fasta.txt   P33557.fasta.txt
P55333.fasta.txt   Q9HFH0.fasta.txt
I1S2K3.fasta.txt   P36217.fasta.txt
P81536.fasta.txt   V9TXH2.fasta.txt
O43097.fasta.txt   P36218.fasta.txt
Q12550.fasta.txt   W0HJ53.fasta.txt
O74716.fasta.txt   P55328.fasta.txt
Q2LMP0.fasta.txt
P09850.fasta.txt   P55329.fasta.txt
Q2PGY1.fasta.txt
```

These are the 30 sequences for modeling GH10 subfamily. Let's open one of them.

```
[35]: %use bash
      cat A6YAP7.fasta.txt
```

```
>sp|A6YAP7|XYN1_LEUGO Endo-1,4-beta-xylanase 1 OS=Leucoagaricus gongylophorus
OX=79220 GN=Xyn1 PE=1 SV=1
MVSFIFTRIILFAAAINGAVALPMNTTEPEDFSILSRSGTPSSTGYSNGYYYSWWTDGAA
QATYANGGGGQYSLNWSGNNGNLVGGKGWNPGFNGRVIQYSGTYQPNGNSYLSVYGWTLN
PLIEYYIVESYGSYNPSSAAARKGSVNCDGANYDILTTTRYNEPSINGTQTFQQFWSVRN
PKKNPGGSISGSVSTGCHFTAWGNLGMNLGSTWNYQIVATEGYQSSGFSSITVA
```

```
[36]: %use bash
      cd ../
```

```
[37]: %use bash
      cat Sequences/* > GH11_sequences.fasta
```

```
[38]: %use bash
      head -n 20 GH11_sequences.fasta
```

```
>sp|A6YAP7|XYN1_LEUGO Endo-1,4-beta-xylanase 1 OS=Leucoagaricus gongylophorus
OX=79220 GN=Xyn1 PE=1 SV=1
MVSFIFTRIILFAAAINGAVALPMNTTEPEDFSILSRSGTPSSTGYSNGYYYSWWTDGAA
QATYANGGGGQYSLNWSGNNGNLVGGKGWNPGFNGRVIQYSGTYQPNGNSYLSVYGWTLN
```

```
PLIEYYIVESYGSYNPSSAAARKGSVNCDGANYDILTTTRYNEPSINGTQTFQQFWSVRN
PKKNPGGSISGSVSTGCHFTAWGNLGMNLGSTWNYQIVATEGYQSSGFSSITVA
>sp|B3VSG7|XY11A_BOTFB Endo-1,4-beta-xylanase 11A OS=Botryotinia fuckeliana
(strain B05.10) OX=332648 GN=xyn11A PE=1 SV=1
MVSASSLLLAASAIAGVFSAPAAAPVSENLNVLQERALTSSATGTSGGYYYSFWTDGSGG
VTYSNGDNGQYAVSWTGNKGNFVGGKGWAVGSERSISYTGSYKPNGNSYLSVYGWTTFPL
IEYYIVEDFGTYDPSSAATEIGSVTSDGSTYKILETTRTNQPSIQGTATFKQYWSVRTSK
RTSGTVTTANHFAAWKKLGLTLGSTYDYQIVAVEGYQSGSASITVS
>sp|G0RUP7|XYN2_HYPJQ Endo-1,4-beta-xylanase 2 OS=Hypocrea jecorina (strain
QM6a) OX=431241 GN=xyn2 PE=1 SV=1
MVSFTSLLAGVAAISGVLAAPAAEVESVAVEKRQTIQPGTGYNNGYFYSYWNDGHGGVTY
TNGPGGQFSVNWSNSGNFVGGKGWQPGTKNKVINFSGSYNPNGNSYLSVYGWSRNPLIEY
YIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQRVNQPSIIGTATFYQYWSVRRNHRSS
GSVNTANHFNAWAQQGLTLGTMDYQIVAVEGYFSSGSASITVS
>sp|I1RII8|XYNB_GIBZE Endo-1,4-beta-xylanase B OS=Gibberella zeae (strain ATCC
MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) OX=229533 GN=XYLB PE=1
SV=1
MVSFTYLLAAVSAVTGAVAAPNPTKVDAQPPSGLLEKRTSPTTGVNNGFYFSFWTDTPSA
VTYTNGNGGQFSMNWNGNRGNHVGGKGWNPGAARTIKYSGDYRPNGNSYLAVYGWTRNPL
VEYYIVENFGTYNPSSGAQKKGEINIDGSIYDIAVSTRNCAPSIEGDCKTFQQYWSVRRN
KRSSGSVNTGAHFNAWAQAGLRLGSHDYQILAVEGYQSSGQATMTVSG
```

[39]:
```bash
%use bash
# MSA
mafft --auto GH11_sequences.fasta > MSA_GH11_xylanases.fasta
```

```
outputhat23=16
treein = 0
compacttree = 0
stacksize: 8192 kb
rescale = 1
All-to-all alignment.
tbfast-pair (aa) Version 7.490
alg=L, model=BLOSUM62, 2.00, -0.10, +0.10, noshift, amax=0.0
0 thread(s)

outputhat23=16
Loading 'hat3.seed' …
done.
Writing hat3 for iterative refinement
rescale = 1
Gap Penalty = -1.53, +0.00, +0.00
tbutree = 1, compacttree = 0
Constructing a UPGMA tree …
    20 / 30
done.

Progressive alignment …
```

```
STEP    22 /29
Reallocating..done. *alloclen = 1485
STEP    29 /29
done.
tbfast (aa) Version 7.490
alg=A, model=BLOSUM62, 1.53, -0.00, -0.00, noshift, amax=0.0
1 thread(s)

minimumweight = 0.000010
autosubalignment = 0.000000
nthread = 0
randomseed = 0
blosum 62 / kimura 200
poffset = 0
niter = 16
sueff_global = 0.100000
nadd = 16
Loading 'hat3' … done.
rescale = 1

    20 / 30
Segment    1/  1     1- 299
STEP 007-019-1  rejected..
Converged.

done
dvtditr (aa) Version 7.490
alg=A, model=BLOSUM62, 1.53, -0.00, -0.00, noshift, amax=0.0
0 thread(s)


Strategy:
 L-INS-i (Probably most accurate, very slow)
 Iterative refinement method (<16) with LOCAL pairwise alignment information

If unsure which option to use, try 'mafft --auto input > output'.
For more information, see 'mafft --help', 'mafft --man' and the mafft page.

The default gap scoring scheme has been changed in version 7.110 (2013 Oct).
It tends to insert more gaps into gap-rich regions than previous versions.
To disable this change, add the --leavegappyregion option.
```

[40]:
```bash
%use bash
head -n 20 MSA_GH11_xylanases.fasta
```

```
>sp|A6YAP7|XYN1_LEUGO Endo-1,4-beta-xylanase 1 OS=Leucoagaricus gongylophorus
OX=79220 GN=Xyn1 PE=1 SV=1
```

```
MVSF--------------------IFTRIILFAAAING-AVALPMNT--------TEP
EDFSILSRS-GTPSSTGYS-------NGYYYSWWTDGAAQATYANGGGGQYSLNWSGN--
NGNLVGGKGWNPGFNG-RVIQY-SGTYQP--N-GNSYLSVYGWTLNPLIEYYIVESYGSY
NPS--SAAARKGSVNCDGANYDILTTTRYNEPSINGTQ-TFQQFWSVRNPKKNPGGSISG
SVSTGCHFTAWGNLGMNLGS---TWNYQIVATEGYQSSGFSSITVA---
>sp|B3VSG7|XY11A_BOTFB Endo-1,4-beta-xylanase 11A OS=Botryotinia fuckeliana
(strain B05.10) OX=332648 GN=xyn11A PE=1 SV=1
MVS---------------------ASSLLLAASAIAG-VFSAPAAA--------PVSE
NLNVLQERA-LTSSATGTS-------GGYYYSFWTDGSGGVTYSNGDNGQYAVSWTGN--
KGNFVGGKGWAVG-SE-RSISY-TGSYKP--N-GNSYLSVYGWTTFPLIEYYIVEDFGTY
DPS--SAATEIGSVTSDGSTYKILETTRTNQPSIQGTA-TFKQYWSVRTSKRT-----SG
TVTTANHFAAWKKLGLTLGS---TYDYQIVAVEGYQ-SGSASITVS---
>sp|G0RUP7|XYN2_HYPJQ Endo-1,4-beta-xylanase 2 OS=Hypocrea jecorina (strain
QM6a) OX=431241 GN=xyn2 PE=1 SV=1
MVS---------------------FTSLLAGVAAISG-VLAAPA-----------AEV
ESVAVEKRQ-TIQPGTGYN-------NGYFYSYWNDGHGGVTYTNGPGGQFSVNWS-N--
SGNFVGGKGWQPG-TKNKVINF-SGSYNP--N-GNSYLSVYGWSRNPLIEYYIVENFGTY
NPS--TGATKLGEVTSDGSVYDIYRTQRVNQPSIIGTA-TFYQYWSVRRNHRS-----SG
SVNTANHFNAWAQQGLTLG----TMDYQIVAVEGYFSSGSASITVS---
>sp|I1RII8|XYNB_GIBZE Endo-1,4-beta-xylanase B OS=Gibberella zeae (strain ATCC
MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) OX=229533 GN=XYLB PE=1
SV=1
MVS---------------------FTYLLAAVSAVTG-AVAAPNPT------KVDAQP
```

```
[41]: %use bash
      # Modeling with HMM
      hmmbuild GH11_xylanase.hmm MSA_GH11_xylanases.fasta
      hmmsearch --tblout GH11_results.txt GH11_xylanase.hmm ../../clustered_sequences.
        ↪fasta
```

```
# hmmbuild :: profile HMM construction from multiple sequence alignments
# HMMER 3.3.2 (Nov 2020); http://hmmer.org/
# Copyright (C) 2020 Howard Hughes Medical Institute.
# Freely distributed under the BSD open source license.
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# input alignment file:          MSA_GH11_xylanases.fasta
# output HMM file:               GH11_xylanase.hmm
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

# idx name                  nseq  alen  mlen eff_nseq re/pos description
#---- ------------------- ----- ----- ----- -------- ------ -----------
1     MSA_GH11_xylanases      30   289   222     0.88  0.589

# CPU time: 0.07u 0.00s 00:00:00.07 Elapsed: 00:00:00.09
# hmmsearch :: search profile(s) against a sequence database
# HMMER 3.3.2 (Nov 2020); http://hmmer.org/
# Copyright (C) 2020 Howard Hughes Medical Institute.
# Freely distributed under the BSD open source license.
```

```
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# query HMM file:                 GH11_xylanase.hmm
# target sequence database:       ../../clustered_sequences.fasta
# per-seq hits tabular output:    GH11_results.txt
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -


