

Supplementary material

Novel Insights from Comparative *In silico* Analysis of Green Microalgal Cellulases

Gea Guerriero, Kjell Sergeant, Sylvain Legay, Jean-Francois Hausman, Henry-Michel Cauchie, Irshad Ahmad, Khawar Sohail Siddiqui

List of Supplementary tables and figures

Suppl. Fig. 1a	page 2
Suppl. Fig. 1b	page 37
Suppl. Fig. 2	page 38
Suppl. Fig. 3	page 59
Suppl. Table 1	page 60
Suppl. Table 2	page 61
Suppl. Fig. 4	page 63
Suppl. Fig. 5	page 64
Suppl. Fig. 6	page 70
Suppl. Table 3	page 71
Suppl. References	page 72

1UT9	-----	0
1CLC	-----	0
Fungal	-----	0
Amoeba	-----	0
CSA	-----	0
1JS4	-----	0
Ascidian	MARRSFLLSIFIVACAKLSFAGVCNELRPTATVRMSCDIGRNPNSVCRFRCSGGYMLTN	60
1KS8	-----	0
Cnidaria	-----	0
Bryophyte	-----	0
Pine	-----	0
Tomato	-----	0
NSpinach	-----	0
CSpinach	-----	0
CR9D	-----	0
GPKXZ44756	-----	0
VC2952174	-----	0
CR9B	-----	0
CR9C	-----	0
VC2958622	-----	0
NGP51468	-----	0
GP51466	-----	0
CGP51468	-----	0

1UT9	-----	0
1CLC	-----	0
Fungal	-----	0
Amoeba	-----	0
CSA	-----	0
1JS4	-----	0
Ascidian	SRNRIRICRCTGDTCLWTGGEATCRRRSQNNNNNQRRPQRVTTTTTRRPVTRRPPTTRPPIR	120
1KS8	-----	0
Cnidaria	-----	0
Bryophyte	-----	0
Pine	-----	0
Tomato	-----	0
NSpinach	-----	0
CSpinach	-----	0
CR9D	-----	0
GPKXZ44756	-----	0
VC2952174	-----	0
CR9B	-----	0
CR9C	-----	0
VC2958622	-----	0
NGP51468	-----	0
GP51466	-----	0
CGP51468	-----	0

1UT9	-----	0
1CLC	-----	0
Fungal	-----	0
Amoeba	-----	0
CSA	-----	0
1JS4	-----	0
Ascidian	TTRPLCPSPQFHGHTFQVIDSWPTGAILRVTINTGTNEIQNGWTVLFTFTRNLPRNLRFM	240
1KS8	-----	0
Cnidaria	-----	0
Bryophyte	-----	0
Pine	-----	0
Tomato	-----	0
NSpinach	-----	0
CSpinach	-----	0
CR9D	-----	0
GPKXZ44756	-----	0
VC2952174	-----	0
CR9B	-----	0
CR9C	-----	0
VC2958622	-----	0
NGP51468	-----	0
GP51466	-----	0
CGP51468	-----	0

1UT9	-----MKFRRSICTAVLLAVLLTLLV	21
1CLC	-----	0
Fungal	-----	0
Amoeba	-----	0
CSA	-----	0
1JS4	-----	0
Ascidian	SWTSRKIYSGTKYLAVGNLQHNRRLLSSYEQFSFTVVLLDTSMPRAMQGYTALVGLYTQVVT	300
1KS8	-----	0
Cnidaria	-----	0
Bryophyte	-----	0
Pine	-----	0
Tomato	-----	0
NSpinach	-----	0
CSpinach	-----	0
CR9D	-----	0
GPKXZ44756	-----	0
VC2952174	-----	0
CR9B	-----	0
CR9C	-----	0
VC2958622	-----	0
NGP51468	-----	0
GP51466	-----	0
CGP51468	-----	0

1UT9	PTSVFALEDNSSTLPPYKNDLLYERTFDEG-----LCYPWHTCEDSGGKCSFDV-----	70
1CLC	-----	0
Fungal	-----	0
Amoeba	-----	0
CSA	-----	0
1JS4	-----	0
Ascidian	DTSCFSLQSNTMALPPTTHWLVSTPKLSLTLHVFLYKATPWLSHQQLKTPTTTTTRTTTH	360
1KS8	-----	0
Cnidaria	-----	0
Bryophyte	-----	0
Pine	-----	0
Tomato	-----	0
NSpinach	-----	0
CSpinach	-----	0
CR9D	-----	0
GPKXZ44756	-----	0
VC2952174	-----	0
CR9B	-----	0
CR9C	-----	0
VC2958622	-----	0
NGP51468	-----	0
GP51466	-----	0
CGP51468	-----	0

1UT9	-----VDVPGQPG	78
1CLC	-----	0
Fungal	-----	0
Amoeba	-----	0
CSA	-----	0
1JS4	-----	0
Ascidian	RPTTRRTTQRPQPRQTTRRTTQRPQPRQTTRRTTRPTVRTTTRRTTQQTITSTPS	420
1KS8	-----	0
Cnidaria	-----	0
Bryophyte	-----	0
Pine	-----	0
Tomato	-----	0
NSpinach	-----	0
CSpinach	-----	0
CR9D	-----	0
GPXZ44756	-----	0
VC2952174	-----	0
CR9B	-----	0
CR9C	-----	0
VC2958622	-----	0
NGP51468	-----	0
GP51466	-----	0
CGP51468	-----	0

1UT9	NKAFAVTVLDKGQNRWSVQMRHRGLTL-----EQGHTYRVRLKIWADASCKVYIKIG	130
1CLC	-----	0
Fungal	-----	0
Amoeba	-----	0
CSA	-----	0
1JS4	-----	0
Ascidian	NIQIDESSVSR--HSRGCNVLRNGLTIQNSGYEVVEQGVENSRRFRFNADVW----I-AG	473
1KS8	-----	0
Cnidaria	-----	0
Bryophyte	-----	0
Pine	-----	0
Tomato	-----	0
NSpinach	-----	0
CSpinach	-----	0
CR9D	-----	0
GPXZ44756	-----	0
VC2952174	-----	0
CR9B	-----	0
CR9C	-----	0
VC2958622	-----	0
NGP51468	-----	0
GP51466	-----	0
CGP51468	-----	0

1UT9	QMGEPYAEYWNNKWSPTYTLTAGKVLEIDE-TFVMDKPTDDTCEFTFHLG-----	178
1CLC	-----TMITNSR-----	7
Fungal	-----	0
Amoeba	-----	0
CSA	-----	0
1JS4	-----	0
Ascidian	-----TQNRMNGWSLKLVFSKRITNIQVWEAILSRSDDGRVFIFQPHSWNEELRDDFS	527
1KS8	-----	0
Cnidaria	-----	0
Bryophyte	-----	0
Pine	-----	0
Tomato	-----	0
NSpinach	-----	0
CSpinach	-----	0
CR9D	-----	0
GPKXZ44756	-----	0
VC2952174	-----	0
CR9B	-----	0
CR9C	-----	0
VC2958622	-----	0
NGP51468	-----	0
GP51466	-----	0
CGP51468	-----	0

1UT9	---GE-----LAATPP--YTVYL-DDVSLYDPEYTKPVEYILPQPDVRV	216
1CLC	---GS-----VDLQPS--LTGVFPSGLIETKVSAAKITENYQFDSRIRL	46
Fungal	-----	0
Amoeba	-----	0
CSA	-----	0
1JS4	-----	0
Ascidian	FLIIPEMSSQGLPQVVMFLCPREVTNMMNWDGIFIDRSTT-----SSNEAV	573
1KS8	-----	0
Cnidaria	-----	0
Bryophyte	-----	0
Pine	-----	0
Tomato	-----	0
NSpinach	-----	0
CSpinach	-----	0
CR9D	---MPDVCGN-----PFQDSPPINF'TTRFYGFVANYT---QGQE-VDITINIAT	42
GPKXZ44756	-----	0
VC2952174	-----	0
CR9B	-----	0
CR9C	-----	MV 2
VC2958622	-----	0
NGP51468	-----	0
GP51466	-----	0
CGP51468	-----	0

1UT9	NQVGYP-----EGKKVATVV-----CNSTQPVKWQLKNA	246
1CLC	NSIGFIP-----NHSKKATIA-----ANCST---FYVVKE	73
Fungal	-----	0
Amoeba	-----	0
CSA	-----	0
1JS4	-----	0
Ascidian	NSQNRDRLRQEQLRQRQEEIAREQRRQVEERRRQQELERRQREGQSTQVTTTTQLQTQRT	633
1KS8	-----	0
Cnidaria	-----	0
Bryophyte	-----	0
Pine	-----	0
Tomato	-----	0
NSpinach	-----	0
CSpinach	-----	0
CR9D	NHGGRMAMRVCPL-----SRGLISHDCFNNPAN--QLRRVSS---NPQYDAKLYWYVRPN	92
GPKXZ44756	-----	0
VC2952174	-----	0
CR9B	-----	0
CR9C	SESGSLPLLLHNIVLLEPQSTWSSREVIEWARR--ALGRASS---ASRWR-----	47
VC2958622	-----	0
NGP51468	-----	0
GP51466	-----	0
CGP51468	-----	0

1UT9	AGVVVLEGYTEPKGLDKDSQDY-VHWLDFSDFATEGIGIYYFELPTVNS-----PT	295
1CLC	DGTIVYTG-ATSMFDNDTKET-VYIADFSSVNEEG-TYYLAVPGVGK-----SV	120
Fungal	-----MKILA-----T----ILT	9
Amoeba	-----MKILKNCILL-----I----IFG	14
CSA	-----	0
1JS4	-----	0
Ascidian	QPATT-QTTRRPTRRPNTSSSRCTNP-----MGIPPSNPGQTRV----RFR	676
1KS8	-----	0
Cnidaria	-----	0
Bryophyte	-----	0
Pine	-----MKVVSEACVAFSLAYVYVLLL-IGTATVEATPFHRIIPPLQS	41
Tomato	-----	0
NSpinach	-----MGSFRLYGLLL-VSLQ-----LFYV-L--TST	23
CSpinach	-----FI-----GLL	5
CR9D	DIDIT-QRF-----RLPPGVS--C-----AD--GC-VLQ--VR-----PSP	120
GPKXZ44756	-MGAS-QGA-----DGPAGLP--R-----LALLGL-AAL--LC-----CSA	29
VC2952174	-----	0
CR9B	-----	0
CR9C	-----NRF-----LLGTGIVSPCLQALRKMLASLVVL-TLL--A-----AA	80
VC2958622	-----MALKVLRPSLLVC-LIT--A-----LC	19
NGP51468	-----	0
GP51466	-----	0
CGP51468	-----	0

1UT9	NYSHPFDIRKDIYTQMKYDALAFFYHKRSGIPIEMPYAGGEQWTRPAGHIGIEPNKGD TN	355
1CLC	NFKIAMNVYEDAF----KTAMLGMYLLRCGTSVSATYNGIHYSHG P-----	162
Fungal	CAPAFIKAASQDYARHLELSILFYEAQRSGKLPAN--NRI-----	47
Amoeba	LLSTQLINADTDYCSLLENALMFYKMN RAGRLPD---NDI-----	51
CSA	-----GSFNYGEALQKAIMFYEFQMSGKLPNW--VRN-----	30
1JS4	-----EPAFN YAEALQKSMFFYEAQRSGKLPEN--NRV-----	31
Ascidian	-RSPPRERRPYDYNEVIAMSILFYEAQRSGKLP SN--NRI-----	713
1KS8	-----MAYDYKQVLRD SLLFYEAQRSGRLPAD--QKV-----	30
Cnidaria	-----YDYDLVLHKSILFYEAQRSGKLPST--NRI-----	28
Bryophyte	-----MFLFLCLFLFSSGKLPAD--FPI-----	21
Pine	LYGRRGPSLSHDYRDALTKSILFYEGQRSGKLP LN--QRM-----	79
Tomato	-----GHNYGEALSKSFLFYEAQRSGYLPRN--QRV-----	29
NSpinach	ATIKVVATATFDYNDALDKSLLFFEAQRSGSLPVN--RRV-----	61
CSpinach	ALEAITMVAGFDYGEAVDKTLLFFEAQRAGKLPYD--NRV-----	43
CR9D	SPAANFSSGEYDYAALIDASYFFYEAQQTGPLPPW--NRAAQVNG-----	163
GPKXZ44756	-LPRFALSTEYNYTEALDGSYFFYEAQQAGPLPTW--NRAARWNG-----	71
VC2952174	-----MVVLYRFYEAQMSGGEVPAW--SRASQAQG-----	27
CR9B	-----QMSHNYASVLGLSYRFYEAQMSGNVPSW--SRASQAAG-----	36
CR9C	TPFVIEAQVKHNYGNLLDMSFRFYEAQMSGNVPSW--SRASQAVG-----	123
VC2958622	FHVSNVVAQQHNFSQILGLSYKFYEAQMSGDVPTW--SRASQAAG-----	62
NGP51468	-----	0
GP51466	-----MAWALGRLLRFYEAQMSGDVPSW--SRASQAAG-----	31
CGP51468	-----GLQLNYSHVLSLSYRFYEAQMSGDVPSW--SRASQAAG-----	36

c c

```
1UT9      VPTWPQDDEYA-GI-----PQKNYTKDVTGGWYDAGDHGKYVVNGGI AVWTL MNMYER 407
1CLC      --CHTNDAYLD-YI-----NGQHTKKDSTKGWHDAGDY NKYVVNAGITV GSMFLAWEH 212
Fungal    --YWRHDSMVDAGK---DN-----NVDLTGGYYDAGDNV KFNFPQASALTLL--AWS- 92
Amoeba    --PWRGNSALNDAS---PNSAKDANGDGNLSSGGYFDAGDGV KFGFLPMAYSMTML--GWS- 103
CSA       --NWRGDSALKDQG---DN-----GLDLTGGWFDAGDHV KFNLPMSTGTML--SWA- 75
1JS4      --SWRGDSGLNDGA---DV-----GLDLTGGWYDAGDHV KFGFPMFTA TML--AWG- 76
Ascidian  --PWRGDSGLRDGC---DV-----GVDLTGGWYDAGDHV KFGFPLAWSVTTL--AWG- 758
1KS8      --TWRKDSALNDQG---DQ-----GQDLTGGYFDAGDFV KFGFPMAYTATVL--AWG- 75
Cnidaria  --SWRGDSALGDHG---DN-----GEDLTGGWYDAGDYV KFGFPMAS SATVL--AWG- 73
Bryophyte --KWRGDSNLLDGS---DV-----NVSLSGGIYDAGDSV KFGFPMFTA TIL--SWS- 66
Pine      --RWRGDSALS DGA---AG-----HVDLTGGYYDAGDNV KFGFPMFTA TTTML--SWS- 124
Tomato    --QWRGNSGLNDGK---AS-----GIDL VGGYYDAGDNV KFGLPMAFTVTML--SWS- 74
NSpinach  --TWRGDSGLNDGF---SE-----QADLVGGYYDAGDHV KFGLPMAYSVT LI--SWA- 106
CSpinach  --KWRDTSGM RDGY---SQ-----GVDLVGGYYDAGDHV KFGLPMAFSVTMM--AWA- 88
CR9D      --GWRNDSY MADGA---DI-----GADLRGGWFDAGDHMK FALPYSWAVSTL--AWS- 208
GPKXZ44756 --GWRDASFLNDGS---DI-----GKNLTGGWFDAGDHMK FQLPFGWSASTL--AWS- 116
VC2952174 --GWRNWSHT HDGFGPDGI-----GMSLSSGGWYDAGDHLK I SLPLGVTASML--SYG- 75
CR9B      --GWRNKSHALDGTGPGGV-----NLDLSSGGWYDAGDHLK LHLPLGVSVSLL--SYG- 84
CR9C      --GWRNKSHALDGTGPGGV-----NLDLSSGGWYDAGDHLK LHLPLGVSVSLL--SYG- 171
VC2958622 --GWRNKSHLLDGTGPNGI-----GVDLSSGGWYDAGDHLK LHLPLGVSASLL--SYG- 110
NGP51468 -----MQDGFGPSGI-----SVGLSSGGWYDAGDHLK LHLPLGQAASTL--AYG- 41
GP51466   --GWRNRSHMQDGFGPSGI-----SVDLSSGGWYDAGDHLK LHLPLGQAASTL--AYG- 79
CGP51468 --GWRNRSHMQDGFGPSGI-----SVDLSSGGWYDAGDHLK LHLPLGQAASTL--AYG- 84
```