Query:       MSA_GH11_xylanases  [M=222]
Scores for complete sequences (score includes all domains):
   --- full sequence ---    --- best 1 domain ---    -#dom-
    E-value  score  bias    E-value  score  bias    exp  N  Sequence
Description
    -------  ------ -----    -------  ------ -----    ---- --  --------
-----------
    6.4e-63  207.3  13.1    7.4e-63  207.0  13.1    1.0  1  k141_2912295
    3.5e-60  198.3   6.0    4.8e-60  197.8   6.0    1.1  1  k141_2003823
    4.8e-56  184.8   9.8    1.1e-55  183.6   9.8    1.5  1  k141_9005574
    1.9e-55  182.8   6.0    2.7e-55  182.3   6.0    1.2  1  k141_5844946
    3.8e-55  181.8  12.2    3.8e-55  181.8  12.2    1.6  2  k141_7538601
    6.9e-55  181.0  12.3      9e-55  180.6  12.3    1.1  1  k141_8367260
    6.3e-54  177.8  12.6    1.3e-53  176.8  12.6    1.5  1  k141_1296036
    4.4e-52  171.8  13.1      6e-52  171.4  13.1    1.1  1  k141_8720139
    3.4e-47  155.8   7.0    4.5e-47  155.4   7.0    1.1  1  k141_2049582
    5.6e-47  155.1   3.9    1.1e-46  154.2   3.9    1.5  1  k141_2606760
      4e-45  149.1   2.2    4.8e-45  148.8   2.2    1.1  1  k141_5257166
    1.5e-44  147.1   8.9      3e-44  146.2   8.9    1.4  1  k141_7441232
    8.9e-44  144.6   2.4      1e-43  144.4   2.4    1.0  1  k141_2387523
    2.4e-42  139.9  10.4    4.9e-42  139.0  10.4    1.4  1  k141_7730058
    2.9e-42  139.7   2.8    3.3e-42  139.5   2.8    1.0  1  k141_1928726
    1.3e-41  137.6   2.2    1.5e-41  137.3   2.2    1.0  1  k141_2356616
    8.7e-41  134.9  13.6    3.2e-40  133.0  13.6    1.7  1  k141_5463473
    3.5e-40  132.9   5.3    3.7e-40  132.8   5.3    1.0  1  k141_4491313
    1.5e-39  130.9   9.3    2.2e-39  130.3   9.3    1.2  1  k141_6411968
      1e-37  124.8   3.0    1.4e-37  124.4   3.0    1.0  1  k141_6801310
    1.7e-37  124.1   5.1    1.9e-37  123.9   5.1    1.0  1  k141_4644390
    1.4e-36  121.1  13.2    1.8e-36  120.8  13.2    1.1  1  k141_6776299
    1.8e-36  120.7   5.2    2.2e-36  120.5   5.2    1.0  1  k141_3276475
    2.2e-36  120.4   4.8    2.9e-36  120.1   4.8    1.1  1  k141_127344
    3.9e-28   93.5   2.7    4.8e-28   93.2   2.7    1.1  1  k141_3001072
    2.5e-26   87.6   7.7    2.6e-26   87.5   7.7    1.1  1  k141_5776627
    4.2e-25   83.6   2.4      5e-25   83.3   2.4    1.0  1  k141_4500609
    2.9e-23   77.6  11.1    3.7e-23   77.2  11.1    1.1  1  k141_4891430
    8.9e-20   66.2   0.0    1.2e-19   65.8   0.0    1.1  1  k141_8326139
    2.9e-14   48.2   5.1    5.6e-14   47.2   5.1    1.4  1  k141_124775
    2.1e-12   42.1   4.1    1.2e-08   29.7   0.0    2.2  2  k141_7411831
    2.9e-07   25.3  15.1    2.2e-06   22.4  11.0    2.3  2  k141_7367989


Domain annotation for each sequence (and alignments):
```

```
>> k141_2912295
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom   env to      acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  207.0 13.1   4.1e-64   7.4e-63      32     218 ..      10     202 .]
2     202 .] 0.88

  Alignments for each domain:
  == domain 1  score: 207.0 bits;  conditional E-value: 4.1e-64
  MSA_GH11_xylanases  32 kraltssstgasngyyysfwtdgggevtytngsggeysveWensgnfvgGkGWnp
gss…rai…kysgsyspsgnsylavYGWtrn 114
                         + ++++++tg ++gy y+ w+d +g++++t ++gg+++ +W+n +n    kG +
s+   ++i      +y  +y+p+gnsyl+vYGWt +
        k141_2912295  10 ADTIYNNKTGNQDGYDYELWKD-
TGNTSMTLNAGGTFDCSWSNINNALFRKGKKFDSTktyQQIgnisfDYGCDYRPNGNSYLCVYGWTVD 99
                         4567899**************9.6889999*************9888666555554
443113333222336899***************** PP

  MSA_GH11_xylanases 115 plveyYivenygtynPssgatkkGtvtsdGstYdiytstrvnqpsieGtatFtqy
wsvRqskrtsgtvttanhfnaWaklGlnlgtfnYqi 205
                         plveyYiv+++gt++P  g+  kG+++
dG+tYd+y++tr+n+psi+G++tF+qy+svR+skrtsgt+++++hf+aW+++G++ g+++
        k141_2912295 100 PLVEYYIVDSWGTWRPP-
GGSPKGQIQVDGGTYDVYETTRYNAPSIQGDTTFKQYFSVRTSKRTSGTISVSEHFKAWERMGMRCGKIYEAA 189
                         ***************9.8999*******************************
********************************** PP

  MSA_GH11_xylanases 206 vategyqssgsas 218
                         +++egyqssgsas
        k141_2912295 190 LNIEGYQSSGSAS 202
                         **********96 PP


>> k141_2003823
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom   env to      acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  197.8  6.0   2.7e-61   4.8e-60       8     219 ..       8     239 ..
1     241 [. 0.81

  Alignments for each domain:
  == domain 1  score: 197.8 bits;  conditional E-value: 2.7e-61
  MSA_GH11_xylanases   8 laaaaaaagalaapa…eeeeaaelekraltssstgasngyyysfwtdggg
evtytngsggeysveWensgn..fvgGkGWnpgss. 89
                         ++++  ++g+ ++       + +ea++ ++   t++ t +++gy y+ w+d+g
++  ++  gg++s eW+n +n  f  Gk +  +++
        k141_2003823   8 VCMMGISTGCSSTSSnsdgksSAKEAEKSKALVFTENVTDTADGYDYELWKDNGD
```

202

```
TTFTVEPGGGNFSCEWSNINNalFRRGKKYDCTQTy 98
                           4444444443333334454333344444455555788999999**********877
7777788899*******9777335567766554322 PP


  MSA_GH11_xylanases   90 …raikysgsyspsgnsylavYGWtrnplveyYivenygtynPssgatkkGt
vtsdGstYdiytstrvnqpsieGtatFtqywsvRqs 175
                             +i+y   +y+p+gnsy++vYGWtr+pl+eyYive++gt++P  +
+Gtv+ dG++Ydiy++trv+qpsi+  +tF+qywsvRq+
        k141_2003823   99 demgnISINYGVDYQPDGNSYMCVYGWTREPLIEYYIVESWGTWRPPGAPMALGT
VKVDGAVYDIYKTTRVEQPSIDDIQTFDQYWSVRQE 189
                           11122579************************************************
*******************************9 PP


  MSA_GH11_xylanases  176 krt…sgtvttanhfnaWaklGlnlgtfnYqivategyqssgsasi 219
                           k +      +gt+++++hf+aW+k Gl+lg+++   +++egyqs g+a+i
        k141_2003823  190 KPKpngtkiEGTISVSKHFDAWKKCGLELGKMYEVALNIEGYQSQGKATI 239
                           9766777789*****************9999************98 PP


>> k141_9005574
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  183.6   9.8   6.2e-57   1.1e-55       5     220 ..      24     254 ..
15     256 .. 0.83


  Alignments for each domain:
  == domain 1  score: 183.6 bits;  conditional E-value: 6.2e-57
  MSA_GH11_xylanases    5 ksllaaaaaaagalaapaeeeeaaelekraltssstgasngyyysfwtd.gggev
tytngsggeysveWensgnfvgGkGWnp… 86
                           +++ a a++++g+ a p    e+ +l+++a  ++  g  +gy y++w++
g+g++++ + s g+++ + +n +nf +  G n
        k141_9005574   24 SAVTASALLLVGTTAFP----
ETGMLSAKAADAQDRGNVGGYDYEMWNQnGQGQASM-KPSEGSFTCSLSNIENFLARMGKNYdskklnyk 109
                           34445555566666666…5777888888888999999998888876155666
66.788899***********977766511222222 PP


  MSA_GH11_xylanases   87 ..gssraikysgsyspsgnsylavYGWtrnplveyYivenygtynPssgatkkGt
vtsdGstYdiytstrvnqpsieGtatFtqywsvRqs 175
                             gs+  ++y  +ysp gnsy++vYGWtr+pl+eyYive +g+++P++
++kkGtvt dG+tYdi++++r+nqps++Gt+tF qywsvRq
        k141_9005574  110 diGSNIVLTYDVEYSPRGNSYMCVYGWTRTPLMEYYIVEGWGSWRPGADGEKKGT
VTLDGNTYDIAKTMRYNQPSLDGTQTFPQYWSVRQT 200
                           225555789**********************************************
**************************98 PP


  MSA_GH11_xylanases  176 krt…sgtvttanhfnaWaklGlnlgtfnYqi.vategyqssgsasit
220
```

```
                              +        sg + +++hf+aW+++Gl+++   Y + +++egy+s gsa+++
         k141_9005574 201 SGSrdnvqnnmSGIIHVGKHFDAWSQKGLDMSGTLYEVsLNIEGYRSNGSANVK
254
                              655557778889********************888988689**********985
PP


>> k141_5844946
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  182.3   6.0   1.5e-56   2.7e-55      84     219 ..      16     150 ..
5      153 .. 0.95


  Alignments for each domain:
  == domain 1  score: 182.3 bits;  conditional E-value: 1.5e-56
  MSA_GH11_xylanases  84 WnpgssraikysgsyspsgnsylavYGWtrnplveyYivenygtynPssgatkkG
tvtsdGstYdiytstrvnqpsieGtatFtqywsvRq 174
                          +++  + +++y  +y+p+gnsyl+vYGW+r+pl+eyYiv+++gt++P  g+++
Gt++ dG+tYdiy++ r nqpsi+G++tF+qywsvR+
        k141_5844946  16 YKQMGAISVEYGVDYKPDGNSYLCVYGWSRDPLIEYYIVDSWGTWRPP-
GSKSMGTIEVDGGTYDIYETIRENQPSIDGNTTFKQYWSVRT 105
                          556667789****************************************9.899***
********************************* PP


  MSA_GH11_xylanases 175 skrtsgtvttanhfnaWaklGlnlgtfnYqivategyqssgsasi 219
                          +krtsgt+++++hf+aW++lGl+lg+ +   +++egyqs g a++
        k141_5844946 106 EKRTSGTISVTEHFKAWEQLGLTLGKLYEASLTIEGYQSNGWADV 150
                          ***************************************9987 PP


>> k141_7538601
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  181.8  12.2   2.1e-56   3.8e-55      38     219 ..       9     210 ..
2      213 .. 0.83
   2 ?   -3.0   0.3       7.1   1.3e+02      46      58 ..     248     260 ..
231      276 .. 0.54


  Alignments for each domain:
  == domain 1  score: 181.8 bits;  conditional E-value: 2.1e-56
  MSA_GH11_xylanases  38 sstgasngyyysfwt.dgggevtytngsggeysveWensgnfvgGkGWnp…
…gssraikysgsyspsgnsylavYGWtrnplv 117
                          +  g  +gy y++w+ +g+g+v++t g +g+++ +W+n +nf +  G n
gs  +++y  +y+p gnsy++vYGWtrnpl+
        k141_7538601   9 QDRGNIGGYDYEMWNqNGQGQVSMTPG-
AGSFTCSWSNIENFLARMGKNYdskkqrygqiGSDITLTYDVEYTPRGNSYMCVYGWTRNPLM 98
```

```
                              5566667776777752688999996665.678***********977765411112
222224555799********************* PP