. * .***** * . . : : :

1UT9	AKIRGLDNWGPYRDGGMNIPEQNNGYPDILDEARWEIEFFKKMQVTEKEDPSIAGMVHH-	466
1CLC	FKD-----QLEPVALEIPEKNNSIPDFLDELKYEIDWILTMQYPDG-----SGRVAH-	259
Fungal	-----AVDWKDGYPEAG--QWEYMKDLLKWGMDYFIKCHT-----DKYVLYGQ-	133
Amoeba	-----FIEYESNIAQCG--LTSLYLDTIKYGTDWLIAAHT-----ADNEFAGQ-	144
CSA	-----AYEYKDAFVKSG--QLEHILNQIEWVNDYFVKCHP-----SKYVYYYQ-	116
1JS4	-----AIESPEGYIRSG--QMPYLKDNLRWVNDYFIKAHP-----SPNVLYVQ-	117
Ascidian	-----VIEFKDAYVDAN--EYRRVLDLKWVADYFVKAHT-----SRYELYGQ-	799
1KS8	-----LIDFEAGYSSAG--ALDDGRKAVKWATDYFIKAHT-----SQNEFYGQ-	116
Cnidaria	-----LVEYRDAYQAAG--ELDNALNSIKWATDYFIKAHT-----KKFEFYGQ-	114
Bryophyte	-----VLEYGPAMEKAG--QLASAKNSIKWITDYLIKAHA-----APNVLYFQ-	107
Pine	-----VLEFGGRMG--D--NLDHAKAAIRWATDYLLKATA-----RPGVIYVQ-	163
Tomato	-----ILEYGRQMAASG--ELSHAMDAVKWGTDYLLKAHP-----EPYVLYGE-	115
NSpinach	-----AIDFRKEILAAN--QMDYTLETIRWGTDYFLKAHC-----DKNVLWAQ-	147
CSpinach	-----AIDFSKDVLAAN--KMDQTLWAIWGTDYFLKAHT-----HPNVLWAQ-	129
CR9D	-----VLEFPAAAYSSAPG--LWATAKRNLLFAADYLVRSHVTASDVPSENRFVAQ-	256
GPKXZ44756	-----MVEFPAAAYGPPSGSLFQTVRRNLLFAADYIVRSHVNASDVPGENVYAAQ-	165
VC2952174	-----MLTWESTYRSAG--QWDLAVRNLDWVASYLKCHVNASDNPADNAFVAQA	123
CR9B	-----ALTFEAAAYRAAG--QWDIAVRNLDWAASYIAKCHTQASDTPADNKFVAQ-	131
CR9C	-----ALTFEAAAYRAAG--QWDIAVRNLDWAASYIAKCHTQASDTPAYNKFVAQ-	218
VC2958622	-----VLTWEAAYRAAG--QWDIAVRNLDWVASYYLKCHYQASDTPSANAFVAQ-	157
NGP51468	-----ILTWESAYRTAG--VWDTAVRNMDWIASYMLKCHYKNSDTPSGNAFVAQ-	88
GP51466	-----ILTWESAYRTAG--VWDTAVRNIDWIASYMLKCYKNSDTPSGNAFV---	124
CGP51468	-----ILTWESAYRTAG--VWDTAVRNIDWIASYMLKCHYKNSDTPSGNAFVAQ-	131

: .:

S S

1UT9	-----KI H DFR W TALGMLPHED-----PQPRYLRPVSTA----A	496
1CLC	-----KV S TRN F GGF-IMPENE-----HDERFFVPWSSA----A	288
Fungal	-----VGNGSLD H GA- W VPPPEID-----YKYPSYKIT-ASAPGSDL	168
Amoeba	-----VGDGNVD H SW- W GPPEDMT-----MARPTYMLT-TEAPGTEI	179
CSA	-----VGDGGKD H AW- W GPAEVMQ-----MERPSFKVT-QSSPGSAV	151
1JS4	-----VGDGDAD H KW- W GPAEVMP-----MERPSFKVD-PSCPGSDV	152
Ascidian	-----VGSGRAD H LY- W GRSEDLR-----MNRPSYKID-ASNPGTEL	834
1KS8	-----VGQGDAD H AF- W GRPEDMT-----MARPAYKID-TSRPGSDL	151
Cnidaria	-----VGDGHVD H AY- W GRPEDMT-----MQRPAFKIT-TSRPGSDL	149
Bryophyte	-----VGNASTD H KC- W YRPEDGGS-----IARPSLVLN-TTLPGSEV	143
Pine	-----VGDPNLD H KC- W ERPEDMD-----TSRNVYKID-ADHPGSDV	198
Tomato	-----VGDGNTD H YC- W QRPEDMT-----TSRAAYRID-PNHFGSDL	150
NSpinach	-----VGDGAD H SC- W QRAEEMT-----TPRIAYRLD-SSHFGSDV	182
CSpinach	-----VGDGASD H LC- W ERAEDMT-----TSRTAYKLD-SSNPGSDL	164
CR9D	-----VGDTDTD H SR- W CRPEQCGAVE----GPYRPTWLTT-ATKPGSDV	295
GPKXZ44756	-----IGDTDTD H AR- W CRPEQCPEIQ----GPYRPTWVAD-RTRPGADI	204
VC2952174	REGQEGAQLGNGFVWVGDDTD H NLH W GRPEQQAEGGEEGALGWRPVYLLTAEGGKGADI	183
CR9B	-----IGDVATD H NT W GRPEQQPEGGAQGSAGYRPVYVITSSSGKGADI	176
CR9C	-----IGDVATD H NT W GRPEQQPEGGAQGSAGYRPVWLITANGKGADI	263
VC2958622	-----VGDVDTD H NT W GRPEQQAQGSQGSQSPGWRPVHVITAAGGRGADI	202
NGP51468	-----VGDVDTD H SK W GRPEQQPEGGAQGSTGWRPVYSIT-AGGRGADI	132
GP51466	-----GDVDTD H SK W GRPEQQPEGGAQGSTGWRPVYSIT-AGGRGADI	167
CGP51468	-----VGDVDTD H SK W GRPEQQPEGGAQGSNGWRPVYSIT-AGGRGADI	175

:

1UT9	TLNFAATLAQSARLWKDY----DPTFAADCLEKAEIAWQAALKHPD	IYA	-----	541
1CLC	TADFVAMTAMAARIFRPY----DPQYAEKCINAAKVSYEFLKNNPANVF		-----	333
Fungal	AAETSASMVAASMAFRDE----DPSYADILLKHGKELYEFAEKYRGTYD		-----	213
Amoeba	AMEAASALAAASIAFKSS----NPTYAATCLAHAKTLHNFYGYTYRGVYS		-----	224
CSA	VAETAASLAAASIVLKDR----NPTKAATYLQHAKDLYEFAEVTKSD		-----	194
1JS4	AAETAAMAASSIVFADD----DPAYAATLVQHAKQLYTFADTYR	GVYS	-----	197
Ascidian	AAETAALAACSIVFKNA----RPGYSRMLLRHATELYEFADRYRRSYH		-----	879
1KS8	AGETAALAAASIVFRNV----DGTYSNNLLTHARQLFDFANNYR	GKYS	-----	196
Cnidaria	AGETAALAAASIAFKPT----NPSYAAEMLQHAEELYEFADTYRGKYS		-----	194
Bryophyte	AAETAAMAASMVFRST----DATYADTLVAHAQQLFNFSDTYQASYS		-----	188
Pine	AAETAALAAASMVFRRT----DPIYSRHLLQTAMQVDFADKHRGAYS		-----	243
Tomato	AGETAAMAASIVFRRY----NPGYSNELLNHAHQLFEFADKYRGKYD		-----	195
NSpinach	AGETAALAAASLAFRSH----NSSYSTLLLRHAKEIFSFADTFRGVYD		-----	227
CSpinach	AGETAALAAASLAFRPY----NSSYAQQLVQHAEQLFYFADTFRGLYD		-----	209
CR9D	VGEAVAALAAMVVAADPEAS--PVAAQLLVHARQLYAFGKA	FPG	-----	339
GPKXZ44756	VGEAVASLVGVASVLKMPAD--PAIPLLMTHARQLYAFKA	FPG	-----	248
VC2952174	VSEAVAAMVGTALVLRPPIHSNPAKAQELLRRATQLFEFAKLLPGM	CVSRVGLSGVASL		243
CR9B	VAEAAASLASVSLLLKRPGTYSNTTKAAFLARAKQLFEFAKTLTGG	THTDRRLV-HTSV		235
CR9C	VAEAVASLASVSLLLKRPGAYSNTTKAASFLARAKQLFEFAKT	LNSG	-----	310
VC2958622	VGEAVATLAGVSLLLKRPGAYSNPTRAATLLSRAKQLFEFAKTI	KN	-----	248
NGP51468	AAQGVATMVGAAMLLKRPGSFANATKAALLSRARQLFEFAKTV	PG	-----	178
GP51466	AAQGVATMVGAAMLLKRPGAFANATKAALLSRARQLFEFAKTV	PG	-----	213
CGP51468	AAQGVATMVGAAMLLKRPGSFANATKAALLSRARQLFEFAKTV	PG	-----	221

. : : . :

	SS	MM	
1UT9	-----EYTPGSGGGPGGG P YND-DY	VG DEF YWAACELYVTTG-----	KDEYK 581
1CLC	-----ANQSGFSTG E YAT-VSDA	DDRLWAAAEMWETLG-----	DEEYL 370
Fungal	-----LSITD----AKG Y RSYSGFN DEL	VWGAAWLYRATG-----	DKTYK 250
Amoeba	-----DSITN----AQ A FYNSWSGYK DDL	VWGSIWLYKATQ-----	DSDYL 261
CSA	-----SGYTA----ANG Y NSWSGFY DELS	SWAAVWLYLATN-----	DSTYL 231
1JS4	-----DCVP----AG A FYNSWSG YQ	DELWGAYWLYKATG-----	DDSYL 233
Ascidian	-----LSIPD----VTS Y RSYNGYN DEL	WVGALWLYKATG-----	MRSYL 916
1KS8	-----DSITD----ARN F YAS-AD YR	DELWAAAALYRATN-----	DNTYL 232
Cnidaria	-----DAIPN----AG S FYKSWSGYK DEL	VWGAAWLYRATK-----	KASYL 231
Bryophyte	-----ETIPE----FQD Y NS-TGY DEL	LLWGATWLYYATG-----	DNTYL 224
Pine	-----DSLQSE---VCP F YCSYSGYN DELL	WGAAWLQRASR-----	NVSYI 281
Tomato	-----SSITV----AQK Y RSVSGYA DELL	WGAAWLYKASN-----	NQFYI 232
NSpinach	-----DSYPD----AET F YPS-SGY DEL	LWAAWLYRATN-----	NDYYL 263
CSpinach	-----DSITN----AEK Y YTS-SGY Q	DELLWAAVWLYRATN-----	KDRYL 245
CR9D	-----AWSLTSDEGDYP Y RGN-HVW Q	DDMLWAAAMCRAGQ-----	GAGYC 380
GPKXZ44756	-----TWEIP--AGDYP Y RGT-HKW Q	DDMLWAAAWMCRAE-----	GASYC 287
VC2952174	TSPALGWWSPPAGR---QT L YGS-AR	WR DDL LAWAAAWLCRAAVETGVGGGAGTSAGSSAC	299
CR9B	AEPNMRRWAPPDNN----G A YGS-SS	WN DD MAWAAAWLCRASVDEGVT----P-TNSAAC	285
CR9C	-----VWAPPEGQ----N A YTS-SS	WN DD MAWAAAWLCRADVDAGAS----A-ATSSAC	354
VC2958622	-----TWGPTSGS----N A YPS-SS	YN DD LAWAAAWLCRADVDGGAM----SLTASAAC	293
NGP51468	-----SWSPPWGS----N A YPS-SS	YL DD MTWAAAWLCRADVDAGIA----T-GTSTAC	222
GP51466	-----SWSPPWGS----N A YSS-SS	YL DD MTWAAAWLCRADVDAGVA----T-GASTAC	257
CGP51468	-----SWSPPWGS----S A YSS-SS	YL DD MAWAAAWLCRADVDAGVA----T-GASTAC	265

* * : * . : : :

B MSMM

1UT9	NYLMNSPHYLEMPAKMGENGANGEDNGL---	WGCF	WGT	TQGLGTITLALVENGL-PA	636				
1CLC	RDFENRAAQF-----	SKKI---	EADF	WNVANLGMFTYLLSERPGKNP	411				
Fungal	DKVDKIWDTP-----	Y---GDLDPDKFLGSG---	GPIS	WDDKKAAYALMALTT-----	293				
Amoeba	TKAVADYASG-----	GVGMAQG---	NSHDWN	KAPGCCLLLSKLV-----	300				
CSA	TKAESYVQNW-----	PKISGSNIIDYK---	WAHCWDD	VHNGAALLLAKIT-----	273				
1JS4	AKAEYEYDFL-----	STEQQTDLRSYR---	WTIA	WDDKSYGTYVLLAKET-----	275				
Ascidian	EDAKRKYDQY-----	GQGNTP---	IMFS	WDDKRAQSQVLLANFT-----	952				
1KS8	NTAESLYDEF-----	GLQNWG---	GGLN	WDSKVSQVLLAKLT-----	268				
Cnidaria	TKAKKYFNDF-----	GIGGTA---	WAFS	WDDKKAGAQVLLAQIT-----	267				
Bryophyte	AYVTGA-----	NGEKFADWGVFP	SWFS	WDSKRPVQVLLARLQMLK-PP	267				
Pine	SYIQ-S-----	HGQNLGGED-NV	NI	FSWDDKHAGARVLLAKEVLLR---	320				
Tomato	NYLG-R-----	NGDALGGTG	WSMTE	FGWV	KYAGVQTLVAQFLMSG-KA	274			
NSpinach	QYAS-Y-----	NAASLGGTGNSV	KMFS	WDNKYAGLQILLAKVLLDG-DG	305				
CSpinach	EYVV-Q-----	NAASMGGTG	WAVRE	FSWDNKYAGVQVLVSKLLLEG-KG	287				
CR9D	ADAVTYWNAA-----	ANMGV	GW-S	SGMDW	DN	AFNEASVMMLGMADKL-SP	423		
GPKXZ44756	ADAVSFWNVG-----	SNMGIG	W-C	PGMDW	DN	AFNQASVMMLGMADRF-SA	330		
VC2952174	AEAA	SLWIDA-----	ADTGGE	YGR	DVIA	WAA	VFPLASMMLRDV-GAG-GP	342	
CR9B	AAAL	AYWKPF-----	VGNAWEVQ--	DV	N	WDR	MAGMAAVLLRDV-GAG-TA	326	
CR9C	SVAV	SYWKPF-----	IGNANV	YG--	DV	N	WDR	MAGMAAVLLRDV-GAG-TA	395
VC2958622	NAAP	SLWDAT-----	KY-AN--L--	DLS	W	DN	VAAAAALLLRDT-GAG-GA	331	
NGP51468	STAL	SYWDQI-----	KSGS--Y--	DFS	W	Q	VAGLAAVLLRDT-GAG-GA	261	
GP51466	STAL	SYWDQV-----	KNSGS--Y--	DVV	W	Q	VAGLAAVLLRDT-GAG-GA	296	
CGP51468	STAL	SYWDQV-----	KSGS--Y--	DVV	W	Q	VAGLAAVLLRDT-GAG-GA	304	