   MSA_GH11_xylanases 118 eyYivenygtynP.ssgatkkGtvtsdGstYdiytstrvnqpsieGtatFtqyws
vRqskrt…sgtvttanhfnaWaklGlnlg 199
                              eyYive +g+++P + ga++kGtvt dG+tYdi++++r+nqps++GtatF
qyws+Rq   +        +gt+ +++hf+aW+k+Gl+++
         k141_7538601   99 EYYIVEGWGDWRPpGDGAERKGTVTLDGNTYDIAKTMRYNQPSLDGTATFPQYWS
IRQTSGSrnntqnnmKGTIHVGKHFDAWSKAGLDMS 189
                              ***********96268999***************************************
**97544446677889***************** PP


   MSA_GH11_xylanases 200 tfnYqi.vategyqssgsasi 219
                              Y + +++egy+s gsa++
         k141_7538601 190 GTLYEVsLNIEGYRSNGSANV 210
                              888988689**********98 PP


   == domain 2  score: -3.0 bits;  conditional E-value: 7.1
   MSA_GH11_xylanases  46 yyysfwtdgggev 58
                              y++s ++ g+g+
         k141_7538601 248 YFTSTFESGAGDW 260
                              3345555555543 PP


>> k141_8367260
    #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
    1 !  180.6  12.3     5e-56     9e-55      15     220 ..      15      239 ..
5     241 .] 0.79


   Alignments for each domain:
   == domain 1  score: 180.6 bits;  conditional E-value: 5e-56
   MSA_GH11_xylanases  15 agalaapaeeeeaaelekraltssstgasngyyysfwt.dgggevtytngsggey
sveWensgnfvgGkGWnpgssra…ikys 95
                              +ga aa +    ++   ++a  +++ g  +g+ y++w+ +g+g++++ n
+g+++ +W+n +nf +  G n  s+++         ++y
         k141_8367260  15 IGAGAAAMMVAVSVPAVASAADQQTRGNIGGFDYEMWNqNGQGQASM-
NPGAGSFTCSWSNIENFLARMGKNYDSQKKnykafgnivLTYD 104
                              4433333322223333333334556666666666665166777777.888999*
***********98888877664223334443379** PP


   MSA_GH11_xylanases  96 gsyspsgnsylavYGWtrnplveyYivenygtynP.ssgatkkGtvtsdGstYdi
ytstrvnqpsieGtatFtqywsvRqskrt… 178
                              +y+p gnsy++vYGWtrnpl+eyYive +g+++P ++ ++ kGtvt++G+tYdi
+++r+nqps++GtatF qywsvRq   +
         k141_8367260 105 VEYTPRGNSYMCVYGWTRNPLMEYYIVEGWGDWRPpGNDGEVKGTVTANGNTYDI
RKTMRYNQPSLDGTATFPQYWSVRQTSGSannqtny 195


                              205
```

```
                                **********************************9636899**************
************************976555566688 PP

  MSA_GH11_xylanases 179 .sgtvttanhfnaWaklGlnlgtfnYqi.vategyqssgsasit 220
                         +gt+++++hf+aW+ +Gl+++   Y + +++egy+s gsa+++
        k141_8367260 196 mKGTIDVTKHFDAWSAAGLDMSGTLYEVsLNIEGYRSNGSANVK 239
                         89*******************888988689**********985 PP


>> k141_1296036
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  176.8  12.6   7.2e-55   1.3e-53      47     220 ..      2     195 ..
1     197 [. 0.86


  Alignments for each domain:
  == domain 1  score: 176.8 bits;  conditional E-value: 7.2e-55
  MSA_GH11_xylanases  47 yysfwtdgggevtytngsggeysveWensgnfvgGkGWnpgssr…a
ikysgsyspsgnsylavYGWtrnplveyYivenygt 127
                         y  + ++g+g+v++ n s+g+++ +W+n +nf +  G n  s++
+++y  +y+p gnsy++vYGWtrnpl+eyYive +g+
        k141_1296036   2 YEMWNQNGQGQVSM-
NPSAGSFTCSWSNIENFLARMGKNYDSQKkkykqigediTLTYDVEYTPRGNSYMCVYGWTRNPLMEYYIVEGWGD 91
                         56667789999999.999***************9777665544212222333226
79******************************** PP


  MSA_GH11_xylanases 128 ynPs..sgatkkGtvtsdGstYdiytstrvnqpsieGtatFtqywsvRqskrt..
…sgtvttanhfnaWaklGlnlgtfnYqi.va 207
                         ++P   +g ++kGtvt dG+ Ydi++s+r+nqps++Gt+tF qywsvRq   +
+gtv ++ hf+aW+++Gl+++   Y + ++
        k141_1296036  92 WRPPgnNGVESKGTVTLDGNKYDICKSMRYNQPSLDGTKTFPQYWSVRQTSGSrn
ntqnnmKGTVHVGRHFDAWSNAGLDMSGTLYEVsLN 182
                         **964468899******************************************9754444
6677889******************888988689 PP


  MSA_GH11_xylanases 208 tegyqssgsasit 220
                         +egy+s gsa+++
        k141_1296036 183 IEGYRSNGSANVK 195
                         **********985 PP


>> k141_8720139
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  171.4  13.1   3.3e-53      6e-52      47     220 ..      4     195 ..
1     198 [. 0.86
```

206

```
  Alignments for each domain:
  == domain 1  score: 171.4 bits;  conditional E-value: 3.3e-53
  MSA_GH11_xylanases  47 yysfwtdgggevtytngsggeysveWensgnfvgGkGWnpgssra…i
kysgsyspsgnsylavYGWtrnplveyYivenygty 128
                          y  + ++g+g++++ n s+g+++ +W+n +nf +  G n  s+++
++y  +y+p gnsy++vYGWtrnpl+eyYive +g++
        k141_8720139   4 YEMWNQNGQGNAQM-
NPSAGSFTCSWSNIENFLARMGKNFDSQKKnykalgdivLTYDVEYTPRGNSYMCVYGWTRNPLMEYYIVEGWGDW 93
                          45555667777777.999**************988887766542333444337
9******************************** PP


  MSA_GH11_xylanases 129 nP.ssgatkkGtvtsdGstYdiytstrvnqpsieGtatFtqywsvRqskrt…
…sgtvttanhfnaWaklGlnlgtfnYqi.vate 209
                          +P ++ +++kG++t +G+tY+i++++r+nqps++GtatF qyws+R+   +
+gt+++++hf+aW+++Gl+++   Y + +++e
        k141_8720139  94 RPpGNDGERKGNITLNGNTYEIAKTMRYNQPSLDGTATFPQYWSIRTTSGSannq
tnymKGTIDVSKHFDAWSQKGLDMSGTLYEVsLNIE 184
                          9637999*****************************************876555556
67889******************888988689** PP


  MSA_GH11_xylanases 210 gyqssgsasit 220
                          gy+s gsa+++
        k141_8720139 185 GYRSNGSANVK 195
                          *******985 PP


>> k141_2049582
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  155.4   7.0   2.5e-48   4.5e-47      93     220 ..      2     139 ..
1     143 [. 0.92


  Alignments for each domain:
  == domain 1  score: 155.4 bits;  conditional E-value: 2.5e-48
  MSA_GH11_xylanases  93 kysgsyspsgnsylavYGWtrnplveyYivenygtynP.ssgatkkGtvtsdGst
YdiytstrvnqpsieGtatFtqywsvRqskrt… 178
                          +y  +y+p gnsy++vYGWtrnpl+eyYive +g+++P ++ +++kGt t
+G+tYdi +++r+nqps++GtatF qyws+R+   +
        k141_2049582   2 SYDVEYTPRGNSYMCVYGWTRNPLMEYYIVEGWGDWRPpGNDGENKGTTTQNGNT
YDIRKTMRYNQPSLDGTATFPQYWSIRTTSGSannq 92
                          6999*****************************963799*************
**********************876555556 PP


  MSA_GH11_xylanases 179 …sgtvttanhfnaWaklGlnlgtfnYqi.vategyqssgsasit 220
                          +gt+++++hf+aW+++Gl+++   Y + +++egy+s gsa+++
        k141_2049582  93 tnymKGTIDVSKHFDAWSQKGLDMSGTLYEVsLNIEGYRSNGSANVK 139
```

```
                             67889*********************888988689**********985 PP


>> k141_2606760
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  154.2   3.9     6e-48   1.1e-46     110     219 ..       1     109 [.
1     112 [. 0.98


  Alignments for each domain:
  == domain 1  score: 154.2 bits;  conditional E-value: 6e-48
  MSA_GH11_xylanases 110 GWtrnplveyYivenygtynPssgatkkGtvtsdGstYdiytstrvnqpsieGta
tFtqywsvRqskrtsgtvttanhfnaWaklGlnlgt 200
                            GWt +plveyYiv+++gt++P  g+  kG+++
dG+tYd+y++tr+n+psi+G++tF+qy+svR+ krtsgt+++++hf+aW+++G++ g+
        k141_2606760   1 GWTVDPLVEYYIVDSWGTWRPP-
GGSPKGQIQVDGGTYDVYETTRYNAPSIQGDTTFKQYFSVRTTKRTSGTISVSEHFKAWERMGMRCGK 90
                            9*******************9.8999******************************
********************************** PP


  MSA_GH11_xylanases 201 fnYqivategyqssgsasi 219
                            +   +++egyqssgsas+
        k141_2606760  91 LYEAALNIEGYQSSGSASV 109
                            ****************98 PP


>> k141_5257166
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  148.8   2.2   2.6e-46   4.8e-45      24     188 ..      11     189 .]
3     189 .] 0.85


  Alignments for each domain:
  == domain 1  score: 148.8 bits;  conditional E-value: 2.6e-46
  MSA_GH11_xylanases  24 eeeaaelekraltssstgasngyyysfwtdgggevtytngsggeysveWensgn.
.fvgGkGWnpgss…raikysgsyspsgnsyl 106
                            +e++ + e+ + t++ t +++gy y+ w+d g ++  ++  gg +s eW+n +n
f  Gk + +++      +++y +y+p+gnsy+
        k141_5257166  11 QETEPAAEALEFTENITDTADGYDYELWKDEGDTLFRVEPGGGCFSCEWKNINNa
lFRRGKKFDCTQTyeelgnISVDYGVDYQPQGNSYM 101
                            4444556666788999999***********999999999999********97773
355676665555332112114799************ PP


  MSA_GH11_xylanases 107 avYGWtrnplveyYivenygtynPssgatkkGtvtsdGstYdiytstrvnqpsie
GtatFtqywsvRqskrt…sgtvttanhf 188
                            +vYGWtr+pl+e+Y+ve++gt++P  +    G+vt dG+ Ydiy++tr++qpsi+
```

```
                      +tF+qywsvR++k +        +gt+++++hf
          k141_5257166 102 CVYGWTREPLIEFYVVESWGTWRPPGAPFAIGSVTVDGAEYDIYKTTRYEQPSID
DIQTFDQYWSVRREKPKgsgtklEGTISVSKHF 189
                          ********************************************************
*************99776677778999999998 PP


>> k141_7441232
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to     alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  146.2   8.9   1.7e-45     3e-44      47     176 ..       5     143 ..
1     146 [. 0.87


  Alignments for each domain:
  == domain 1  score: 146.2 bits;  conditional E-value: 1.7e-45
  MSA_GH11_xylanases  47 yysfwtdgggevtytngsggeysveWensgnfvgGkGWnp…gssra
ikysgsyspsgnsylavYGWtrnplveyYivenygt 127
                         y   ++g+g+v++ n s+g+++ +W+n +nf +  G n           gs+
++y  +ysp gnsy++vYGWtr+pl+eyYive +g+
          k141_7441232   5 YEMCNQNGQGQVSM-
NPSAGSFTCSWSNIENFLARMGKNYdskklnykdiGSNIVLTYDVEYSPRGNSYMCVYGWTRKPLMEYYIVEGWGS 94
                          666678999***99.999***************9777665112222222255557
89****************************** PP


  MSA_GH11_xylanases 128 ynPssgatkkGtvtsdGstYdiytstrvnqpsieGtatFtqywsvRqsk 176
                         ++P++ ++kkGtvt dG+tYdi++++r+nqps++Gt+tF qywsvRq+
          k141_7441232  95 WRPGADGEKKGTVTLDGNTYDIAKTMRYNQPSLDGTQTFPQYWSVRQKS 143
                          *******************************************975 PP


>> k141_2387523
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to     alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  144.4   2.4   5.7e-45     1e-43      90     191 ..      21     128 .]
11     128 .] 0.95


  Alignments for each domain:
  == domain 1  score: 144.4 bits;  conditional E-value: 5.7e-45
  MSA_GH11_xylanases  90 raikysgsyspsgnsylavYGWtrnplveyYivenygtynPssgatkkGtvtsdG
stYdiytstrvnqpsieGtatFtqywsvRqskrt.. 178
                         +i+y  +y+p+gnsy++vYGWtr+pl+eyYive++gt++P +   +Gtv+
dG++Ydiy++tr++qpsi+   +tF+qywsvR++k +
          k141_2387523  21 ISIDYGVDYQPDGNSYMCVYGWTREPLIEYYIVESWGTWRPPGAPVALGTVEVDG
AVYDIYKTTRYEQPSIDDIQTFDQYWSVRKEKPVps 111
                          479***************************************************
*****************************97777 PP


                                      209
```

```
  MSA_GH11_xylanases 179 …sgtvttanhfnaW 191
                          +gt+++++hf+aW
       k141_2387523 112 gtkiEGTISVSKHFDAW 128
                          77779*********** PP


>> k141_7730058
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  139.0  10.4   2.7e-43   4.9e-42      16     177 ..      16     185 ..
3     193 .. 0.78


  Alignments for each domain:
  == domain 1  score: 139.0 bits;  conditional E-value: 2.7e-43
  MSA_GH11_xylanases  16 galaapaeeeeaaelekraltssstgasngyyysfwtd.gggevtytngsggeys
veWensgnfvgGkGWnpgssr…aikysg 96
                         ga++a +   +a+ + ++a  +++ g  +gy y++w++ g+g++++ n  +g+++
+W+n +nf +  G n  s++        +++y
        k141_7730058  16 GAVSAMM-IASAVPVVASAADQQTRGNVGGYDYEMWNQnGQGQASM-
NPGAGSFTCSWSNIENFLARMGKNFDSQKinykalggiTLTYDV 104
                         2333333.333444555556788888889888887615566666.888999**
**********99888876654233333433578889 PP


  MSA_GH11_xylanases  97 syspsgnsylavYGWtrnplveyYivenygtynPssgatkkGtvtsdGstYdiyt
strvnqpsieGtatFtqywsvRqskr 177
                         +ysp gnsy++vYGWtrnpl+eyYive +g+++P  +a ++G+vt +G+ Y+i
+s+r+nqps++G+atF qywsvRq
        k141_7730058 105 EYSPRGNSYMCVYGWTRNPLMEYYIVEGWGSWEPPGNADNLGNVTLNGNGYKIRK
SMRYNQPSLDGNATFPQYWSVRQTSG 185
                         ********************************************************
*****************9754 PP


>> k141_1928726
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  139.5   2.8   1.8e-43   3.3e-42     100     205 ..       1     115 [.
1     117 [. 0.91


  Alignments for each domain:
  == domain 1  score: 139.5 bits;  conditional E-value: 1.8e-43
  MSA_GH11_xylanases 100 psgnsylavYGWtrnplveyYivenygtynP.ssgatkkGtvtsdGstYdiytst
rvnqpsieGtatFtqywsvRqskrt…sgt 181
                         p gnsy++vYGWt++plveyYive +g+++P ++ +++kGtvt +G+tYdi
+s+r+nqps+eGt+tF qywsvR + +         +gt
```

210

```
        k141_1928726    1 PRGNSYMCVYGWTKSPLVEYYIVEGWGDWRPpGNDGENKGTVTLNGNTYDIRKSM
RYNQPSLEGTSTFPQYWSVRLTRGSannqtnymKGT 91
                          68*************************963799********************
********************65544445567889** PP


  MSA_GH11_xylanases 182 vttanhfnaWaklGlnlgtfnYqi 205
                         +++++hf+aW+++Gl+++   Y +
        k141_1928726   92 IDVSKHFDAWSQAGLDMSGTLYEV 115
                          ****************9888876 PP


>> k141_2356616
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  137.3   2.2   8.4e-43   1.5e-41      99     220 ..       4     122 ..
1     124 [. 0.91


  Alignments for each domain:
  == domain 1  score: 137.3 bits;  conditional E-value: 8.4e-43
  MSA_GH11_xylanases  99 spsgnsylavYGWtrnplveyYivenygtynPssgatkkGtvtsdGstYdiytst
rvnqpsieG.tatFtqywsvRqskrtsgtvttanhf 188
                         s++gns l+vYGW ++plveyYi+e++ +++P+ +     tvt dG+ Y+i++
+   p i G t+tF+qy+svR++krtsgt+t++ hf
        k141_2356616    4 SSQGNSRLCVYGWFKDPLVEYYIIEDWVNWRPTGS---
SKTVTIDGAEYEIFQLDH-TGPTILGdTRTFKQYFSVRKQKRTSGTITVSDHF 90
                          467***************************43…459**********9977
6.5688888356*********************** PP


  MSA_GH11_xylanases 189 naWaklGlnlgtfnYqivategyqssgsasit 220
                         +aWa++G n+g+     +++eg++ssg+a+++
        k141_2356616   91 QAWANAGWNIGNLTEVALNVEGWESSGKANVS 122
                          **************************985 PP


>> k141_5463473
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom   env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  133.0  13.6   1.8e-41   3.2e-40      38     220 ..      25     229 ..
3     231 .. 0.78


  Alignments for each domain:
  == domain 1  score: 133.0 bits;  conditional E-value: 1.8e-41
  MSA_GH11_xylanases  38 sstgasngyyysfwtd.gggevtytngsggeysveWe…nsgnfvgGkGWnpgs
sra…i…ky..sgsyspsgnsylavYG 110
                         + + + +gy y+ w d +gg+ t+t g+g+++++eW+   n gnf + +G
gs+++       +     +y +gs++  gns l+vYG
```

```
        k141_5463473   25 QFKNTCDGYSYEIWLDqTGGSGTMTLGKGATFKTEWNcsvNAGNFLARRGLDFGS
KKKatdyeyigMdykaTYaqTGSFNGGGNSRLCVYG 115
                          33334466666666551678899**************987789*************9
864222222222111133444 7788899******** PP


  MSA_GH11_xylanases 111 Wtrn…plveyYivenygtynPssgatkkGtvtsdGstYdiytstrvnqp
sieG.tatFtqywsvRqskrtsgtvttanhfnaWak 193
                          W +n       plveyYi+e++ ++ Ps    +  tv+ dG+ Y+i++   +  p
i+G t+tF+qy+svRq+krtsg +t+++hf+aWa+
        k141_5463473 116 WFENqgaagnpPLVEYYIIEDWKDWCPS---GNSKTVQIDGADYKIFQLD-
HTGPTIHGrTETFKQYFSVRQQKRTSGHITVSEHFKAWAQ 202
                          *87655666669**************9…34459**********9876.568*
****456************************ PP


  MSA_GH11_xylanases 194 lGlnlgtfnYqivategyqssgsasit 220
                          +G  +g+ +   ++ eg+qssg a++t
        k141_5463473 203 QGWGIGNLYEVALNAEGWQSSGVADVT 229
                          ********9999*************997 PP


>> k141_4491313
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  132.8   5.3     2e-41   3.7e-40      82     182 ..       2     101 ..
1     102 [] 0.97


  Alignments for each domain:
  == domain 1  score: 132.8 bits;  conditional E-value: 2e-41
  MSA_GH11_xylanases  82 kGWnpgssraikysgsyspsgnsylavYGWtrnplveyYivenygtynPssgatk
kGtvtsdGstYdiytstrvnqpsieGtatFtqywsv 172
                          k W++  + +++y+ +y+p+gnsy++vYGW+r+pl+eyYiv+++gt++P  g+++
Gt++ dG+tYd+y s r n+psi+G++ F+q+wsv
        k141_4491313   2 KTWQQLGTITVNYNVDYRPDGNSYMCVYGWSRDPLIEYYIVDSWGTWRPP-
GGNSIGTINVDGGTYDLYISDRWNAPSIDGNRDFKQFWSV 91
                          679999999*****************************************9.999*
******************************** PP


  MSA_GH11_xylanases 173 Rqskrtsgtv 182
                          R++k+tsgt+
        k141_4491313  92 RREKKTSGTI 101
                          *********9 PP


>> k141_6411968
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to    acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
```

```
     1 !   130.3   9.3   1.2e-40   2.2e-39      56      219 ..        7      184 ..
2       187 .. 0.80


  Alignments for each domain:
  == domain 1  score: 130.3 bits;  conditional E-value: 1.2e-40
  MSA_GH11_xylanases  56 gevtytngsggeysveWe…n..sgnfvgGkG..Wnpgssr…aikys
gsysp..sgnsylavYGWtrnplveyYivenygtyn 129
                         +++t   ++gg +s++W+   n +gnf + +G  W   + +       + ++
++s+  sgns +++YGWt+nplveyYi+e++ ++
        k141_6411968   7 STMTL-ADEGGGFSTKWQcgpNnsRGNFLARRGlfWGRNNPNhwqdygnfTCDFD
CDWSAgsSGNSRICIYGWTENPLVEYYIIEDWKNWV 96
                         44444.677888*****865524689***98875554444431111111145555
666655469*********************** PP


  MSA_GH11_xylanases 130 PssgatkkGtvtsdGstYdiytstrvnqpsieGta.tFtqywsvRqskrtsgtvt
tanhfnaWaklGlnlgtfnYqivategyqssgsasi 219
                         Pss+++k  +vt dGs+Yd++t+  +n   i+ t+  Ftqy+svR+
rtsgt+++ +hf+aW++lG+++g+ +    +++eg++s g+a++
        k141_6411968  97 PSSASAK--QVTIDGSVYDVFTNA-
MNSYNITNTNgPFTQYISVRRTPRTSGTISIYKHFEAWESLGMKMGNLYEVAFNVEGWESDGQANV 184
                         **77665..7999*******9986.667777777758*****************
******************9999*************98 PP


>> k141_6801310
    #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
    1 !  124.4   3.0   7.7e-39   1.4e-37      93      220 ..       11      142 ..
4       143 .. 0.86


  Alignments for each domain:
  == domain 1  score: 124.4 bits;  conditional E-value: 7.7e-39
  MSA_GH11_xylanases  93 kysgsyspsgnsylavYGWtrn…plveyYivenygtynPssgatkkGtv
tsdGstYdiytstrvnqpsieGta.tFtqywsvRqs 175
                         +y  + s++gns l+vYGW +n        plveyYi+e++ ++ Ps    +
tvt dG+ Y+i++   + p i+G++ tF+qy+svRqs
        k141_6801310  11 SYRQTGSAQGNSRLCVYGWFENqgapgnpPLVEYYIIEDWKDWCPS---
GNSKTVTIDGAEYKIFQLD-HTGPTIHGNTeTFKQYFSVRQS 97
                         3444446789*********97656666669*************9…34459*
*********9876.568*****655*********** PP