*

1UT9	T-----DIQKARNNIKAADRWLENIE-----E	QGYRLPIK-QAEDERGG	---	675	
1CLC	A-----LVQSIKDSLLSTADSIVRTSQ-----	NHGYGRT-----	LGTT	---	444
Fungal	-----GESKYVEESTKHSELMV-----	-----	NYNTTPGGLWY		321
Amoeba	-----TTSTYKTD FEGWLN YWLPG-----	-----	GGV TYTPGGLAW		331
CSA	-----DKDTYKQIIESHLDYWT TGYN-----	-----	GERIKYTPKGLAW		307
1JS4	-----GKQKYIDDANRWLDYWTVGVN-----	-----	GQR	VPYSPGGMAY	309
Ascidian	-----GEAKYKGHVANYQRFLN-----	-----	GALKTPRGLVW		980
1KS8	-----NKQAYKDTVQSYVNYLIN-----	-----	N	QQKTPKGLLY	297
Cnidaria	-----GESSFVNAAQASLNAWMPG-----	-----	GSV TYTPKGLAW		298
Bryophyte	TNAVNTVSKGLTDYKTTADGLMCAFLPGSP-----	-----	TASTDR TKGGYIW		310
Pine	-----NSKSLEEYRGHADNFVCSLLPGTP-----	-----	NSQAQYTPGGLLY		357
Tomato	G----HNAPVFEKYQQKAENFMCSMLGKGN-----	-----	R-NTQKTPGGLIY		312
NSpinach	Q----SYTDTLTQYKARADFFVCAYLQKNN-----	-----	GDNVPMT PGGLAF		344
CSpinach	G----AYASTLKQYQAKADYFACACVQKNN-----	-----	GFDVQLTPGGLVY		326
CR9D	A-----FLANVRTRMDWNLNLWHVSTLCTAPPAGTDSNGDGLVDD		GHICYSPRGLVH		475
GPKXZ44756	S-----FLTTRTRLDYNLNLWHVSTVCTQPPPNTDSNGDGLVDD		GHICYSPKGFAH		382
VC2952174	A-----MVGRFEQHISYVLDRWISPAA-----	APPC--NGTSLE	FQVCYTPGGLAW		386
CR9B	T-----DVATYNTAINAVLSRWMEPGT-----	RTCS--SG---A	APPCYTS GGLVW		367
CR9C	T-----DVATYNTAISNIMKRWLIPST-----	QTCV--GG---A	ALPCYTPGGLVW		436
VC2958622	T-----YVASYDDFVNRLLTRWTGSG-----	ACS--T---G	ATPCMT PGGLAW		369
NGP51468	A-----YTASWDGYIQGIQNRWKSSI-----	-----	PYTPGGLAF		291
GP51466	T-----YTASWDGYIQSIQNRWKSSL-----	-----	PYTPGGLAW		326
CGP51468	A-----YTASWDGYIQSIQNRWKSSL-----	-----	PYTPGGLAW		334

	S	SS	
1UT9	---	YPWGSNSF	ILNQMIVMGYAYDFTG-----DSKYLDGMFDGISYLLG 716
1CLC	---	YYWGCNGT	VVRQTMILQVANKISP-----NNDYVNAALDAISHVFG 485
Fungal	---	DSNLSMWGSNRY	ASNAAFVAMLASTMD-----ANNS--KRKEYVKFVKKQIDYILG 371
Amoeba	---	IRQWGPARYA	AATAAFLGSLAGT-----EKGTDFTQKQVDYLIG 369
CSA	---	LDQWGSRLRY	ATTTAFLAFVYSDWSG-----CPTG--KKETYRKFGESEQIDYALG 354
1JS4	---	LDTWGALRYA	AANTAFVALVYAKVID-----DPV---RKQRYHDFAVRQINYALG 355
Ascidian	---	LDQWGSNRYA	AANAALAAKVPG-----IA---NRNEMVRFAEAQIHYMLG 1025
1KS8	---	IDMWGTLRHA	AANAALFIMLEAAELGL-----SASSYRQFAQTQIDYALG 340
Cnidaria	---	RAEWGANRYA	AANTAFLLVAADAGI-----NPATYREFAKKQIHYMLG 341
Bryophyte	---	LNEWSALQH	GINSALLASFYS DYLVAAKSSGITCSGKSFTHAQLRAFASSQANYVLG 367
Pine	---	KMSDCNLQY	VTTSTFLLFTYPKYLRVSK-QVVRRCGNMVVTPTRIRTLAKRQVDYILG 413
Tomato	---	RQRWNNMQF	VTSAAFLATTYS DYLASAG-KYLCSSGFVSPNELLSFAKSQVDYILG 368
NSpinach	---	LLASNNLQYA	AASASFLLAIS DYLSGSS-SVIDCPDGKVPQDLLNFAKSQADYILG 400
CSpinach	---	VRQWNNMQY	ASSAFLAVYS DYLSQAK-AVVNCPEGTAQPQDLFNFAKSQADYILG 382
CR9D	---	QMQWGTLRV	TANAAATKLVYSKYTT-----ANTADTQRQRCWARRQMRLMLG 522
GPKXZ44756	---	ESTWGTARI	TANAAALKLAYS KYLP-----TNPEDAKRQRCWARKQMRLMLG 429
VC2952174	---	YSNWGSARC	AANMAMAALMSSRTGTETNT---NTPEVALTQQRRCWAWRQASYLLG 440
CR9B	---	GSEWGS CRH	TANAALVALAAARGDAGAGL-----EVAYSTRVNRNCWARSQVDYMLG 419
CR9C	---	RDAWGS NRH	TANAALVALAAARGDAGAGL-----EVAYSTRVNRNCWARSQVDYMLG 488
VC2958622	---	YSDWGSARY	AANVALVALAAARS DGGGGA-----ALTS AARASRICWAKNQVSYMLG 421
NGP51468	---	LSGWGS CRY	SANTALVLLAAARPDGGSGS-----GLTADARRERHCWARKQVSYMLG 343
GP51466	---	LTAWGS CRH	SANTALVLLAAARPDGGSGP-----GLTADARRERHCWARKQVSYMLG 378
CGP51468	---	LTAWGS CRH	SANTALVLLAASRPDGGSGP-----GLTADARRERHCWARKQVSYMLG 386

:*

S S

1UT9	RNAMDQSYVTGYG----ERPLQNP HDR FWTPQTSKR-----FPAPP---	753
1CLC	RNYYNRSYVTGLG----INPPMNP HDR RSGAD---G-----IWEPW---	519
Fungal	DNPAKVDYVVGAD----PSSPKAV HR RGASGSKG-----ADKGPSENVFI	412
Amoeba	NNPNQQSFVVGMG----PNYPINP HR RAAHSTT-----NDINNPVNNLYL	411
CSA	STG--RSFVVGFG----TNPPKRP HR RTAHSSWA-----DSQSIIPSYHRHT	394
1JS4	DNPRNSSYVVGFG----NNPPRNP HR RTAHGSLT-----DSIASPAENRHV	397
Ascidian	GAG--RSYVVGYG----RNPTQP HR RGSSCPAAPT-----ECSW-GNFHSSAANHFT	1071
1KS8	DGG--RSFVCGFG----SNPPTRP HR RSSSCPAPAPA-----TCDW-NTFNSPDPNYHV	386
Cnidaria	DSG--HSYVVGFG----VNPPKRP HG RSSSCPSPPA-----TCGW-SLYNADVDNAHV	387
Bryophyte	NNPLSTSFVVGYG----EKHPKYL HR RGASIPVDQIK---TDCASW-GWYDSKEPNPNI	419
Pine	DNPLRMSYVVGYG----AKFPERI HR RGSSLPSIYQHPQIIPCNDGFQSLYSN-APNPNR	468
Tomato	DNPRATSYMVGYG----NNYPRQV HR RASSIVSFKVNPSFVSCRGGYATWYSRKASDPNL	424
NSpinach	ENPQSMSYLIGYG----TNYPQKA HR RGSSIPSMNELSSRLECSQGFDEWYKNWGPNPNI	456
CSpinach	KNPKSMSYLVGYG----TNYPKQV HR RGASIASISVHNAYVGCVQGFEEWYHRTSANPNV	438
CR9D	DWGR--SFVVGVG----NNPPQRP HS SSMCDPDYS-----VVCDG-NTAALDRPNPSV	569
GPKXZ44756	DWGR--SFVVGFG----CNPPVRP HS STMCDRDYS-----ITCDG-NTAADPRPNPSV	476
VC2952174	GNSRNQSFVVGYPYHSSPTRP VHK SSSCPTDYN-----TTCDW-TALSAPGANPSV	493
CR9B	SNPQSQSYVVGKPTTSHKAPEKP HR RSSSCATNYA-----TPCDW-NALDAPGNPSV	472
CR9C	SNPQSQSYVVGKPTTSHKAPEKP HR RSSSCATNYA-----SPCTW-AALDNTDPNPSV	541
VC2958622	TNPQSQSFVVGKPTTSHKAPEKP HR RSSSCNPSYA-----ITCDW-TALDAAGPNPSV	474
NGP51468	DNPRSQSFVVGFKPTAGHSSPQSP HR SASCSPNYA-----ITCDW-NNLNAAGPSPSV	396
GP51466	DNPRSQSFVVGFKPTAGHSSPQSP HR SASCSPNYA-----ITCDW-NNLNAAGPSPSV	431
CGP51468	DNPRSQSFVVGFKPTAGHSSPQSP HR SASCSPNYA-----ITCDW-NNLNAAGPSPSV	439

. . . *

1UT9	YLDEQYTDSETDKVTIDSPVAGERFEAGKDINISATVKS KTPVSKVEFYNGDTLISS ---	866
1CLC	G FVNY-NSPQNE-V-----LYG DVNDDGKVNSTDLTLLKRYVLK-----AVSTLPSS---	604
Fungal	FLIKEGLNV-----PDPKQTDGAWPPKE-----PKPDV-----KWDWNLEA ---	489
Amoeba	SLVNPSSTS-----V-----PTTTPTV-----TETPT-----ET--PTET ---	479
CSA	KMYLLYGGN-----PIPDFK--AIETPTN-----D EFFV-----EA--GINA---	467
1JS4	MLVEEYGGT-----PLADFP--PTEEPDG-----P EIFV-----EA--QINT---	471
Ascidian	GLKYFKIKQ-----RR----- -----	1122
1KS8	ALVALGY----- -----	433
Cnidaria	GLKSL----- -----	432
Bryophyte	GLVGSSSNS-----VPISWI----- -----	474
Pine	YLAHSFA----- -----	515
Tomato	RLHAGHSGYNQL--LPVVPDPKPT--PKPAPRT-----KVTPA-----PR--PRVLP --	505
NSpinach	KLHSVCSP-----SPPSASP-----AYT-----PG--TPSIPKE ---	523
CSpinach	KLRSSNTY-----STPYARNT--PKSSYST-----PTTYV-----KK--PQNAPKN ---	515
CR9D	GLLQLGAS-----TPDWNAYCGATP-----SPV-----PSPTPTPSPSP ---	643
GPKXZ44756	GLLQLSAS-----TPDWDAYCGTAP-----TPI-----TCPWACSSCDS ---	550
VC2952174	GLIEVESLL-----HEGGCSWEGYCVSTS-----CGT-----PGDR ---	564
CR9B	GLAAVDAAI-----KAAGCTWTS----- -----	533
CR9C	ALSGLDAAI-----TKAGCTWSS----- -----	599
VC2958622	GLTDLEQGL-----QRSGPFPPPSPSPSL-----SPP ---	541
NGP51468	GLTALDQAL-----RATGCN----- -----	451
GP51466	-----	471
CGP51468	GLTALDQAL-----RSTGCN----- -----	494

1UT9	-DTTAPYTAKITGAAVGAYNLKAVAVLSDGRRIESPVTPVLVKVIVKPTVKLTAPKSNVV	925
1CLC	-K-----AEKNADVNRDGRVNSSD-VTILSRYLIRVIEKLP-----	639
Fungal	-----DEP-----SYM-----SGAPKIA-----	502
Amoeba	-----PTE-----TPTE-----	486
CSA	-----SGT-----NFIEIKAIVNNQSGWPARA-----	489
1JS4	-----PGT-----TFTEIKAMIRNQSGWPARM-----	493
Ascidian	-----	1122
1KS8	-----	433
Cnidaria	-----	432
Bryophyte	-----	474
Pine	-----	515
Tomato	--VPANAHVTIQQRATSSWALNGK-----TYYRYSAVVTNKSGKTVK--	545
NSpinach	PSTGEG-----	529
CSpinach	PYTPNVPIREFKHSITGTWNDKGQ-----TVYHHTVLVKNMSMKTVR-----	557
CR9D	SPTPTPSPSPS-----P-----	655
GPKXZ44756	GTQPGS-----	556
VC2952174	GVLPAATCPA-----VQI-----CVVVMVVMVAVV-----	591
CR9B	-----	533
CR9C	-----	599
VC2958622	-----	541
NGP51468	-----	451
GP51466	-----	471
CGP51468	-----	494

1UT9	AYGNEFLKITATASDSDGKISRVDLVDGEVIGSDREAPYEYEWKAVEGNHEISV-IAYD	984
1CLC	-----	639
Fungal	-----TGSGGLKC--AKWCIDL-----EV-----DS-SNVSVQ-----	526
Amoeba	-----	486
CSA	-----TNK-LKF--RYFVDLSELIKAGY-----SP-NQLTLSTNYN	521
1JS4	-----LDK-GTF--RYWFTLDE----GV-----DP-ADITVSSAYN	521
Ascidian	-----	1122
1KS8	-----	433
Cnidaria	-----	432
Bryophyte	-----	474
Pine	-----	515
Tomato	-----	545
NSpinach	-----	529
CSpinach	-----	557
CR9D	-----	655
GPKXZ44756	-----	556
VC2952174	-----	591
CR9B	-----	533
CR9C	-----	599
VC2958622	-----	541
NGP51468	-----	451
GP51466	-----	471
CGP51468	-----	494

1UT9	DDDAASTPDSVKIFVKQARDVKVQYLCENTQTSTQEIKGKFNIVNTGNRDYSLKDIVLRY	1044
1CLC	-----	639
Fungal	-----	526
Amoeba	-----TPT-----	489
CSA	-----QGAKVSGP-----	529
1JS4	-----QCATPE-----	527
Ascidian	-----	1122
1KS8	-----	433
Cnidaria	-----	432
Bryophyte	-----	474
Pine	-----	515
Tomato	-----	545
NSpinach	-----	529
CSpinach	-----	557
CR9D	-----	655
GPKXZ44756	-----	556
VC2952174	-----	591
CR9B	-----	533
CR9C	-----	599
VC2958622	-----	541
NGP51468	-----	451
GP51466	-----	471
CGP51468	-----	494

1UT9	YFTKEHNSQLQFICYTPIGSGNLI PSFGGSGDEHYLQLEFKDVKLPAGGQTGE---IQF	1101
1CLC	-----	639
Fungal	-----NW-----GGKITENKGNKF	541
Amoeba	-----	489
CSA	-----YVWDSSRNIYYILVDFTGTLIYPGGQDKYKKEVQF	564
1JS4	-----DVHHVSGDLYYVEIDCTGEEKIFPGGQSEHRREVQF	562
Ascidian	-----	1122
1KS8	-----	433
Cnidaria	-----	432
Bryophyte	-----	474
Pine	-----	515
Tomato	-----NLKL	549
NSpinach	-----	529
CSpinach	-----ELKL	561
CR9D	-----	655
GPKXZ44756	-----	556
VC2952174	-----V	592
CR9B	-----	533
CR9C	-----	599
VC2958622	-----	541
NGP51468	-----	451
GP51466	-----	471
CGP51468	-----	494

1UT9	VIRYADN-----SFHDQSNDYSFDPTIKAF-----QDYGKVTLYKN	1137
1CLC	-----	639
Fungal	TICSEYDNGYL-DGKGTSQHWN-----FNFKKPNGGKGTDILPKTA-ILYCN	586
Amoeba	-----	489
CSA	RIAAPQNVQ-----WDNSNDYS-----F--QDIKGVSSGSVVKTKYIPLYDE	604
1JS4	RIAG--GPG-----WDPSNDWS-----F--QGIGN----ELAPAPYIVLYDD	596
Ascidian	-----	1122
1KS8	-----	433
Cnidaria	-----	432
Bryophyte	-----	474
Pine	-----	515
Tomato	SIVKLYGPLWGLTKYGNS--FIFPAWLNSLPAGKSLEFVYIHTASP AIVSVSSYTLV	604
NSpinach	-----	529
CSpinach	KIENLSGPIYGLIPTGEKNIFQVPPHLRVLLAGGELDFVYIQGGPQAKVSVYSFH	616
CR9D	-----	655
GPKXZ44756	-----	556
VC2952174	-----AVVRAAA-III	602
CR9B	-----	533
CR9C	-----	599
VC2958622	-----	541
NGP51468	-----	451
GP51466	-----	471
CGP51468	-----	494

1UT9	GELVWGTPPGGTEPE-----EPEEPEEPEEPAIVY-----	1167
1CLC	-----	639
Fungal	GKEH-GDAYL-VNTDGS GAKPYGWTAGTCKPTF-LCDGSTPAPSTTV----KKNTTTVKK	639
Amoeba	-----ETPTE--TPT--ETPTETPTETPTETPTETPTETPTETPTETPTETPTETPTET	539
CSA	DIKVVGEEPGTSGVS---PTPTASVTPTPTPTPTATPTPTPTPTPTVTPTPTVTATPTPTPT	661
1JS4	GVPVWGTAPEEGEPPGGGEGPGGGGEEPGEDVTPPSAPGSPAVRDVTSTSAVLTWSASS--	654
Ascidian	-----	1122
1KS8	-----	433
Cnidaria	-----	432
Bryophyte	-----	474
Pine	-----	515
Tomato	-----	604
NSpinach	-----	529
CSpinach	-----	616
CR9D	-----APIPSPS-----PS--PTPSPSPSPSATPSPSPSPSPSPSP--SPSPSPSPS	698
GPKXZ44756	-----	556
VC2952174	-----SRPINTNDMSDNRI RG--GPSQPPPQPPAP-----PPPSP--PPLGLPSDP	644
CR9B	-----	533
CR9C	-----	599
VC2958622	-----PSPPPRPSSP-----PSQSP--P-----	557
NGP51468	-----	451
GP51466	-----	471
CGP51468	-----	494

1UT9	-----GDCNDDGKVNSTDVA-----VMKRYLK	KENVNINL 1197
1CLC	-----	639
Fungal	TTTTKKIEPTSALCYGYKCCETCEVQYSD-----ETGSWGIENNDWCGIPDSCN	-- 688
Amoeba	VTPTPTVTPTETPSSGESLSIYKSGL-----KNDFQDWSWGEHSLT	-- 580
CSA	PTSTPTVTPTPTPVSTPATSGQIKVLYANK-----ETNSTTNTIRPWLKVVNSGS	-- 711
1JS4	-----DTGGSGVAGY-DVF-----LRAGT	-- 672
Ascidian	-----	1122
1KS8	-----	433
Cnidaria	-----	432
Bryophyte	-----	474
Pine	-----	515
Tomato	-----	604
NSpinach	-----	529
CSpinach	-----	616
CR9D	PSGNPSCPPTTEYDCQQCAANADAVQSLLPGMTAPCQTCAA----AIADGWPC--YNCL	-- 750
GPXZ44756	--N--LASQRSNCYSCV-----NAR----GVSKSWQC--HACV	-- 584
VC2952174	SKAPATCRPTDAAC-----RSLGNT-----	-- 665
CR9B	-----YCALTCT-----GLDAGKC--TNSC	-- 551
CR9C	-----YCSMACT-----	606
VC2958622	PPPLASCSPTDYACQQCSQSTYTAP-----DACRSCVGAMRSIGQDPYRC--FSCS--	606
NGP51468	-----LVDYC-----G-----GKCSLAPSPSPPPAASPSLK--PS	479
GP51466	-----ACTNALITAQ-----GACRSCVATLTSKGQDPWQC--HSCG	-- 505
CGP51468	-----LACTNALITAQ-----GACRSCVATLTSKGQDPWQC--HSCG	-- 529

1UT9	DNADVADGKVNSTDFS-----ILKR-----YVMK-----NIEEL--	1227
1CLC	-----	639
Fungal	-EQDDE-----YPTCSINTEVAYVDEYKSWGIEGECIIEK-----EIP	725
Amoeba	-DTTNVESGETNSISFTPKAY--GAVFLGC----FECI-----	611
CSA	-SS-IDLSRVITIRYWYTVDGERAQA-----I--SDWAQIGASNVTFKFKLSSSVS	759
1JS4	-GQ-EQKVGSTTRTSFTLTGLEPDTTYIAA----VVARDNAGNVSRSTVSFTTLAENGG	726
Ascidian	-----	1122
1KS8	-----	433
Cnidaria	-----	432
Bryophyte	-----	474
Pine	-----	515
Tomato	-----	604
NSpinach	-----	529
CSpinach	-----	616
CR9D	-ATPLVSTNPS---IMQGCFCDC---AAAGVNGWA--CTQCTKGALS-----ATDNAN	793
GPXZ44756	-GNATYV--AS---QGQHCLSC---VSAGADAWA--CQSYCTDLSS-----DIAVLPS	626
VC2952174	-----NVTNTTA	672
CR9B	---SGIATAALQTVCMGTCVFN---SAAKGTDWG--CNQYCGASSLVGT----DPARAQQ	599
CR9C	-----	606
VC2958622	-NG--VTDPTIQGICFTECVPP---TALKGADWS--CSQYCSAPALVAN----DPTRARD	654
NGP51468	---PPSSSSPPP-SPSPSASPS---PS-----PSPSPSPSPG-----	509
GP51466	-TKGYTSDATIQTACFTQCVPS---AVAKGIAWA--CADYCEAQANVAG----DPSRASQ	555
CGP51468	-TKGYTSDATIQTACFTQCVPS---AVAKGIAWA--CADYCEKPAVVAG----DMTRVAQ	579

1UT9	-----PYR-----	1230
1CLC	-----	639
Fungal	GENCVCKAEAQ-----GYKCCSNSNLDVLYTDETGESVENNDWC	765
Amoeba	DTDTYNNIEFDINGGSSG--AQ--LLRITVVKNKSKVGSKLITDLNGGTPIEANSWT	664
CSA	GADYYLEIGFKSGAGQLQPGKDTGEIQIRFNKDDWSNYNQG-----NDWSWI	806
1JS4	GPDASCTV-----GYSTNDWDSGFTASIRITYHGTAPLSSWE	763
Ascidian	-----	1122
1KS8	-----	433
Cnidaria	-----	432
Bryophyte	-----	474
Pine	-----	515
Tomato	-----	604
NSpinach	-----	529
CSpinach	-----	616
CR9D	CATCYRR--ASS-----GNNWGCLEQTA-----GG-SSEG--RR	823
GPKXZ44756	CTSCVADPAVRS-----AGPWRCVCMAP-----SV-LAKGAAAV	660
VC2952174	CSACVAVCAELS-----IIDHRIDMRGRKKVKPA-----TRCLSDWRDAR	712
CR9B	CAACVAGW-----SNPWDCQNCIGV-----	619
CR9C	-----	606
VC2958622	CISCVKGV-----SNPWDCYNMAV-----TASLSDSAAAR	685
NGP51468	-----	509
GP51466	CMSCVTAGKVNS-----GNVWGCQSCMTG-----TS----SSTSR	586
CGP51468	CFSCVTGSGATS-----ANVWGCENCQKA-----TS----TTAAR	610

1UT9	-----	1230
1CLC	-----	639
Fungal	-LIKKC-----	770
Amoeba	-KIKASFIDDFKVSQKVDGIWIQ-----DIKQDTQSTVYISNIIATA-----	705
CSA	-QSMTSYGENEKV-----TAYIDGVLVWGQEPS-----	833
1JS4	-LSFTF-PAGQQVTHGWNATWRQ-----DGAAVTATPMSWNSSLAPGATVEVGF-----	810
Ascidian	-----	1122
1KS8	-----	433
Cnidaria	-----	432
Bryophyte	-----	474
Pine	-----	515
Tomato	-----	604
NSpinach	-----	529
CSpinach	-----	616
CR9D	AACLACVGNN---SDAWACTQCASRYGTPCEAEKCVACLKASGNAWGCYTATYAAQCG--	878
GPKXZ44756	EACMSCVRSL---KGPYACAVSV-----	680
VC2952174	AQCFDCVTSG--VTDAVSCAECALP-TAAARAACMTCQVRPLSA---Q-----	755
CR9B	-----	619
CR9C	-----	606
VC2958622	ATCFKCVTTT--TLGGWSCGDCAASRA-TPAERDSCIKSRGGRLL---A-----	728
NGP51468	-----	509
GP51466	ATCMSCVASN--LLPTWQCPQCANAG-SCRRRQMR-----HSL-----	621
CGP51468	SACSSCVGSN--LRPPSDCATCANSQ-SCTTR-----	639

1UT9	-----	1230
1CLC	-----	639
Fungal	-----	770
Amoeba	-----	705
CSA	-----G--	834
1JS4	NGSWSGSNTPTDFTLNGEPCALA	834
Ascidian	-----	1122
1KS8	-----	433
Cnidaria	-----	432
Bryophyte	-----	474
Pine	-----	515
Tomato	-----	604
NSpinach	-----	529
CSpinach	-----	616
CR9D	GGRRSLGTEF	888
GPXZ44756	-----	680
VC2952174	SAS	758
CR9B	-----	619
CR9C	-----	606
VC2958622	GENF	732
NGP51468	-----	509
GP51466	-----	621
CGP51468	-----	639

Supplementary Figure 1a. Multiple alignment of algal sequences across members from other diverse taxonomic groups. Blue highlight, catalytic domain (CD); pink highlight, carbohydrate-binding module (CBM); turquoise highlight, Fn3-like domain; turquoise highlight within Box, Fn3-like domain within CBM; yellow highlight, Ig-like; light grey highlight, linker; green highlight, dockerin; single boxed within blue region, conserved motifs in algal sequences; pink highlight within a box, putative blocking loops/secondary structure elements; white residues within CD, substrate binding (S), catalytic (C) and metal-

binding/Ca²⁺-binding (M); red font, putative and/or cannot be assigned to any particular function/domain. Organism names are provided as described for Supplementary Figure 1b (below) and [1]

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
1:1UT9	100	29	19	19	22	26	22	23	23	21	21	20	22	20	17	17	20	21	20	20	23	22	21
2:1CLC	29	100	19	19	21	23	21	23	23	18	18	19	19	19	21	22	17	20	18	20	22	21	21
3:Fungal	19	19	100	32	33	36	46	45	49	38	39	39	39	37	25	26	28	31	32	30	33	32	31
4:Amoeba	19	19	32	100	41	39	40	47	50	40	36	40	39	38	28	28	28	31	33	29	33	30	30
5:CSA	22	21	33	41	100	47	44	45	50	36	37	37	38	36	30	29	29	32	36	32	32	32	32
6:1JS4	26	23	36	39	47	100	51	53	55	42	44	40	43	40	30	32	30	33	35	32	34	32	31
7:Ascidian	22	21	46	40	44	51	100	53	58	40	39	43	40	41	33	33	35	38	35	39	39	38	39
8:1KS8	23	23	45	47	45	53	53	100	59	41	44	46	44	43	40	40	38	39	38	41	40	41	41
9:Cnidaria	23	23	49	50	50	55	58	59	100	42	47	46	47	47	39	40	38	41	40	42	41	41	42
10:Bryophyte	21	18	38	40	36	42	40	41	42	100	44	43	40	40	29	27	29	31	31	31	30	30	29
11:Pine	21	18	39	36	37	44	39	44	47	44	100	53	47	46	31	29	30	32	31	31	31	32	32
12:Tomato	19	19	39	40	37	40	43	46	46	43	53	100	51	51	29	28	29	32	33	33	30	31	32
13:N-Spinach	22	19	39	39	38	43	40	44	47	40	47	51	100	63	29	28	30	33	32	32	30	31	31
14:C-Spinach	19	19	37	38	36	40	41	43	47	40	46	51	63	100	30	28	27	30	30	29	28	29	28
15:Cr9D	16	21	25	28	30	30	33	40	39	29	31	29	29	30	100	60	39	39	38	38	38	39	40
16:Gp44756	17	22	26	28	29	32	33	40	40	27	29	28	28	28	60	100	38	39	39	37	39	40	40
17:Vc2952174	20	17	28	28	29	30	35	38	38	29	30	29	30	27	39	38	100	52	54	52	55	53	55
18:Cr9B	21	20	31	31	32	33	38	39	41	31	32	32	33	30	39	39	52	100	85	65	56	60	60
19:Cr9C	20	18	32	33	36	35	35	38	40	31	31	33	32	30	38	39	54	85	100	65	61	64	63
20:Vc2958622	20	20	30	29	32	32	39	41	42	31	31	33	32	29	38	37	52	65	65	100	62	63	63
21:N-Gp51468	22	22	33	33	32	34	39	40	41	30	31	30	30	28	38	39	55	56	61	62	100	85	85
22:Gp51466	22	21	32	30	32	32	38	41	41	30	32	31	31	29	39	40	53	60	64	63	85	100	91
23:C-Gp51468	21	21	31	30	32	31	39	41	42	29	32	32	31	28	40	40	54	60	63	63	85	91	100

Supplementary Figure 1b. Percent identity matrix of GH9 catalytic domain (CD) regions (sequences taken from Supplementary Figure 1a, blue region) across diverse taxonomic groups. PDB 1UT9 and PDB 1CLC, *Clostridium thermocellum*; fungal, *Neocallimastix patriciarum* (AEX92719.1); amoeba, *Dictyostelium discoideum* (P22699.1); CSA, *Caldocellum saccharolyticum*; PDB 1JS4, *Thermobifida fusca*; ascidian, *Ciona intestinalis* (P002126063.2); PDB 1KS8, termite, *Nasutitermes takasagoensis*; Cnidaria, *Nematostella vectensis* (XP001640312.1); bryophyte, *Physcomitrella patens* (XP001781646.1); pine, *Pinus radiata* (AAC12685.1); tomato, *Solanum lycopersicum* (NP001234172.1); N-spinach (N-terminal part) and C-spinach (C-terminal part) of *Spinacia oleracea* (KNA09089);

Cr, *Chlamydomonas reinhardtii*; Vc, *Volvox carterii*; N-Gp (N-terminal part) and C-Gp (C-terminal part) of *Gonium pectorale*. Numbers in brackets refer to sequence ID taken from the NCBI database (<https://www.ncbi.nlm.nih.gov/protein/>). Algal, green; bacterial, grey; metazoan, blue; plant, turquoise; fungal, blue, protist, white.