  MSA_GH11_xylanases 176 krtsgtvttanhfnaWaklGlnlgtfnYqivategyqssgsasit 220
                         krtsg +t+++hf+aW+k+G  +g+ +    ++ eg+qssg a++t
        k141_6801310  98 KRTSGHITVSEHFKAWEKQGWGIGNLYEVALNAEGWQSSGIADVT 142
                         *************************9999************997 PP


>> k141_4644390


                              213
```

```
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  123.9   5.1   1.1e-38   1.9e-37      92     178 ..       6      93 ..
2     103 .. 0.90

  Alignments for each domain:
  == domain 1  score: 123.9 bits;  conditional E-value: 1.1e-38
  MSA_GH11_xylanases  92 ikysgsyspsgnsylavYGWtrnplveyYivenygtynP.ssgatkkGtvtsdGs
tYdiytstrvnqpsieGtatFtqywsvRqskrt 178
                         ++y  +y+p gnsy++vYGWtrnpl+eyYive +g+++P ++ +++kG+vt +G+
Y+i++++r+nqpsieGt+tF qyws+Rq    +
        k141_4644390   6 LTYDVEYTPRGNSYMCVYGWTRNPLMEYYIVEGWGDWRPpGNDGERKGNVTINGN
SYEIAKTMRYNQPSIEGTKTFPQYWSIRQTSGS 93
                        79********************************9637999***********
**************************97644 PP


>> k141_6776299
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 !  120.8  13.2   9.7e-38   1.8e-36      26     199 ..      33     216 .]
6     216 .] 0.74

  Alignments for each domain:
  == domain 1  score: 120.8 bits;  conditional E-value: 9.7e-38
  MSA_GH11_xylanases  26 eaaelekraltssstgasngyyysfwtdgggevtytngsggeysveWensgnfvg
GkGWnpgssra…ikysgsyspsgns…yl 106
                         ++++ ++++ ++ + g s  +y  ++++g+ ++t+   ++g+y+ +W+ +++f +
G++  ++++      i+   ++s +gn+    y+
        k141_6776299  33 KTTQGQNNSSVTGNVGSSPYHYEIWYQGGNNSMTF--
YDNGTYKASWNGTNDFLARVGFKYNEKQTyeelgpIDAYFKWSKQGNAggynYI 121
                        23333344445555565566666677766555555..899***************
****999887622222322234444455333339* PP


  MSA_GH11_xylanases 107 avYGWtrnplveyYivenygtynPssg..atkkGtvtsdGstYdiytstrvnqps
ieGtatFtqywsvRqs.krtsgtvttanhfnaWakl 194
                         +YGWt +plveyYiv+++ + +P+++   + kkG+ t
dG+tY++y+++r+n+psi+G++tF q++s R+   r+ g ++++hf+ W++l
        k141_6776299 122 GIYGWTVDPLVEYYIVDDWFS-
EPGANllGSKKGEFTVDGATYEVYQNMRYNAPSIKGDQTFPQFFSKRKGgARSCGHIDITAHFKKWEEL 211
                        ******************65.6776534799**********************
**************9637999*************** PP


  MSA_GH11_xylanases 195 Glnlg 199
                         G+++g
```

```
          k141_6776299 212 GMKMG 216
                             **997 PP


>> k141_3276475
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  120.5   5.2   1.2e-37   2.2e-36      91     176 ..      21     107 ..
9     117 .. 0.91


  Alignments for each domain:
  == domain 1  score: 120.5 bits;  conditional E-value: 1.2e-37
  MSA_GH11_xylanases  91 aikysgsyspsgnsylavYGWtrnplveyYivenygtynP.ssgatkkGtvtsdG
stYdiytstrvnqpsieGtatFtqywsvRqsk 176
                           ++y  +y+p gnsy++vYGWtrnpl+eyYive +g+++P ++ +++kG+vt
+G+tY+i++++r+nqps++GtatF qyws+R+
        k141_3276475  21 VLTYDVEYTPRGNSYMCVYGWTRNPLMEYYIVEGWGDWRPpGNDGERKGNVTLNG
NTYEIAKTMRYNQPSLDGTATFPQYWSIRTTS 107
                           679*********************************9637999**********
**************************865 PP


>> k141_127344
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !  120.1   4.8   1.6e-37   2.9e-36      53     166 ..       3     125 .]
1     125 [] 0.87


  Alignments for each domain:
  == domain 1  score: 120.1 bits;  conditional E-value: 1.6e-37
  MSA_GH11_xylanases  53 dgggevtytngsggeysveWensgnfvgGkGWnpgssra…ikysgsy
spsgnsylavYGWtrnplveyYivenygtynP.ssg 133
                           +g+g++++ n s+g+++ +W+n +nf +  G n  s+++          ++y
+y+p gnsy++vYGWtrnpl+eyYive +g+++P + g
        k141_127344   3 NGTGNAQM-NPSAGSFTCSWSNIENFLARMGKNFDSQKKnykafgnivLTYDVEY
TPRGNSYMCVYGWTRNPLMEYYIVEGWGDWRPpGDG 92
                           67888888.999*************988877766542223333333379*****
****************************962689 PP


  MSA_GH11_xylanases 134 atkkGtvtsdGstYdiytstrvnqpsieGtatF 166
                           a++kGtvt dG+tYdi++++r+nqps++GtatF
        k141_127344  93 AERKGTVTLDGNTYDIAKTMRYNQPSLDGTATF 125
                           99**************************9 PP


>> k141_3001072
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
```

```
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   93.2   2.7   2.6e-29   4.8e-28      18     138 ..      40     162 ..
23     163 .] 0.81


  Alignments for each domain:
  == domain 1  score: 93.2 bits;  conditional E-value: 2.6e-29
  MSA_GH11_xylanases  18 laapaeeeeaaelekraltssstgasngyyysfwtdgggevtytngsggeysveW
ensgnfvgGkGWnpgssra…ikysgsysp 100
                          la+     ++ ++ ++++l+++ tg+++gy ++ w+d  g++++t ++gg+++
+W+n gn    kG +  s+r+       ++y  +y+p
        k141_3001072  40 LAV----PNIKAYAAETLYDNRTGTQDGYSFELWKD-
YGNTSMTLNAGGNFECSWSNIGNALFRKGQKFDSTRTysqmgnisVEYGCNYQP 125
                          333…456777888899****************8.8999**************
*****9998888776655533333333389****** PP


  MSA_GH11_xylanases 101 sgnsylavYGWtrnplveyYivenygtynPssgatkkG 138
                          +gnsyl+vYGW++nplveyYiv+++g+++P  ga  kG
        k141_3001072 126 NGNSYLCVYGWMKNPLVEYYIVDSWGSWRPP-GASPKG 162
                          **************************98.555555 PP


>> k141_5776627
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   87.5   7.7   1.4e-27   2.6e-26      93     175 ..      32     117 ..
2     118 .] 0.87


  Alignments for each domain:
  == domain 1  score: 87.5 bits;  conditional E-value: 1.4e-27
  MSA_GH11_xylanases  93 kysgsysp..sgnsylavYGWtrnplveyYivenygtynPs..sgatkkGtvtsd
GstYdiytstrvnqpsieGtatFtqywsvRqs 175
                          +y  s+ +  sgns +++YGW++nplveyYi+e++ ++ P+  s+a++kG+ t
dGs+Y++yt+ r n   ieG++ Ftqy+s+Rq+
        k141_5776627  32
DYDCSWYAgsSGNSRICIYGWAQNPLVEYYIIEDWKNWSPAqdSTAQYKGQTTIDGSVYKVYTTSR-
NSYTIEGNKSFTQYISIRQN 117
                          56666654336*****************************9778899********
*******9988.6789**************97 PP


>> k141_4500609
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   83.3   2.4   2.8e-26      5e-25     139     220 ..       1      81 [.
```

```
   1       83 [. 0.96

  Alignments for each domain:
  == domain 1  score: 83.3 bits;  conditional E-value: 2.8e-26
  MSA_GH11_xylanases 139 tvtsdGstYdiytstrvnqpsieGtatFtqywsvRqskrtsgtvttanhfnaWak
lGlnlgtfnYqivategyqssgsasit 220
                            tv+ dGs Y++yts r n   ieG++ Ftqy+svRq++rt+gt+++++hf+aW++
G+++g+f+    +++eg++s g+a+++
        k141_4500609    1 TVNIDGSDYKVYTSAR-
NSYTIEGNKDFTQYISVRQNTRTKGTISISEHFKAWESFGMRMGNFYECAFNVEGWESDGQATVK 81
                            799***********99.6789********************************
**********************986 PP


>> k141_4891430
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   77.2  11.1     2e-24   3.7e-23      48      147 ..       4      113 .]
1      113 [] 0.81

  Alignments for each domain:
  == domain 1  score: 77.2 bits;  conditional E-value: 2e-24
  MSA_GH11_xylanases  48 ysfwtdg.ggevtytngsggeysveWensgnfvgGkGWnpgssra…i
kysgsyspsgnsylavYGWtrnplveyYivenygty 128
                            y++w+++ +g+v++ n  +g+++ +W+  +nf +  G n  s+++
++y   +y+p gnsy++vYGWtrnpl+eyYive +g++
        k141_4891430    4 YEMWNQNyTGNVSM-
NPGAGNFTCSWSGIENFLARMGKNFDSQKKnyksfggivLTYDVEYTPRGNSYMCVYGWTRNPLMEYYIVEGWGDW 93
                            56676661567776.88899*************9888877766422333444337
999****************************** PP

  MSA_GH11_xylanases 129 nP.ssgatkkGtvtsdGstY 147
                            +P + ga++kG+vt +G+tY
        k141_4891430   94 RPpGDGAERKGNVTLNGNTY 113
                            96268999**********9 PP


>> k141_8326139
   #     score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to
envfrom  env to     acc
 ---    ------ ----- --------- --------- ------- -------     ------- -------
------- -------     ----
   1 !   65.8   0.0   6.4e-21   1.2e-19     158      219 ..       1       68 [.
1       70 [. 0.93

  Alignments for each domain:
  == domain 1  score: 65.8 bits;  conditional E-value: 6.4e-21
  MSA_GH11_xylanases 158
```

217

```
psieGtatFtqywsvRqskrt…sgtvttanhfnaWaklGlnlgtfnYqivategyqssgsasi 219
                        psi+  +tF+qywsvR+ k +      sgt+++++hf+aW+k Gl+lg+++
+++egyqs g+a++
        k141_8326139   1
PSIDDIQTFDQYWSVRRTKPQgdgtrlSGTISVSKHFDAWKKCGLELGKMYEVALTIEGYQSKGKATV 68
9*****************9866666666**********************9999***********987 PP


>> k141_124775
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   47.2   5.1   3.1e-15   5.6e-14       38     116 ..      12     100 .]
4     100 .] 0.71


  Alignments for each domain:
  == domain 1  score: 47.2 bits;  conditional E-value: 3.1e-15
  MSA_GH11_xylanases  38 sstgasngyyysfwt.dgggevtytngsggeysveWensgnfvgGkGWnp…
…gssraikysgsyspsgnsylavYGWtrnpl 116
                        ++ g  +g+ y++w+ +g+g++++ + ++g+++ +W+n +nf +  G n
gs+   ++y  +y+p gnsy++vYGWtrnpl
        k141_124775   12 QTRGNIGGFDYEMWNqNGQGQASM-
EPKAGSFTCSWSNIENFLARMGKNYdskkqnykkiGSNIVLTYDVEYTPRGNSYMCVYGWTRNPL 100
                        4556666666666665156677776.88999*************977766511111
111114444679*****************7 PP