>A8JFG8-CrCel9B

LSYRFYEAQMSGNVPSWSRASQAAGGWRNKSHALDGTGPGGVNLDLSSGGWYDAGDHLKLHLPLGVSLSLSYGALTFEAAARAAGQWDIA
VRNLDWAASYIAKCHTQASDTPADNKFVAQIGDVATDHNTWWGRPEQQPEGGAQGSAGYRPVYVITSSSGKGADIVAEAAASLASVSLLL
KRPGTYSNTTKAAAF LARAKQLFEFAKTLTGTHDRRLVHTSVAEPNMRRWAPPDNNGAYGSSSWNDDMAWAAAWLCRASVDEGVTPTN
SAACAAALAYWKPFVGNWEVQDVNWDRMAGMAAVLLRDVGAGTATDVATYNTAINAVLSRWMEPGTRTCSSGAAPP CYTSGGLVWGSEW
GSCRHTANAALVALAAARGDAGAGLEVAYSTRVNRNCWARSQVDYMLGSPQSQS YVVGYKPTTSHKAPEKPHHRSSSCATNYATPCDWN
ALDAPGPNPSVLLYCMGALVGGPDRYDAYTDNRRDYVKNEVALDFNAGYTGALAGLAAVDAAIKAA

>A8JFH1-CrCel9C

MSFRFYEAQMSGNVPSWSRASQAVGGWRNKSHALDGTGPGGVNLDLSSGGWYDAGDHLKLHLPLGVSLSLSYGALTFEAAARAAGQWDI
AVRNLDWAASYIAKCHTQASDTPAYNKFVAQIGDVATDHNTWWGRPEQQPEGGAQGSAGYRPVWLIT TANGKGADIVAEAVASLASVSL
LLKRP GAYSNTTKAASFLARAKQLFEFAKTLNSGVWAPPEGQNAYTSSSWNDDMAWAAAWLCRADVDAGASAATSSACSVAVSYWKPFI
GNANVYGDVNWDRMAGMAAVLLRDVGAGTATDVATYNTAISNIMKRWLIPSTQTCVGGAAALPCYTPGGLVWRDAWGSNRHTANAALVAL
AAARGDAGAGLEVAYSTRVNRNCWARSQVDYMLGSPQSQS YVVGYKPTTSHKAPEKPHHRSSSCATNYASPCTWAALDNTDPNPSVLQ
GALVGGPDRYDAYTDNRRDYVKNEVALDFNAGYTGALAALSGLDAAITKA

>A8HW25-CrCel9D

ASYFFYEAQQTGPLPPWNRAAQVNGGWRNDSYMADGADIGADLRGGWFDAGDHMKFALPYSWAVSTLAWSVLEFPAAAYSSAPGLWAT
AKRNLLFAADYLVRSHVTASDVPSENRFVAQVGD TTDHSRWC RPEQCGAVEGPYRPTWLTTATKPGSDVVG EAVAALAAVAMVVAA
DEPASVAAQLLVHARQLYAFGKAFPGAWSLTSDEGDYPYRYGNHVWQDDMLWAAAMMCRAGQGAGYCADAVTYWNAANMGVWSS
GMDWDNAFNEASVMMLGMADKLS PAFLANVRTRMDWNLN LWHVSTLCTAPPAGTDSNGDGLVDDGHICYS PRGLVHQMQWGTLRVTA
NAAATKLVYSKYTTANTADTQRQRCWARRQMLMLGDWGRSFVVG VGNPPQRPHHSSSMCDPDYSVVC DGNTAALDRPNPSVLRGA
LVGGPRKDDTYEDNRMDYILNEVAIDYNGGFTVALAGLLOLGAS

>VC2952174

MVVLYRFYEAQMSGVPAWSRASQAQGGWRNWSHTHDGFGPDGIGMSLSGGWYDAGDHLKISLPLGVTASMLSYGMLTWESTYRSAG
QWDLAVRNLDWVASYLIKCHVNASDNPADNAFVAQAREGQEGAQLGNGFVWVG DTDHNLHWGRPEQQAEGGEEGALGWRPVYLLT
AEGGKGADIVSEAVAAMVGTALVLRPPIHSNPAKAQELLRRATQLFEFAKLLPGMCVSRVGLSGVASLTSPALGWWSPPAGRQTLY

GSARWRDDLAWAAAWLCRAAVETGVGGGAGTSAGSSACAEAAASLWIDAADTGGGEYGRDVIAWAAVFPLASMMLRDVGAGGPAMVGRF
EQHISYVLDRWISPAAPPNGTSLFQVCYTPGGLAWYSNWGSARCAANMAMAALMSSRTGTETNTNTPEVALTQQRRCWAWRQA
SYLLGGNSRNQSFVVGYPYHSSPTRPVHKSSSCPTDYNTTCDWTALSAPGANPSVLYGALVGGPDQLDGYQDSRGEYVQNEVAL
DYNAGFTGAMAGLIEVESLLHEG

>VC2958622

LSYKFYEAQMSGDVPTWSRASQAAGGWRNKSHLLDGTGPNIGVDLSGGWYDAGDHLKLHLPLGVSASLLSYGVLTWEAAYRAAGQW
DIAVRNLDWVASYYLKCHYQASDTPSANAFVAQVGDVDTDHNTWWGRPEQQAQGGSQSGPWRPVHVITAAGGRGADIVGEAVATLA
GVSLLLKRPGAYSNPTRAATLLSRAKQLFEFAKTIKNTWGPTSGSNAYPSSSYNDLAWAAAWLCRADVDGGAMSLTASAACNAAPS
LWDATKYANLDSLWDNVAAAAALLLRDTGAGGATYVASYDDFVNRLLTRWTGSGACSTGATPCMTPGGLAWYSDWGSARYAANVALV
ALAAARSDGGGAALTSAAARASRICWAKNQVSYMLGTNPQSQSFVVGYPKPTTSHKAPEKPHRSSSCNPSYAITCDWTALDAAGPNP
SVLAGALVGGPGRDSDSYVDNRRDYMKNEVALDFNAGFTAALAGLTDLEQGLQRS

>G.p-KXZ51468

MQDGFPGPSGISVGLSGGWYDAGDHLKLHLPLGQAASTLAYGILTWESAYRTAGVWDTAVRNMDWIASYMLKCHYKNSDTP
SGNAFVAQVGDVDTDHKWWGRPEQQPEGGAQGSTGWRPVYSITAGGRGADIAAQGVATMVGAAMLLKRPGSFANATKAA
LLLSRARQLFEFAKTVPGSWSPWGSNAYPSSSYLDDMTWAAAWLCRADVDAGIATGTSTACSTALS YWDQIKGSGSYDF
SWDQVAGLA AVL LRDTGAGGAAYTASWDGYIQGIQNRWKSSIPYTPGGLAFLSGWGSCRY SANTALVLLAAARPDGGSGS
GLTADARRERHCWARKQVSYMLGDNPRSQS FVVGFKPTAGHSSPQSPHRSASCSPNYAITCDWNNLNAAGPSPSVLLGA
LVGGPGQDDSYLDARGDYMKNEVA VDFNAGYTSALAGLTALDQALRAT

>G.p-KXZ51466

MAWALGRLLRFYEAQMSGDVPSWSRASQAAGGWRNRSHMQDGFPGPSGISVDLSGGWYDAGDHLKLHLPLGQAASTLAYGI
LTWESAYRTAGVWDTAVRNIDWIASYMLKCYKNSDTPSGNAFVGDVDTDHKWWGRPEQQPEGGAQGSTGWRPVYSITA
GGRGADIAAQGVATMVGAAMLLKRPGAFANATKAAALLLSRARQLFEFAKTVPGSWSPWGSNAYSSSYLDDMTWAAAWL
CRADVDAGVATGASTACSTALS YWDQVKNKSGSYDVVWDQVAGLA AVL LRDTGAGGATYTASWDGYIQSIQNRWKSSLPYT
PGGLAWLTAWGSCRHSANTALVLLAAARPDGGSGPGLTADARRERHCWARKQVSYMLGDNPRSQS FVVGFKPTAGHSSPQ
SPHRSASCSPNYAITCDWNNLNAAGPSPSVLLGALVGGPGQDDSYADSRGDYVKNEVA VDYNAGYTGALAACTNALITA

>G.p-KXZ44756

GSYFFYEAQQAGPLPTWNRAARWNGGWRDASFLNDGSDIGKNLTGGWFDAGDHMKFQLPFGWSASTLAWS
MVEFPAAYGPPSGSLFQTVRRNLLFAADYIVRSHVNASDVPGENVYAAQIGDTDTDHARWCRPEQCPEIQ

GPYRPTWVADRTRPGADIVGEAVASLVGVASVLKMNENPADPAIPLLMTHARQLYAFKAFPGTWEIPAGD
YPYRYGTHKWQDDMLWAAAWMCRAGEGASYPADAVSFWNVGSNMGIWCPGMDWDNAFNQASVMMLGMAD
RFSAS

>C.bescii-P96311

GSFNYGEALQKAIMFYEFQMSGKLPNWVRNNWRGDSALKDGDNDGLDLTGGWFDAGDHVKFNLPMSYTG
MLSWAVYEYKDAFVKSGQLEHILNQIEWVNDYFVKCHPSKYVYYYQVGDGSKDHAWWGPAEVMQMERPSF
KVTQSSPGSTVVTETAASLAAASIVLKDRNPTKAATYLQHAKELYEFAEVTKSDAGYTAANGYYNSWSGF
YDELSWAAVWLYLATNDSTYLTKAESYVQNWPKISGSNTIDYKWAHCWDDVHNGAALLLAKITGKDIYKQ
IIESHLDYWITGYNGERIKYTPKGLAWLDQWGLSLRYATTTAFLAFVYSDWVGCPSTKKEIYRKFGE
SQUIDYALGSAGRSFVVGFGTNPCKRPHHRTAHSSWADSQSIPSYHRHTLYGALVGGPGSDDSYTDDIS
NYVNEVACDYNAGFVGALAKMYQLYGGNP

>B.licheniformis-AAR29083.1

MSIASFSEKTRAASAEYPHNYAELLQKSLLFYEAQRSGRLPENSRLNWRGDSGLEDKDVGLDLTGGWY
DAGDHVKFGLPMAYSAAILSWSVYEYRDYKESGQLDAALDNIKWATDYFLKAHTAPYELWGQVNGALD
HAWWGPAEVMMPMKRPAYKIDAGCPSDLAGGTAAALASASIIFKPTDSSYSEKLLAHAKQLYDFADRYR
GKYSDCITDAQYYNSWSGYKDELTDGAVWLYLATEEQYLDKALASVSDWGD PANWPYRWTLSDDDVTY
GAQLLLARLTNDSRFVKSVERNLDYWSTGYSHNGSIERITYTPGGLAWLEQWGLSLRYASNAFLAFVYSD
WVDTEKAKRYRDFAVRQTEYMLGDNPPQRSFVVGYGKNPPKHPHRTAHGSWANQMNVPENHRHTLYGAL
VGGPGRDDSYRDDITDYASNEVAIDYNAAF TGNVAKMFQLFGKGHVP

>B.pumilus-AAF15367.1

MHIFETRLILFNTVQNTNGMTRRWSFLVQCFTFKKKEGVRSDYNYVEVLQKSILFYEAQRSGLPE
SNRLNWRGDSGLEDKDVGHDLTGGWYDAGDHVKFGLPMAYSAAVLAWTVYEYREAYEEAELDDMLDQI
KWATDYFLKAHTGPNFVAQVGDGNADHGWWGPAEVMMPMNRPAFKIDEHCPGTEVAAQTAAALAAGSII
FKETDAPYAAKLLTHAKQLYAFADQYRGEYTDVNTAQPFFYNSWSGYIDELIWGGIWLALATNDQTYLN
KALKAVEEWPKDWDYTF TMSWDNTFFASQILLARITKEKRFIESTERNLDYWSTGFVQNGKVERITYTP
GGLAWLDQWGLSLRYTANAFLAFVYADWVSDQEKKNRYQTFAIRQTHYMLGDNPPQNRSYVVGFGKNPP
MHPHRTAHGSWSNQLTTPSSHRHTLYGALVGGPNAQDQYTDDISDYVSNEVATDYNAAF TGNVAKMVQ
LFGQGSK

>P.barcinonensis-CAB38941.1

KAIYFYEAQRSGPLPANNRVEWRGDSGMQDGADVGVDLTGGWYDAGDHVKFGFPMAASATMLAWSVVEYAD
GYEQAGQLEEIKNIRWATDYFMKAHTKPNELWGQVAGNTDHAWWGPAEVMQMNRPSEFKIDASCPGSDLA
AETAALAASSIVFADSDPVYSAKLLQHAKELYNFADTYRGKYTDCITDAAAFYNSWTGYEDELAWGGAWLY
LATNDNAYLSKALSAADRWSTSGGSANWPYTWTQGWDSKHYGAQILLARITSNLNMPEATKFIQSTERNLDY
WTVGTNGGRVKYTPGGLAWLDQWGLRYAANAFAISFVYSDWVSDPVKKSRYQNFATSQINYLGDNPRQSS
YVVGYGQNSPQHPPHRTAHSSWMNEDI PANHRHILYGAMVGGPNASDQYTDIGDYVSNEVATDYNAGFTG
ALAKMNLLYGQNHQP