>> k141_7411831
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to     acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------    ----
   1 !   29.7   0.0   6.8e-10   1.2e-08      168     202 ..       2      36 ..
1      50 [. 0.87
   2 !   12.3   2.5   0.00014    0.0026       28      81 ..     118     169 ..
77     171 .] 0.70


  Alignments for each domain:
  == domain 1  score: 29.7 bits;  conditional E-value: 6.8e-10
  MSA_GH11_xylanases 168 qywsvRqskrtsgtvttanhfnaWaklGlnlgtfn 202
                         qy+svR+  r gt+++++h+  W+k+G+++g+ +
        k141_7411831   2 QYFSVRDRPRDCGTINISEHMRQWEKMGMTMGKLY 36
                         9*********************************643 PP


  == domain 2  score: 12.3 bits;  conditional E-value: 0.00014
  MSA_GH11_xylanases  28 aelekraltssstgasngyyysfwtdgggevtytngsggeysveWensgnfvgG
81
                         ++ ++++ ++ + g s  +y  ++++g+ ++t+   ++g+y+ +W+ +++f +
        k141_7411831 118 TQGQNNSSVTGNVGSSPYHYEIWYQGGNNSMTF--YDNGTYKASWNGTNDFLAR
```

```
                              33333444455556666666777777766666555..899************9875
PP


>> k141_7367989
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to
envfrom  env to      acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------
------- -------     ----
   1 ?    4.5   0.0     0.034      0.63     185     202 ..       2      19 ..
1       33 [. 0.78
   2 !   22.4  11.0   1.2e-07   2.2e-06      26     118 ..      99     199 .]
80      199 .] 0.65


  Alignments for each domain:
  == domain 1  score: 4.5 bits;  conditional E-value: 0.034
  MSA_GH11_xylanases 185 anhfnaWaklGlnlgtfn 202
                         ++h+   W+k+G+++g+ +
       k141_7367989    2 SEHMRQWEKMGMTMGKLY 19
                         68************643 PP


  == domain 2  score: 22.4 bits;  conditional E-value: 1.2e-07
  MSA_GH11_xylanases  26 eaaelekraltssstgasngyyysfwtdgggevtytngsggeysveWensgnfvg
GkGWnpgssra…ikysgsyspsgns…yl 106
                         ++++ ++++ ++ + g s  +y  ++++g+ ++t+   ++g+y+ +W+ +++f +
G++ ++++      i+   ++s +gn+     y+
       k141_7367989   99 KTTQGQNNSSVTGNVGSSPYHYEIWYQGGNNSMTF--
YDNGTYKASWNGTNDFLARVGFKYDEKHTyeelgpIDAYFKWSKQGNAggynYI 187
                         333334444555566666666777777766666555..899*************
****99988662222233223444444533339* PP


  MSA_GH11_xylanases 107 avYGWtrnplve 118
                         +YGWt +plve
       k141_7367989 188 GIYGWTVDPLVE 199
                         ***********8 PP


Internal pipeline statistics summary:
-------------------------------------
Query model(s):                       1  (222 nodes)
Target sequences:                   583  (111031 residues searched)
Passed MSV filter:                   47  (0.0806175); expected 11.7 (0.02)
Passed bias filter:                  33  (0.0566038); expected 11.7 (0.02)
Passed Vit filter:                   32  (0.0548885); expected 0.6 (0.001)
Passed Fwd filter:                   32  (0.0548885); expected 0.0 (1e-05)
Initial search space (Z):           583  [actual number of targets]
Domain search space  (domZ):         32  [number of targets reported over
```

```
threshold]
# CPU time: 0.02u 0.01s 00:00:00.03 Elapsed: 00:00:00.14
# Mc/sec: 172.47
//
[ok]
```

[42]:
```
%use bash
head -n 20 GH11_results.txt
```

```
#                                                    --- full
sequence ---- --- best 1 domain ---- --- domain number estimation ----
# target name         accession  query name              accession   E-value  score
bias   E-value  score  bias   exp reg clu  ov env dom rep inc description of
target
#------------------- ---------- -------------------- ---------- --------- ------
----- --------- ------ -----   --- --- --- --- --- --- --- ---
--------------------
k141_2912295            -          MSA_GH11_xylanases   -            6.4e-63  207.3
13.1   7.4e-63  207.0  13.1   1.0   1   0   0   1   1   1   1 -
k141_2003823            -          MSA_GH11_xylanases   -            3.5e-60  198.3
6.0   4.8e-60  197.8   6.0   1.1   1   0   0   1   1   1   1 -
k141_9005574            -          MSA_GH11_xylanases   -            4.8e-56  184.8
9.8   1.1e-55  183.6   9.8   1.5   1   1   0   1   1   1   1 -
k141_5844946            -          MSA_GH11_xylanases   -            1.9e-55  182.8
6.0   2.7e-55  182.3   6.0   1.2   1   0   0   1   1   1   1 -
k141_7538601            -          MSA_GH11_xylanases   -            3.8e-55  181.8
12.2   3.8e-55  181.8  12.2   1.6   2   0   0   2   2   2   1 -
k141_8367260            -          MSA_GH11_xylanases   -            6.9e-55  181.0
12.3     9e-55  180.6  12.3   1.1   1   0   0   1   1   1   1 -
k141_1296036            -          MSA_GH11_xylanases   -            6.3e-54  177.8
12.6   1.3e-53  176.8  12.6   1.5   1   0   0   1   1   1   1 -
k141_8720139            -          MSA_GH11_xylanases   -            4.4e-52  171.8
13.1     6e-52  171.4  13.1   1.1   1   0   0   1   1   1   1 -
k141_2049582            -          MSA_GH11_xylanases   -            3.4e-47  155.8
7.0   4.5e-47  155.4   7.0   1.1   1   0   0   1   1   1   1 -
k141_2606760            -          MSA_GH11_xylanases   -            5.6e-47  155.1
3.9   1.1e-46  154.2   3.9   1.5   1   0   0   1   1   1   1 -
k141_5257166            -          MSA_GH11_xylanases   -              4e-45  149.1
2.2   4.8e-45  148.8   2.2   1.1   1   0   0   1   1   1   1 -
k141_7441232            -          MSA_GH11_xylanases   -            1.5e-44  147.1
8.9     3e-44  146.2   8.9   1.4   1   1   0   1   1   1   1 -
k141_2387523            -          MSA_GH11_xylanases   -            8.9e-44  144.6
2.4     1e-43  144.4   2.4   1.0   1   0   0   1   1   1   1 -
k141_7730058            -          MSA_GH11_xylanases   -            2.4e-42  139.9
10.4   4.9e-42  139.0  10.4   1.4   1   1   0   1   1   1   1 -
k141_1928726            -          MSA_GH11_xylanases   -            2.9e-42  139.7
2.8   3.3e-42  139.5   2.8   1.0   1   0   0   1   1   1   1 -
k141_2356616            -          MSA_GH11_xylanases   -            1.3e-41  137.6
```

```
2.2   1.5e-41   137.3   2.2   1.0   1   0   0   1   1   1   1 -
k141_5463473        -           MSA_GH11_xylanases   -           8.7e-41   134.9
13.6   3.2e-40   133.0   13.6   1.7   1   1   0   1   1   1   1 -
```

This file contains the most likely contigs to be xylanase proteins. We will use the top three of them
for the next structural analysis.

1.2.5 Step 4: Predicting the 3D Structure and Structural Alignment

For the final step, we used AlphaFold3 to predict the 3D structures and PyMOL for structural
alignment. Let's explore the results of these two analyses for each of the candidate sequences.

```
[44]: %use bash
      cd ../
```

For GH10 subfamily:

```
[45]: %use bash
      cd GH10/Results/
```

```
[46]: %use bash
      ls
```

k141_2596728   k141_4174516   k141_8751303

k141_2596728   Alphaphold:

Pymol:

RMSD = 0.993
Industrial Xylanase PDB = 1VBR

k141__4174516   Alphaphold:
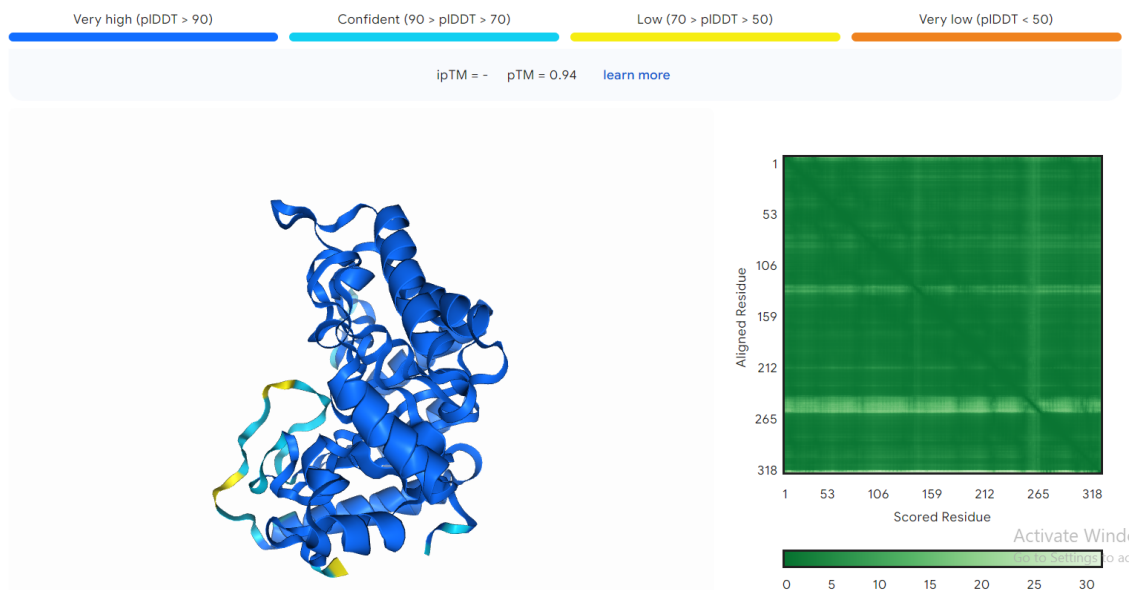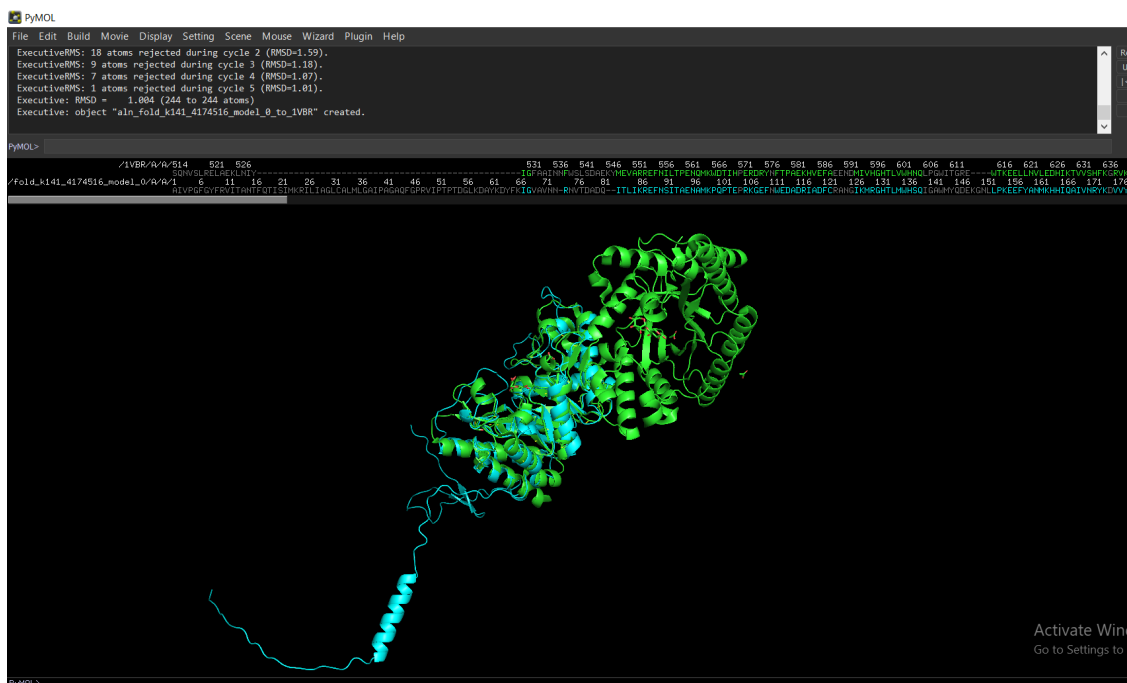
Pymol:

RMSD = 1.004
Industrial Xylanase PDB = 1VBR

k141__8751303   Alphaphold:
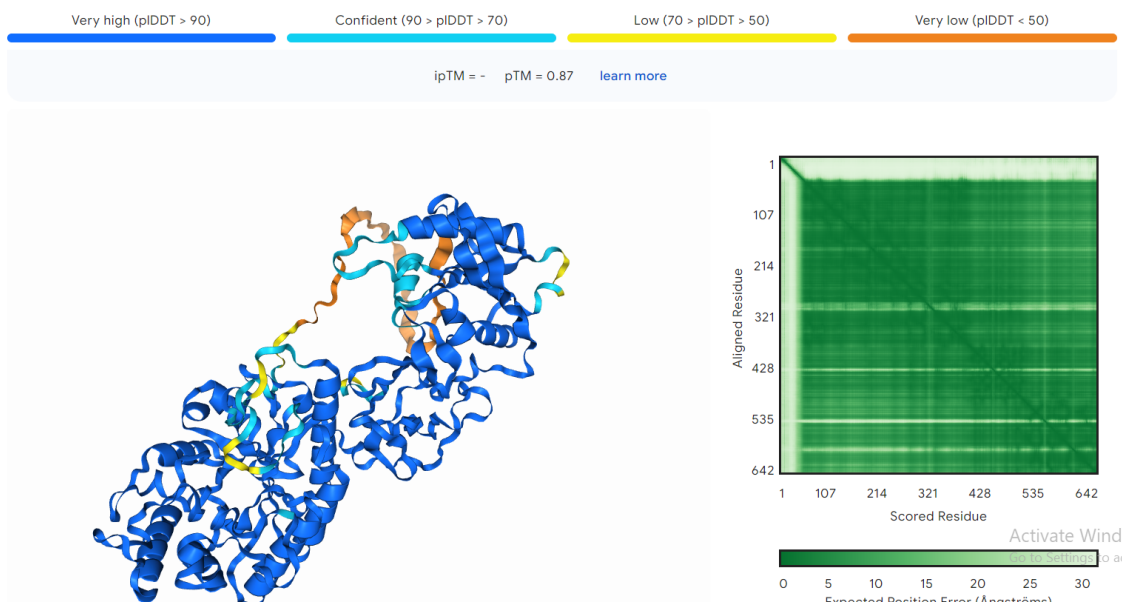
Pymol:
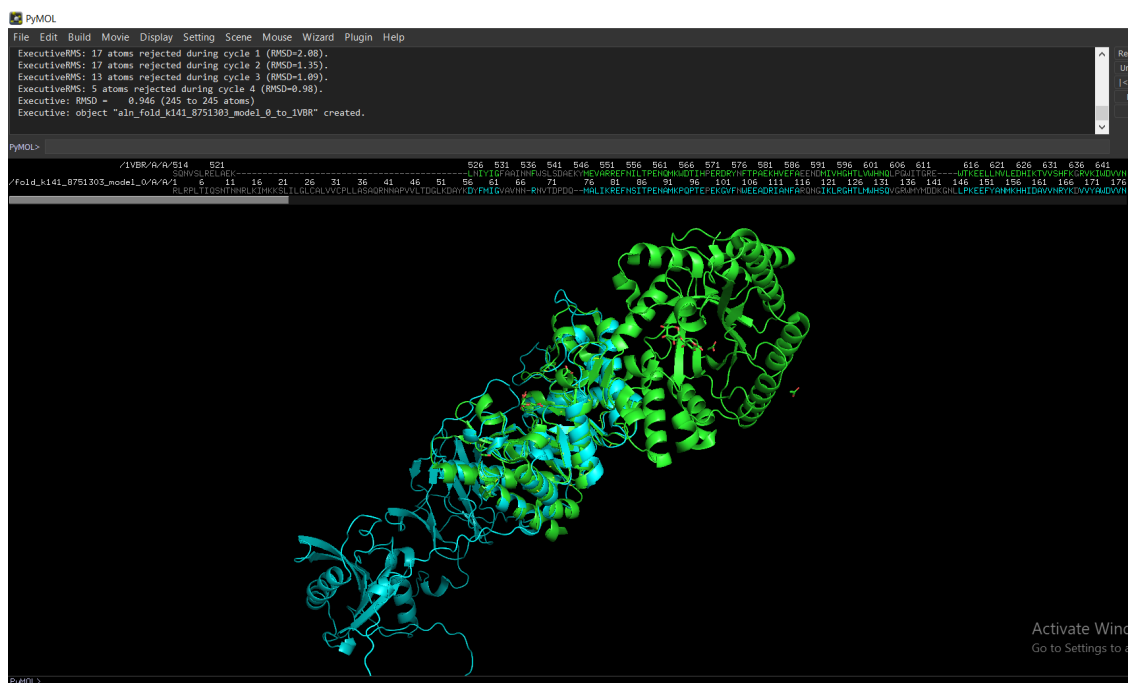
RMSD = 0.946

Industrial Xylanase PDB = 1VBR

For GH11 subfamily:

```
[59]: %use bash
      cd ../../../GH11/Results/
```

```
[60]: %use bash
      ls
```

k141_2003823   k141_2912295   k141_9005574

k141_2003823 Alphaphold:
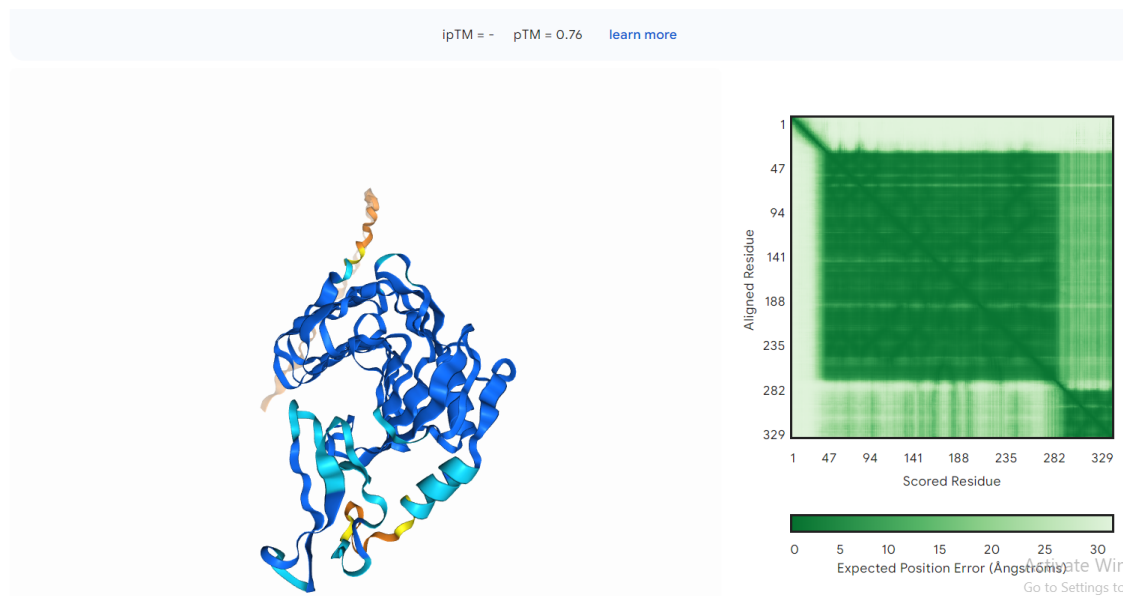
Pymol:
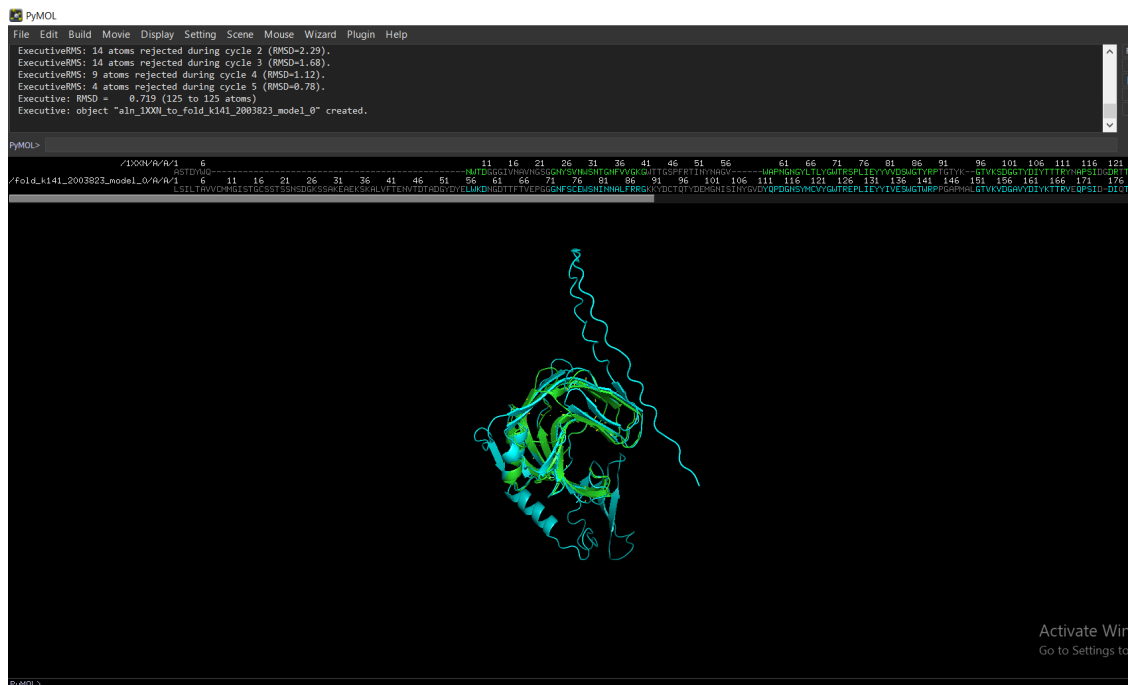
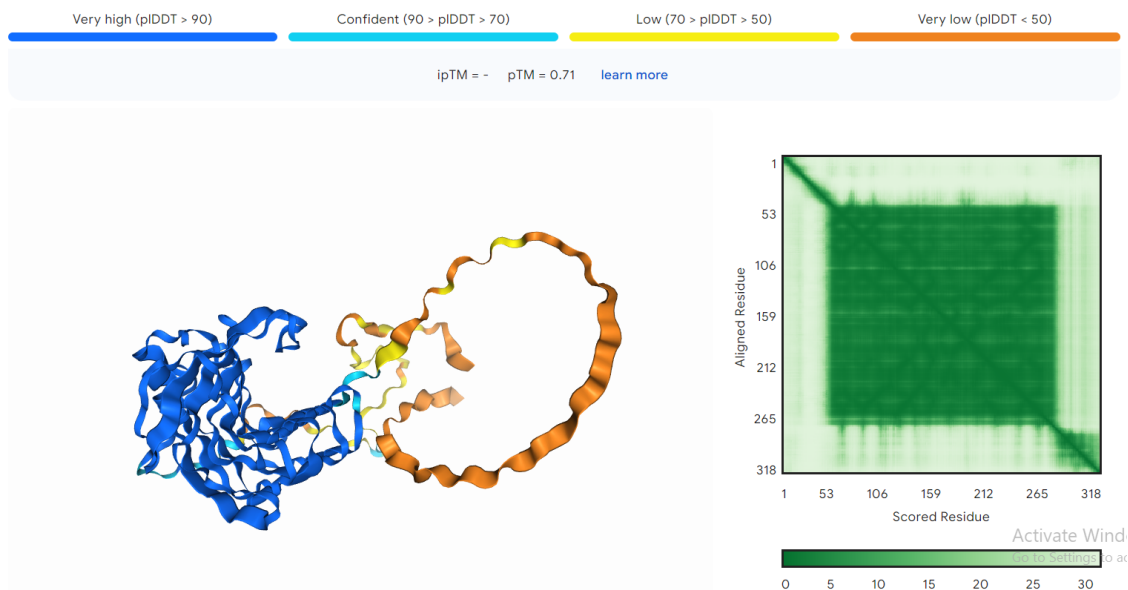RMSD = 0.719

Industrial Xylanase PDB = 1XXN

k141_2912295   Alphaphold:

ipTM = - pTM = 0.93 learn more
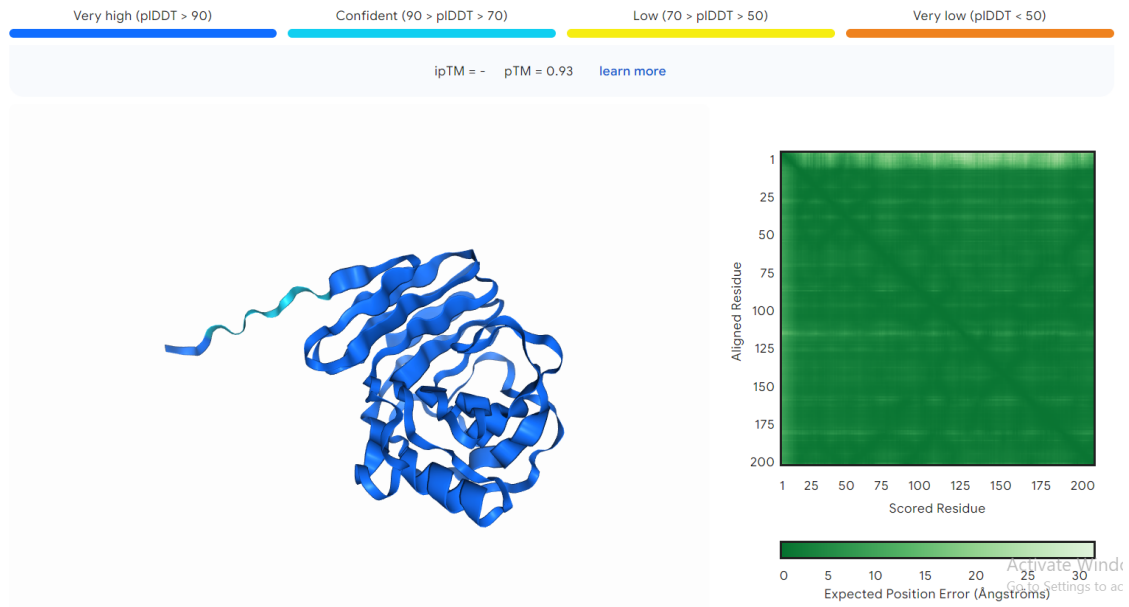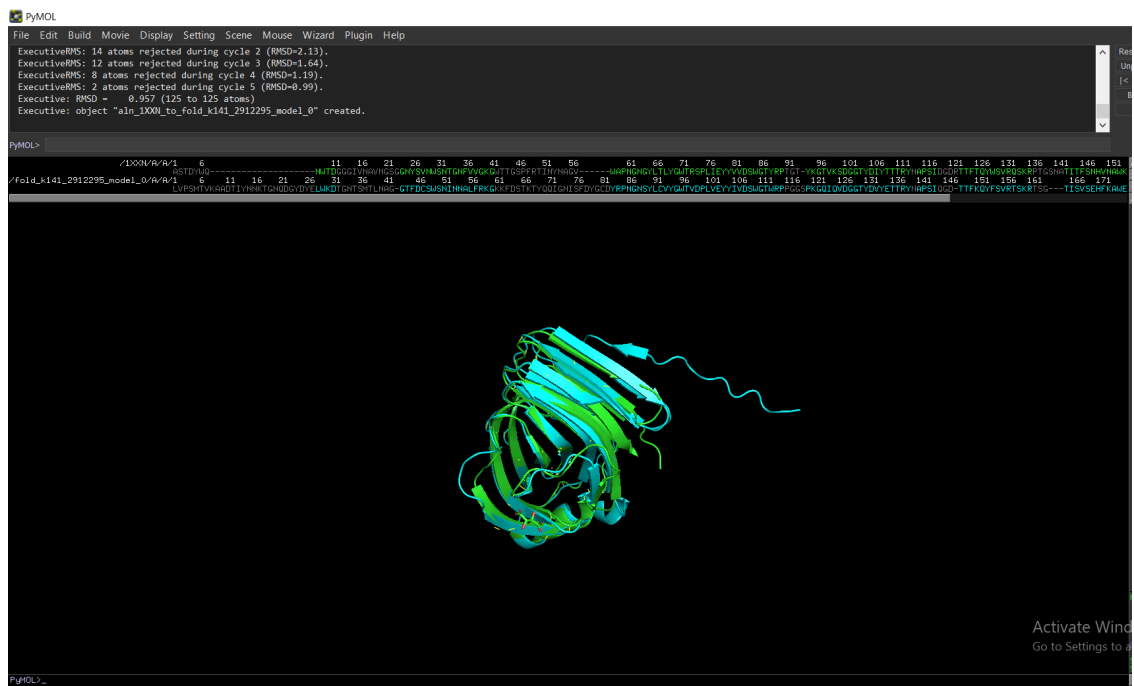
Pymol:

RMSD = 0.957
Industrial Xylanase PDB = 1XXN

k141_9005574 Alphaphold:

Pymol:
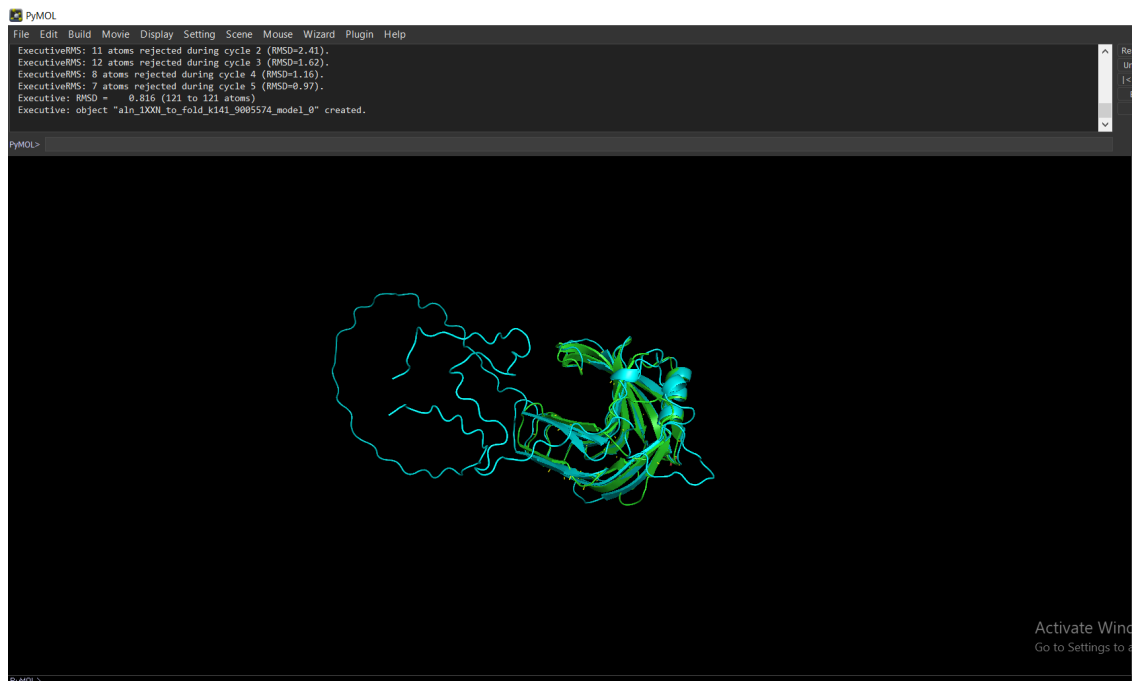
RMSD = 0.816
Industrial Xylanase PDB = 1XXN

1.3   Results

After predicting the 3D structures of each candidate, we performed structural alignment to compare each candidate's structure with that of an industrially known xylanase extracted from the PDB.

For the GH10 subfamily, we used the 1VBR structure, and for the GH11 subfamily, we used the 1XXN structure. We used PyMOL to obtain the RMSD scores and the TM-align website to get the TM-scores for these structural alignments. Here are the final results of the project:

```
[63]: %use bash
      cd ../../
```

```
[67]: %use bash
      cat Final_results.txt
```

```
Contig  Subfamily       Industrial structure    RMSD    TM-score
k141_2596728    GH10    1VBR    0.993   0.8619
k141_4174516    GH10    1VBR    1.004   0.90622
k141_8751303    GH10    1VBR    0.946   0.90775
k141_2003823    GH11    1XXN    0.719   0.91501
k141_2912295    GH11    1XXN    0.957   0.86914
k141_9005574    GH11    1XXN    0.816   0.91279
```

More information and files are available in the "Results" folder for each subfamily.

1.4 Conclusion

As the results show, we successfully modeled two subfamilies of xylanase and identified several potential contigs encoding these enzymes in the rumen of ruminant animals. The structural analysis revealed that our candidate sequences are highly aligned with known industrial xylanases, indicating that these enzymes are indeed encoded within the rumen of ruminants.

This finding suggests that the rumen could be an excellent resource for discovering a diverse array of industrial enzymes. These enzymes have significant potential for further scientific research and industrial applications. Exploring the rumen metagenome may therefore provide valuable insights and lead to new developments in biotechnology.

1.5 References

https://chatgpt.com/
http://www.cazy.org/
https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=tblastn&PAGE_TYPE=BlastSearch&LINK_LOC=blastl
https://www.bioinformatics.org/cd-hit/
https://www.uniprot.org/
https://mafft.cbrc.jp/alignment/software/
http://hmmer.org/
https://alphafoldserver.com/
https://zhanggroup.org/TM-align/
https://pymol.org/
https://www.rcsb.org/