>C.saccharolyticus-P22534.2

KAIMFYEFQMSGKLPNWVRNNWRGDSALKDGDGLDLTGGWFDAGDHVKFNLPMSYTGTMLSWAAYEYKDAF
VKSGQLEHILNQIEWVNDYFVKCHPSKYVYYYQVGDGGKDHAWWGPAEVMQMERPSFKVTQSSPGSAVVAETA
ASLAAASIVLKDRNPTKAATYLQHAHAKDLYEFAEVTKSDSGYTAANGYYNSWSGFYDELSWAAVWLYLATNDST
YLTKAESYVQNWPKISGSNIIDYKWAHCWDDVHNGAALLLAKITDKDITYKQIIESHLDYWTGTGNGERIKYTP
KGLAWLDQWGLRYATTTAFLAFVYSDWSGCPTGKETYRKFGESEQIDYALGSTGRSFVVGFGTNPCKRPHR
TAHSSWADSQSIPSYHRHTLYGALVGGPGSDDSYTDDISNYVNEVACDYNAGFVGALAKMYLLLYGGNP

>Caldicellulosiruptor-AAK06394.1

KTIMFYEFQMSGKLPWVRNNWRGDSGLDDGKDVGLDLTGGWHDAGDHVKFNLPMSYSASMLGWAVYAYK
DAFVKSKQLEHILNQIEWANDYFVKCHPSKYVYYYQVGDPTVDHNFWGPAEVMQMRPAYKCDLSNPASS
VVAETAASLAVASVVIKERNSQKAASYLQHAHAKDLFEFADTTTRSDAGYTAATGFYTSGGFIDDLGWAAVWL
YIATNDSSYLTKAEELMSEYANGTNTWTQCWDDVRYGTLIMLAKITGKELYKGAVERNLDHWTDRITYTP
KGMAYLTGWGLRYATTAFLACVYADWSGCDSNKKTKYLNFAKSEQIDYALGSTGRSFVVGFGTNPQHP
HHRNAHSSWANSMKIPEYHRHILYGALVGGPGSDDSYNDDITDYVQNEVACDYNAGIVGALAKMYQLYGGEP

>C.fimi-P26225.1

KSMFFYQAQRSGDLPADFPVSWRGDSGLTDGADVGVKDLTGGWYDAGDHVKFGFPMAFSATMLAWGAIESP
TGYSKAGSLDELKDNLRVSDYFVKAHTAPNELYVQVGDGEADHKWWGPAEVMTMARPSHKISASCPGSD
VAAETAALASSAIVLKGDDPAYAATLVSHAKQLYTFADTYRGAYSDCVTAASAYYKSWSGYQDELVWGAY
WLYKATGDATYLAKAEAEYDKLGTENQSTTRSYPKWTIAWDNKQFGTYALLAMETGKQKYVDDANRWLDYWT
VGVNGQKVPYSPGGQAVLDSWGALRYAANTSFVALVYSDWMTDATRKARYHDFGVRQINYLGDNPRSSSY
VVGFGANPPTAPHHRTAHGSWLDSTITPAQSRHVLYGALVGGPGSPNDAYTDSRQDYVANEVATDYNAGFT
SALARLVEEYGGTP

>C.cellulovorans-AAC38572.2

FNISKKKAQALLLSGILGATSFTPAVLVKGETTATPTFNYGEALQKSIMFYEFQRSGKLPDIRSNWRG
DSGTKDGSVDVGLTGGWYDAGDHVKFNLPMSYTVAMLAWSLSEDKAAYEKSGQLDYLVKEIKWATDYLM
KCHTAPNEYYYQVGDGGADHKWWGPAEVMQMARPAYKVDLQKPGSSVVAETAALASTAFALKDIDKAYS
EQCIQHAKELYNFADTTKSDAGYTAANTYYNSWSGGYDELSWAAAALYMATNDASYLEKAESYVPFWKVE
QOTTTIAYRWAHCWDDVHFGAQLLLARLTGKSIYKESVERNLDYWTGTDGNKIKYTPKGLAWMDSWGS
RYATTTAFLADVYASSDVCSISKVDTYKNFAKSQADYALGSTGRSFVVGFGENAPKKPHHRTAHSSWSDQ
QVNPTDHRHVLYGALVGGPDASDGYTDAIDNFTNNEVACDYNAGFVGLLARQYSKYGGDP

>C.stercorarium-CAA39010.1

KAIMFYEFQRSGKLPENKRDNRGDSGLNDGAD
VGLDLTGGWYDAGDHVKFNLPMAYSQTMLAWAAEAEALERSGQMGYLLDAIKWVSDYLIKCHPSPNVF
YYQVGDGHLHDHSSWWGPAEVMQMDRPAKVDLANPGSTVVAEAAAALASAAVVFADRDPAYAATCIQHAK
LYNFAEITKSDSGYTAASGFYDHSYGFYDELSWAGVWLYLATGDETYLNKAEQYVAYWGTEPQTNII
SYKWAHCWDDVHYGACLLAKITGKQIYKEAIERHLDYWSVGYNGERVHYTPKGLAWLDSWGS
LRYATTTAFLASVYADWEGCSREKAAIYNDFAKQIDYALGSSGRSYVVGFGVNPCKRPHHRTAHSS
WADSMSVDPDYHRHVLIGALVGGPGKDDSYTDDINNYINNEVACDYNAGFVGLAKMYEDYGGSP

>R.thermocellum-CAB76935.1

KAILFYKANRLGDL
PDDYILPYRADAAMTDGQDVGLDLTGGWADAGDGIKFTHPMSYAAGQLGWAVVEYRQAFKAGLLDDILD
EIKWATDFFIKAHPEPNVLYMCGYNDSDHSVWVPHELLDYVTDRKSFVLPSTPGSDVAGQTAACLAIA
LIIIFEPTDPEYAETCLTHAKQIFFGDKYRAKSSGCFYTPSGGYLDDLAWGAVWLYIKTGDSTYLEKAK
SFLPVTSLGGGHTHCWDDVSYGAALKIAQLTHDEGYAAMVEKNLDFWLPGGGITYTPGGLAWLSPWGS
LR YASTAAFLAFVWADDPTVGTSPSKKETYRAFAEKQINYIILGDNPRKGSYVVGFGENSPKHPH
HRTAHGSWVSMLEVPSFHRHILYGALVGGPTDDDSWEDDISDYTRNEVATDYNAGFVGLAKMYD
MYGGEP

>D.discoideum-P22699.1

NALMFYKMNRRAGRLPDNDIPWRGNSALNDASPN
SAKDA
NGDGNLSGGYFDAGDGVKFGFLPMAYSMTMLGWSFIEYESNIAQCGLTSLYLDTIKYGTDWLI
AAHTADNE
FAGQVGDGNVDHSSWWGPPEDMTMARPTYMLTTEAPGTEIAMEAASALAAASIAFKSSNPT
YAATCLAHAK
TLHNFYTYRGVYSDSITNAQAFYNSWSGYKDDLWGSIWLYKATQDSDYLT
KAVADYASGGVGGMAQGN

SHDWDNKAPGCCLLLSKLVPTTSTYKTD FEGWLNWLPGGGVTYTPGGLAWIRQWGPARYAATAAFLGSL
AGTEKGTDFEQVDYLIGNPNPQQSFVVMGPNYPINPHHRAAHSTTNDINNPVNNLYLLKGALVGGP
GSNDEYTDRTDYISNEVATDYNAGFVGALASLVNPSSTSV

>A.mellifera-XP_396791.3

LSLLFYEAQRSGKL
PENNRI PWRGDSALDDRGLNGEDLTGGYYDAGDFVKFGFTMASTTTLLAWGAVSWPEAYNAAGQLDELK
AIKWATDYFIKCHVSEYVFGQVGFSLDHTFWGRPEELNTRPAYKIDPDHPSDLAGETAALAASSI
VFRNYP EYSANCLKHAKELYKFASKYRGLYHEAIRGAAQYYESTDYGDELAWAAVWLFKATNDTMYLEE
AEHHYQH FHLKERPNEFFYNKKVAGVQVLLAQMTGQPEYQNAARAFCD FSVYQQKRTPKGLLYIDKFGTL
CHAANVAFVVCLEAADSSGIGDSQKYREFAEQQIYYMLGGGGRSYVVGWGRNPPKQPHHAASSCPDRPAIC
GWSEFDKDAPNPQILY GALVSGPDEADKFHDHREDYVYTEVTL DYNAGFTSALAGLLQLRVKSTA

>C.quadricarinatus-AAD38027.1

MSYVFYEAQRSGKLP GDQRVTWRGD
SALNDGSDVGHDLTGGYYDAGDHVKFGFPMAFTATMLAWGQIDFANGH SKAGQTSYGHAAALKWATDYFLK
AHTATNEFYGQVGE GNTDHAYWGRPEDMTMSRPSYKIDQSRPGSDLAGETAALAASIVFKSSDSSYSS
QVLSVAKELYEFADQHRDIYTNAITDAASFYNSWSGYGDELAWAALW LARATGDNSYLDRAKGHVSEFNL
LGTSPSQFGWDDKKAGVQALLVLLDGSSEYTNALNQLFN FVRNQAPYTP EGLVFLDAWGSNRHAANVAFIA
LYAAKLGIDAGTNQQWARGQIGQLLGDNSRYQS FVVGFGVNPPT RPHHRSSCPDRPADCSNGLTNSGPN
PQTLWGALVGGPAQDGSYND DRQDYQHNEVACDYNAAYTGALAA LEVELS

>H.discushannai-BAD01504.1

KSILFYDAQRSGKLPANNPIKWRGDSALGDKGDNGEDLTGGWYDAGDHVKFSLP
MSSTSTVLLWG YLQWKDAYATTKQTD MFFDMIKWPLDYFLK CWIPKSQTLYAQVGE GNDHFWGRAEDM
KMARPAYKLT PPSKPGSDVAGEIAASLAAGYLAFKQRDAKYAATLLSTSKEIYEF GKKYPGIYSSSIQDAG
QFYSSSGYKDEMCEGAMWLYKATGDKSYLADAKGYHENAWAWALGWDDKKIACQLLLYEATKDTAYKTEV
EGFFKGWLP GGSITYTPCGQAWRDKWGSNRYAANS AFALVAADAGIDTVTYR KWAVEQMNYILGDNKYG
ISYQIGFGTKYPRNPHRSASCPDI PAPCSETNLHTAGPS PHILVGAIVGGPDNDDSYKDNREDYVHNEV
ACDYNSGFQSALAGLTHLAHAKELPAIPAPKCHG

>C.savigny-ENSCSAVT00000011362

KSLLFYEAQRSGKLPANNRVLWRKSAFVDDRGLNGEDLSGGYFDAGDYVKFNLPMAFTTTVLSWGLAYTD

AYNATDQLAHAHSAIKWATDYFIKCHVKKEYEYYAQVGEVIDHLLWRSPPRNSTRHRRRAFKLTTTSPGTEV
VAETAAMAAASVVFRSVNPSYSEELIRHARDLYDFGNRYREVVYHRSIRDVQNFYRSYSGYKDELAWAASW
LYFATEEQEFLTDAQAKYNEFNLDNRKPAGFWDDKTAGVQLLLAQMTSDPKFNRSVEQFCDRFLPGGDFP
YTPKGLVFIQEWGVLRHAAGVAFICMGAANLGVKPEIYRDFAKRQIHYMLGDSGLGSYVIGYGPSPPTRPH
HRSSSCPIPPAPCSFEALRNPSNPHVLTGALVGGPDGNDRFTDDRRNHRSSSEVALDYNAAFQSAVAGLKY
LEL

>C.intestinalis-XP002126063.2

MSILFYE

AQRSGKLPNNRI PWRGDSGLRDGCDVGVDLTGGWYDAGDHVKFGFPLAWSVTTLAWGVIEFKDAYVDAN
EYRRVLDLSLKWVADYFVKAHTSRYEYLYGQVGSGRADHLYWGRSEDLRMNRPSYKIDASNPGTELAETA
ALAACSVVFKNARPGYSRMLLRHATELYEFADRYRRSYHLSIPDVTSYYSYNGYNDLVWALWLYKAT
GMRSYLEDAKRKYDQYQGNTPIMFSWDDKRAGSQVLLANFTGEAKYKGHVANYQRFLNGALKTPRGLVW
LDQWGSNRYAANAALAAKVPFIANRNEMVRFVFAEQIHYMLGGAGRSYVVGGRNPPTQPHHRGSSC
PAAPTECSWGNFHSSAANHFLLHGALVAGPGRDDSYTDNRGDYIANEVAVDYNAGFQSAVAGLKYFKIKQ
RR

>C.intestinalis-XP018668452.1

KSILFYEAQRSGPLPQNNRI

PWRGDSGLKDGCDQSIDLTGGWYDAGDNIKFGFPMAYSATVLAWGLIEFRDAYVESRELNNARKSLEWAT
DYFVKAHPSPNELYVQVGDPAADHAKWERPEDAINTVRRSYKIDTQNPGEVAAETAALAAASIVFRQS
KPNYANTLVAHARQLFEFANSHRRNYHLSVPGVASYYKSWNGYNDLLWAAVWLHKATNEASYLNFTTN
YNNFGAGNVAPEFSWDNKYAGVQVLMAQITGNNNYKSDVDRFLQAMNNGKTPDGLTWKSQWGPNNRYAA
NFAFIATVAGRVDSTKRSQYVTYAKNQIYYMLGSNTNGQKYVIGMGANSPOKPHHRASSCPAWTAVPVQT
CDFNALNMQGANPHVLYGALVGGPARNGAYTDDRSYISNEVATDYNAGFQSAVAGLLHYAKAGQL

>N.vectensis-83869

YDYDLVLHKSILFYEAQRSGKLPSTNRI SWRGDSALGDHGDNGEDLTGGWYDAGDYVKFGFPMASATVLA
WGLVEYRDAYQAAGELDNALNSIKWATDYFIKAHTKKFEFYQVGDGHVDHAYWGRPEDMTMQRPFAFKITT
SRPGSDLAGETAALAAASIAFKPTNPSYAAEMLQHAEELEFADTYRGKYSDAIPNAGSFYKSWSGYKDE
LVWGAAWLYRATKKASYLTKAKKYFNDFGIGGTAWAFSWDDKKAGAQVLLAQITGESSFVNAAQASLNAWM
PGGSVTYTPKGLAWRAEWGANRYAANTAFLALVAADAGINPATYREFAKKQIHYMLGDSGHSYVVGFGVNP
PKRPHHGSSSCPSPPATCGWSLYNADVDNAHVLLHGALVGGPDKSDNYKDDRKYIKNEVTTDYNAGFQSAV

AGLKSL

>L.gigantea-23538

KSILFYEAQRSGRLPAIRNIAWRGDSALQDQGI FGEDLSGGWYDAGDCVKFGFPMAASTLLLLWGFIEFYD
GYEYAGLVNEMYDCVQWPLTYFMKAHPTKFEFYAQVGDPIFDHDYWGRPEDMTMYRPAYRLSPERPGSDVI
GETAAALAAGSIVFRTRDPALAGEMLRHSEELFEFAQNYQGLYSESI PSVKEFYPPSSQFQDEL CWAAAWLY
RATGKFTYLDTAEQYYVSKHSWAFNWEDKTDATSLMLFMLTKKEKYRDDIERSLRDWLPGGTVPYTPKGLV
FRAKWGSLRFAGNVAFLLVAANADINPSMYRRWAKQOIHYILGDTGRSYVVGFGNNPPTRPHHASSSCNS
PPLPCTWDDFSKSTPNSHILYGAVVGGPDKFDHFVDDREDFIQNEVACDYNAGFQSALAEVMMWAILLT

>B.floridae-118867

KSILFYEAQRAGNLPNNRI PWRRNCCQGDGSDVGLDLSGGWFDAGDHLKLFPLAYTITVLSWGMIEFKSA
YEAAGEMGYAMDSIKWVTDYFIKCHPSKFEFVAQVGDTEPDHQFWGKPDQDMTMRRAKKVTANQPGSDVTAE
TAAAMAAASIVFRENGDPGYADTLLSHAKDLYEFADTYRGEYQNVVHDTYPYPSFGGMNDELVWGAAWLHRAT
QDGSYLSKAESYYDQYGISSGGFSWDEKQSGTMLVLFKATNKDKYKNDIVGYLSRKMPGGGDTYTPKGMLWL
NEWGSCRHSANHAFLALVAADMGINVDQYRGFAAQQINYM LGDAGRSMVVGFGNNPPVRPHHRAATCPVDGH
CDWNTYNSWDANANVLQ GALVGGPDAHDNYSDDRSNFHTNEVAVDYNAGFQGCLAALIKLGMK

>S.purpuratus-XP_782526.2

KSILFFEAERSGELPNDNNIDYRGDSAMGDKGNNEEDLTGGWYDA
GDHVKFGFLPMAASTLLAWGIIIEFEGVYNACGEYNHALDQIRWATDYFIKCHVSSNELYIQVGDGHVDHA
YWGRPEDMTMDRPAKVTASLPGSDVVGETAAALAAASIVFKDNDSSYSNELLDHAKTLFDFADQYRGKY
TDSLSEPGSFYRSYGYNDELAWAAAWLYKATGNQSYLTKAMSFYSSGTPWALS WDDKNAGVQMLMYQLTG
SNDYKNAVIGFLDSWQPGSITYTPNGLAWRSEWGPLRYAANTAFIAAIACRDNINGNKYCSFVEQQIHYM
LGSTGRSFVVGFGNNPPQRPHHRSSSCPDPQSCSWNEYN SASANPQTLYGALVGGPDEYDNYNDDRGDY
ISNEVACDYNAGFQSAVAGIKQLVTDGKI

>C.formosanus-BAB40693.1

NSLLFYEAQRSGKLPADKKVTWRKDSALNDKGQKGEDLTGGYYDA
GDFVKFGFPMAAYTVTVLAWGLVDYESAYSTAGALDDGRKALKWGTDYFLKAHTAANEFYQVVGQGDVDHA
YWGRPEDMTMSRPAYKIDTSKPGSDLAAETAALAATAIAYKSADSTYSNNLITHAKQLDFANNYRGKY
SDSITDAKNFYASGDYKDELVWAAAWLYRATNDNTYLTKAESLYNEFGLGSWNGAFNWDNKISGVQVLLA

KLTSKQAYKDKVQGYVDYLVSSQKKTPKGLVYIDQWGTLRHAANSALIALQAADLGINAASYRQYAKKQI
DYALGDGGRSYVVGFGTNPVRRPHRSSHSSCPDAPAACDWNTYNSAGPNAHVLTGALVGGPDSNDSYTDSDR
SDYISNEVATDYNAGFQSAVAGLLKAGV

>*C.acinaciformis*-AF336120

SSLLFYEAQRSGKLPADQKVTWRKDSALDDKGNNGEDLTGGYYDAGDFVKFGFPLAYTATVLAWGLVDYE
AGYSSAGATDDGRKAVKWATDYLLKAHTAATELYGQVGDGDADHAYWGRPEDMTMARPAYKIDASRPGSD
LAGETAALAAASIVFKGVDSSYSDNLLAHAKQLFDFADNYRGKYSDSITQASNFYASGDYKDELVWAAT
WLYRATNDNTYLTKAESLYNEFGLGNWNGAFNWDNKVSGVQVLLAKLTSKQAYKDTVQGYVDYLINNQQK
TPKGLLYIDQWGTLRHAANAALIILQAADLGISADSIRQFAKKQIDYALGDGGRSYVVGFGDNPPHPPHHR
SSSSCPDAPAVCDWNTFNSPDPNFHVLTGALVGGPDQNDNYVDDRSDYVSNEVATDYNAGFQSAVAALVTLGV

>*N.takasagoensis*-BAA33708.1

DSLLFYEAQRSGRLPADQKVTWRKDSALNDQGDQGDLTGGYFDA
GDFVKFGFPMAYTATVLAWGLIDFEAGYSSAGALDDGRKAVKWATDYFIKAHTSQNEFYGQVGGDADHA
FWGRPEDMTMARPAYKIDTSRPGSDLAGETAALAAASIVFRNVDGTYSNLLTHARQLFDFANNYRGKY
SDSITDARNFYASADYRDELVWAAWLYRATNDNTYLNTEAESLYDEFGLQNWGGGLNWDSDKVSQVLLA
KLTKQAYKDTVQSYVNYLINNQQKTPKGLLYIDMWGTLRHAANAAFIMLEAAELGLSASSYRQFAQTQI
DYALGDGGRSFVCGFGSNPPTRPHHRSSHSSCPAPATCDWNTFNSPDPNYHVLVSGALVGGPDQNDNYVDDR
SDYVHNEVATDYNAGFQSALAAALVALGY

>*L.stagnalis*-CN810987

KSILFYNAQRSGKLPNTNPIPWGRDSSLTDCVVGWHDAGDHVKFQLPASASTLLAWSLVQFSAGYQNA
SQLTAMYDMIKWPLDYFLKAWSPSKSQLVVQVGGADHAYWGRPEDMTMARPCKTVSAATKGSQAAGT
AAALAAGSIAFKTKGDTAYATSLDDAAKTLTYTFAKANRGVFTGSAEFYSSSGDRDEMCEAAVWLYKATGN
SSYLTDARSFVETTTAYALSWDDKKAACQALLYGVTKEAQYQTPVVNFFNAWLPGGSVQYTPCGLAWRDQ
WGATRYAANAFLALAAADFGIDAAKYRKWGVQINYLILGDNKYSGGCYSFEIGYGTKYPKNPHHRASSC
PNKPAACGWNEYNAQTNNPQVLNVALVGGPDVNDNYEDKRSYIKNEVALDYNAGFQAALAAINSLVAKN
ALPATANKCPCP

>*M.darwiniensis*-CAD54727.1

KSLLFYEAQRSGKLPDQKVTWRKDSALNDKQNGEDLTGGYYDA
GDYVVKFGFPMAYTATVLAWGLVDHPAGYSSAGLLDDGRKALKWVTDYLIKAVSENELYGQVGDGDADHA

YWGWRPEDMTMARPAYKIDTSRPGSDLAGETAALAAASIVFTSTDSNYANTLLTHAKQLFDFANNYRG
KYSDSITQASNFYSSSDYRDELVWAAAWLYRATNDQTYLNTAESLNDDYGLQYWNVHFTWDSKALGATAL
LAKITGKQTYKDGLTSYCDSLVSQQTPKGLTFLDQWGSRLMISNAVYICLQAADLSINSDTYRQFAKSQ
LNYILGDAGRSFVVGFGNNPPTHPHRSSSCPDPATCDWNNYNSADPNPHVLYGALVGGPDSNDNYEDL
RSDYVANEVATDYNAAFQSLLSQAIELNL

>Pyromyces-AAP30753.1

TQDYARHLELSILFYEAQRSGLPENNGIFWRHDSMVDAGKDNNVDLTGGYDAGDNVKNFNPQASALTIL
AYGAYKWKDGYKQAGQWEYMKDLLKWGMDYFLKCHTDKYVLYGQVGNGLDHGAWVPPEDITYKYPSYKI
TASAPGSDLAAETSASMVAASMALREDDPTYADTLLKHGRELYDFAEKYRGTYDLSIDDAKGYRSYSGF
NDELVWGAAMLYAATGEEQYKAKVDKIWDTPYGDLDPKFLGSTGPI SWDDKKAAYALMAITTTGESKYV
EESTRHS DLMVNYQTT PGGLWYDTNLSMNASRYAANAFTVAMLATTTMDENDSKRKQYVKFIKKQIDYI
LGDNPAKVDYVVGADPSSPKAVHHRGASGSKGADKGPDENVFILY GALAGGPGQKDNYKDARNNYEMNEV
ALDYNAAFQGLLAFLITEGLNVPDP

>P.chrysosporium-AAM22492.1

NTLYFYEEQRSGK
LPVTNRVPWRNDSATDDGRDVGLDLSGGYYDAGDYIKYTFPMSFVSMSICWGALDYGKGYDLANQTAYLD
DMLRWSLDWLMKAHPDPNTLYVQVGADLDNAYWGGDRGIPTPRTSYAINSTSPGTDAAAQAAAAFAACS
ALYNNRRTLSQPAPNGITSTSYASTLLQHAQQLYNFATNSSVPQVQTYQASEPSVADAYASSGFQDELAIAA
LFISLAGNSSDAYPQASQVYRKQGLSKHLEDDAVFNWDEKSPGVALLAAQIAQKYPELANGTGVDWKS
DLN NYFDRIVSNSGRSFLTSGGLLYPGDSDDATLNPALNAAMLLRYADSGLASSSEKQSAYRQFAQSQID
YFLGNNPMTVQYMGVHPNAPS NPHSALATGATPQDIANIDTVPEHEAYVLYGGVGGPNDDDLFWDLRS
DWVESEVGLDYVAPVVTIAARELVSGAGDPWY

>N.patriciarum-AEX92719.1

LSILFYEAQRSGLPANRIYWRHDSMVDAGKDNNVDLTGGYY
DAGDNVKNFNPQASALTLLAWSAVDWKDGKEAGQWEYMKDLLKWGMDYFIKCHTDKYVLYGQVGNGLD
HGAWVPPEEIDYKYPSYKITASAPGSDLAAETSASMVAASMAFRDEDPSYADILLKHGKELYEFAEKYR
TYDLSITDAKGYRSYSGFNDELVWGAAWLYRATGDKTYKDKVDKIWDTPYGDLDPKFLGSGGPI SWDD
KKAAYALMALTTGESKYVEESTKHSELMVNYNTTPGGLWYDSNLSMWGSNRYASNAFTVAMLASTMDA
NNSKRKEYVKFVKKQIDYILGDNPAKVDYVVGADPSSPKAVHHRGASGSKGADKGPSENVFILY GALAGG
PGARDNFKDARDNYEMNEVALDYNAAFQGLLAFLIKEGLNVPD

>P.cribrata-AAF80584.1

YSLLFYEAQRSGKLPADQKVTWRKDSALNDKGQNGEDLTGGY
YDAGDFVKFGFPMAYTATVLAWGVISHEQGYQKANALEDARKAVKWATDYFIKAHVSENEFYGQVGRGDL
DHNWWRPEDMTMERPAYKIDAQHPSDLAAETAALAAASIVFKSVDPTYSENTLLTHAKQLYNFADMHR
GKYSDSITDAAQYYSYGYEDDLVWGAVWLYKATNDNSYLTKAEQYYTQFGLADYDGYFSWDQKISGVEV
LLAEITKDQGHISRITQYCDNMVRGQTRTPKGLVYISDWGSLRMAANAVYLCLEAAKDGHNPTQYREFAT
QQIGYILGDTGKSYVVGFGQNYPTHESHRSSCPDAPAACDWNTYNGNQPNHAVLYGALVGGPGQNDDE
DLRSDYVHNEVADDYNAAFQGALAALVELS

>S.lycopersicum-NP_001234172.1

KSFLFYEAQRSGYLPRNQRVQWRGNSGLNDGKASGIDLVG
GYYDAGDNVKGFLPMAFTVTMLSWSILEYGRQMAASGELSHAMDAVKWGTDYLLKAHPEPYVLYGEVGDG
NTDHYCWQRPEDMTTSRAAYRIDPNHPGSDLAGETAAMAAAASIVFRRYNPGYSNELLNHAHQLEFADK
YRGKYDSSITVAQKYRSVSGYADELLWGAAWLYKASNNQFYLNLYLGRNGDALGGTGWSMTEFGWDVKYA
GVQTLVAQFLMSGKAGHNAPVFEKYQQAENFMCMSMLGKGNRNTQKTPGGLIYRQRWNNMQFVTSAAFLA
TTYSDYLASAGKYLKCSSGFVSPNELLSFAKSQVDYILGDNPRATSVMVGYGNNYPRQVHHRASSIVSFK
VNPSFVSCRGGYATWYSRKASDPNLLTGALVGGPDAYDNFADQRDNYEQTEPATYNNAPLIGVLARLHAG
HS

>S.oleracea-KNA09089.1

KTLLFFEA
QRAGKLPYDNRVKWRTDSGMRDGYSGQVDLVGGYYDAGDHVKFGLPMAFSVTMMAWAAIDFSKDVLAANK
MDQTLWAIWGTDYFLKAHTHPNVLWAQVGDGASDHLWCWERAEDMTTSRTAYKLDSSNPGSDLAGETA
LAAASLAFRPNSSYAQQLVQHAEQLFYFADTFRGLYDDSI TNAEKYYTSSGYQDELLWAAVWLYRATNK
DRYLEYVVQNAASMGGTGWAVREFSWDNKYAGVQVLVSKLLLEGKGGAYASTLKQYQAKADYFACACVQK
NNGFDVQLTPGGLVYVRQWNNMQYASSAAFLAVSYDYLQAKAVVNCPEGTAQPQDLFNFAKSQADYIL
GKNPKSMSYLVGYGTNYPKQVHHRGASIASISVHNAYVGCVQGFEWYHRTSANPNVHGGGLVGGPDNND
EFDDDRSNYEQTEPTISGTAPLVGLFSKLR

>M.domestica-AAQ55294.1

KSVLFFQQRSGRLPAGAAQQITWRSNSGL
SDGRQAYVDLTGGYYDAGDNVKNFPMMAFTTTMLSWGALYGKRMGPQLPETRAAIRWATDYLIKCARQT

PGRLYVGVGDPNVDHKCWERPEDMDTTRTVYSVSPSPNPGSDVAGETAALAAASLVFRRVDPKYSKLLLN
TARNVMQFAIQYRGAYSDSLGSVAVCPFYCSYSGYNDELLWGAAWLFRATNELYYNFIKSLGASDSTDIF
SWDNKFAGAYVLLSRRALLNNDKNFEPYKQEAEQFMCRI LPNSPSSSTQYTQGGLIYKLPGSNLQYVTSI
TFLLLTYSKYMAARKLTFDCGNLVVTPMALRNLAKQQVDYILGVNPLKMSYVMVGYGPYYPKRIHHRGSSL
PSLTSHRQSIGCDGGFQPFYSLNPNPNILVGAVVGGPNQNDGFPDDRGDYSHSEPATYINGAIVGPLAF
FAGSYRS

>P.radiata-064402

KSILFYEGQRS

GKLP LNQRMRWRGDSALS DGAAGHV DLTGGYYDAGDNV KFGFPMAFTTTML SWSVLEFGGRMGDNLDHAK
AAIRWATDYLLKATARPGVIYVQVGDPNLDHKCWERPEDMDTSRNVYKIDADHPGSDVAAETAALAAAS
MVFRTTDPIYSRHL LQTAMQVFD FADKHRGAYSDSLQSEVCPFYCSYSGYNDELLWGAAWLQRASRNVSY
ISYIQSHGQNLGGEDNVNIFSWDDKHAGARVLLAKEVLLRNSKSL E EYRGHADNFVCSLLPGTPNSQAQY
TPGGLLYKMSDCNLQYVTSTTFL LFTY PKYLRVSKQVVR CGNMVVTPTRI RTLAKRQVDYILGDNPLRMS
YMVGYGAKFPERIHHRGSSLPSIYQHPQIIPCNDGFQSLYSNAPNPNRLVGAVVGGPDNDHFS DERNDY
AHSEPTYINAPLVGSLAYLAHSFA

>P.taeda-PITA_000080312

KSIMFYEAQRSGKLP SNQRVSWRDDSGLSDGSANGVNLVGGYYDAGDNV KFGLPMAFTVTML SWSLIEYSNQ
LTSSGELGHSMEAIRWGTDYLLKAHTEADVLYGEVGDGNSDHKCWQRPEMDTTPRQAYRIDANNPGSDLAGE
TAAALAAASIVFRHSDPAYSNELLNHAEQLFTFADKYRGKYDSSITVAQKY YASKSGYEDELLWAAAWLHEA
TGDL SYMNYVIDNADSLGGTGWKMTEFSWDVKYAGVQVLASKFLMQGRGGQSNV LQSYQENAEYFMCSCLO
KGNKNVQRTPGGLLFWQKWNNIQFVTSASFLLSVYS DYL TATHKNIQCPGGAVQPSELLSFAQSQIDYILGD
NPRATSYMVGYGSNYPQQVHHRASSIVSYKVSRSFVTCTGGYSTWYSSKGS DPNVLHGALVGGPDQNDNFAD
ERNNYEQTEPATYNNAPIVGV LARLHAGGN

>P.alba-BAA77239.1

KSILFFEGQRSGKLPVNQRLTWRGDSGLSDGS

AYHVNLVGGYYDAGDNV KFGLPMAFTTTLLAWSVIEFGSSMQNQITNAEAAIRWSTDYLLKAATATPDTL
YVQVGDPNMDHRCWERPEDMDT PRNVYKVTTQNP GSDVAAETAALAAASIVFKESDPSY STELLHAATK
VFD FADRHRGSYSDSLSSAVCPFYCSYSGYQDELLW GASWLHKASLNGTYLAIYIQSNGHTMGSDDDDYSF
SWDDKRPGTKILLSKEFLDKTTEEFQIYKSHSDNYICSLMPGSSSFQAQYTPGGLFYKATESNLQYVTST
TFLLLTYAKYLG SNGGVAKCGGSTVTAESLIAQAKQVDYILGDNPAKMSYMVGF GNKYPQHVHHRGSSV

PSIHAHPNRISCNDGFQYLYSSSPNPNVLVGAIVGGPDNRDHFADDRNNYQQSEPATYINAPFVGALAFF
SAKN

>A.thaliana-AAK59818.1

KALKFFNAQKSGKLPKHNNVSWRGNS
GLQDGKGETGSFYKDLVGGYYDAGDAIKFNFPMAYAMTMLSWSVIEYSAKYEAAAGELTHVKELIKWGTDY
FLKTFNSTADSIDDLVSQVGSNTDDGNTDPNDHYCWMPEDMDYKRPVTTTCNGGCSDLAAEMAAALASA
SIVFKDNKEYSKKLVHGAKVVYQFGRTRRGRYSAGTAESSKFYNSSMYWDEFIWGGAWMYATGNVTYLN
LITQPTMAKHAGAFWGGPYGVFSWDNKLAGAQLLSRLRFLSPGCPYEEILRTFHNQTSIVMCSYLP
FNKFNRTNGGLIELNHGAPQLQYSVNAAFLATLYSDYLDAAADTPGWYCGPNFYSTSVLRDFARSQIDYI
LGKNPRKMSYVVGFGTKYPRHVHHRGASIPKNKVYNCKGGWKWRDSKKPNPNTIEGAMVAGPDKRDGYR
DVRMNYNYTEPTLAGNAGLVAAL

>A.thaliana-NP_849349.1

KSILFFEGQRSGKLPNTQRVKWRADSGLSDGASANVNLIGG
YYDAGDNV KFVWPMSFTTTLLSWAALEYQNEITFVNQLGYLRSTIKWGTNFILRAHTSTNMLYTQVGDGN
SDHSCWERPEDMDTPRTLYSISSSSPGSEAAGEAAAALAAASLVFKLV DSTYSSKLLNNAKSLFEFADKY
RGSYQASCPFYCSHSGYQDELLWAAAWLYKATGEKS YLNYVISNKDWSKAIN EFSWDNKFAGVQALLASE
FYNGANDLEKFKTDVESFVCALMPGSSSQQIKPTPGGILFIRDSSNLQYVTTATTILFYYSKTLTKAGVG
SIQCGSTQFTVSQIRNFAKSQVDYILGNNPLKMSYMGVFGTKYPTQPHHRGSSSLPSIQSKPEKIDCNGGF
SYYNFDTPNPNVHTGAIVGGPNSSDQYSDKRTDYSHAEPTTYINAAFIGSVAALISS

>A.lentiformis-BAB32662.1

KSILFFEGQRSGPLPSSQRLNWRGDSGLSDGSSYH
VDLVGGYYDAGDNV KFGLPMAFTTTMLAWSVIEFGSSMHDQLSAAKDAVRWGADYLLKAAATPGTLYVQV
GEPNLDHQCWERPEDMDTPRN VYKVSTQNP GSDVAAETAALAAASIVFKDSDPSYSSKLLHTAIQVDFD
ADKYRGSYSDSLNSVVC PFYCSYSGYQDELLWGAAWIHKASGDSSYLSYIQSNGHILGAEDDDFSFSWDD
KKAGTKVLLAKDFLQDRVEQFQVYKAHADNFICSFIPGANDYQAQYTPGGLLFKQSDSNLQYVTTTSFLL
VAYAKYLGKNGDITTCGSTVITAKKLISVAREQVDYILGDNPATMSYMGVFGNKYPQHIHHRASSLPSVH
AHPSRIGCNDGFQYLN S GSPNPNVLVGAILGGPDSGDKFTDDRNNYRQSEPATYINAPFVGAAAFFSAYN
ERY

>B.napus-CAB51903.1

KALKFFNAQKSGKLP RHNNVSWRGNS

GLQDGGKDGSGSFYKDLVGGYYDAGDAIKFNFP MAYAMTMLSWSVIEYSAKYEAAAGELVHVKELIKWGTDY
FLKTFNSTADSIDDLVSQVGSNTDDGSTDPNDHYCWMRPEDMDYKRPVTT CNGGCSDLAAEMAAALASA
SIVFKDNREYSKKL VHGAKTVYQFGRTRRGRYSAGTAESA KFYNSSMYWDEFIWGGAWLYYATGNVTYLD
LITKPTMAKHAGAFWGGPYG VFSWDNKLAGAQLLSRLRFLSPGYPYEEIVRTFHNQTSIVMCSYLPY
FNKFNRTRGGLIELNHGDPQLQYAANA AFLATLYSDYLDAAADTPGWYCGPNFYSTNVLREFARTQIDYI
LGKNPRKMSYLVGFGTKYPKHVHHRGASIPKNKVYCNCKGGWKWRDSKKPNPNTIEGAMVAGPDKRDGFR
DVRTNYNYTEPTLAGNAGLVAALVALS

>C.annuum-CAA65828.1

KSILFFEGQRSGKLPANQRVKWRGNSGLSDGS

GSHVNLVGGYYDAGDNVKFGLPMAFTTTLLAWSVIEFGSSMHSQ LGHAKEAIRWSTDYLLKAATASPDTL
YVQVGDPNQDHRCWERPEDMDTPRNVYKVS PQNPGSDVAAETAALAAASIVFKDSDPSYSSTLLRTAQK
VFAFADKYRGSYSDSLSSVVC PFYCSYSGYNDELLWGASWLHRASQDTSYLSYIQSNGQTMGANDDDYSF
SWDDKRPGTKIVLSKDFLEKSTQEFQAYKVHSDNYICSLIPGSPSFQAQYTPGGLLFK GSESNLQYVTSS
SFLLLTYAKYLRNNGGVVSCGSSRFPANKLVELARKQVDYILGDNPAKISY MVGFGQKYPLRVHHRGSSL
PSVRTHPGHIGCNDGFQSLYSGSPNPVNLVGAIVGGPDSRDNFEDDRNNYQQSEPATYINAPLVGALAF
L SAESTAV

>C.sinensis-022297

KSILFFEGQRSGRLPPNQQLTWRG

NSGLSDGSSYHVLDLVGGYYDAGDNVKFGLPMAFTTTLLSWSVIEFGSSMQNHLENAKAAIRWGTDYLLKA
STATPGALYVQVGDPNMDHHCWERPEDMDTPRNVYKVSTQNPGSDVAAETAALAAASV VFKDSDPSYST
KLLKTAMKVFDFADKYRGSYSDSLNSVVC PYYCSYSGYLDELLWGASWLHRASQNSSYLYIYIQSNGHILG
ADDDYSFSWDDKRAGTKVLLSKGFLEKNTQEFQLYKAHSDNYICSLIPGSSSFQAQYTAGGLFYKASES
NLQYVTTTAFLLLLTYAKYLSNNGGVATCGSSSTVKAENLIALAKKQVDYILGDNPAKMSY MVGFGGERYPQH
VHHRGSSLPSIHAPDHIACNDGFQYLYSRSPNPVNLTGAILGGPDNRDNFADDRNNYQQSEPATYINAP
FVGAVAFFSSKTTTN

>F.ananassa-AAC78298.2

KSILFFEAQRSGVLP HNQRVTWRSHSGLYDGKASGVN

LVGGYYDAGDNVKGFLPMAFTVTMMSWSIIIEYGKQMASSGELGHALDAVKWGTDYFIKAHPEPNVLYGEV
GDGNTDHYCWQRPEDMTTDRRAYKISPSNPGSDLAGETAAMAAAASIVFRRTNPAYSRELLQHAYLLFDF
ADKYRGKYDSSITVAQKYRSISGYNDELLWAAAWLYQASNNEYLYNLAVNGDSMGGTGWGMTEFGWDV
KYSQVQTLVAKFLMQGKAGKHAAVFQKYTAKAEYFMCSCLGKGSRNAQKTPGGLLFRQRWNNMQFVTSAS
FLATVYSDYLTSSRRTLKCSGNVAPSELLSFAKSQVDYILGDNPRATSYMVGYGNNYPQQVHHRGSSIV
SIKKDSSFVSCRGGYATWFSRKASDPNLLTGAIVGGPDAYDNFADQRDNYEQTEPATYNNAPLIGILARL
GGGQ

>H.vulgare-BAA94257.1

KALMFFNAQRSGHLPKHNGVSWRG
NSGMKDGLPDSTVKKSLVGGFYDAGDAIKFNFPMAWSMTMLSWTVIEYRAKYEAI GELDHVKEI IKWGTD
YMLKTFNSSADTIDRIVAQVGVGDTSKGPMNDHYCWMRPEDIDYKRPVIECHSCSDLAAEMAAAALAAAS
IVFKDSKAYSDKLVHGAKALYKFGRLQRGRYSPNGSDQSLFYNSTSYWDEFVWGGAWMYFATGNTSYLTI
ATAPGMAKHAGAFWIGSPNYGVFTWDDKLPQSQVLLSRLRFLSPGYPYEEILRTFHNQTDNVMCSYLPV
FNSFNFTKGLIQLNHGGPQLQYVVNAAFSLASYADYLDTADTPGWYCGPNFYTTDVLRFKFAKSQLDYI
LGKNPQKMSYVVGFGKKYPKRVHHRGASIPHNGVKYCKGGFKWRESKKNPNILVGAMVAGPDKHDGFK
DIRTNYNYTEPTLAANAGLVAALISLAD

>N.tabacum-AAL30452.1

KSILFFEGQRSGKLPHNQRVSWRGSSGLSDGSLAK
VDLTGGYYDAGDNVKNFPMAYTTTLLSWNTLEYGKRMGPQLQNARAAIRWATDYLLKCANAAAPNKL FVG
VGDPNSDHKCWERPEDMTVRSVYVSPSSPGSDVAGEMAAALAAASLVFRTVDPVYSKLLGNVAVKVF
FAVQYRGSYSDSLGSAACPFYCSYSGYKDELYWGAAWLLRATNDISYLNFINTLGANDVPDLFSWDNKYA
GAHVLMAARRSVVGNDRKRFDPFRQQAEDFVCKILPNSPYTSTQYTKGGLIYKLTENLQYVTSITSLLTTY
AKYMASKKHTFNCGSLLVTEKTIRILAKRQVDYILGNNPMKMSYMGYGTNYPRRVHHRGSSLP SMAMHP
QSFGCDGGFQPYYYTANANPNILVGAIVGGPNQNDFFPDERTDYSHSEPATYINAAIVGPLAYFDSSER

>O.sativa-AAP03405.1

KALMFFNAQRSGPLPKHNGVSWRGN
SCMKDGLSDSTVRKSLVGGFYDAGDAIKFNYPMAWSMTMLSWSVIEYKAKYEAI GELDHVKELIKWGTDY
LLKTFNSSADTIDRIVAQVGVGDTSKGGAQPNDHYCWMRPEDIDYPRPVTECHSCSDLASEMAAAALAAAS
IVFKDSKTYSDKLVRGAKALYKFGRLQRGRYSPNGSDQAI FYNSTSYWDEFVWGGAWMYFATGNNTYLSV
ATAPGMAKHAGAYWLDSPNYGVFTWDDKLPQAQVLLSRLRFLSPGYPYEEILRTFHNQTDNVMCSYLP

YNSFNFTKGGMIQLNHGRPQPLQYVVNA AFLASLYSDYLDAADTPGWYCGPTFYTTEVLRKFARSQLDYV
LGKNPLKMSYVVGFGNKYPKRAHHRGASIPHNGVKYGCKGGFKWRETKKPNPNILIGALVAGPDRHDGFK
DVRTNYNYTEPTLANAGLVAALISLTNIH

>P.americana-P05522.1

KSILFFEGQRSGKL

PTNQRLTWRGDSGLSDGSSYHVLDLVGGYYDAGDNLKFGLPMAFTTTMLAWGIIIEFGCLMPEQVENARAAL
RWSTDYLLKASTATSNSLYVQVGEPNADHRCWERPEDMDTPRNVYKVSTQNPAGSDVAAETAALAAASIV
FGDSDSSYSTKLLHTAVKVFE
FADQYRGSYSDSLGSSVPCPFYCSYSGYNDELLWGASWLHRASQNASYMTYIQSNGHTLGADDDDY SFSWD
DKRVGTKVLLSKGFLQDRIEELQLYKVHTDNYICSLIPGTSSFQAQYTPGGLLYKGSASNLQYVTSTAFLL
LLTYANYLNSSGGHASC GTTTVTAKNLISLAKKQVDYILGQNPAKMSYMVGFGERYPQHVVHHRGSSLPSV
QVHPNSIPCNAGFQYLYSSPPNPNIILVGAILGGPDNRDSFSDDRNNYQQSEPATYINAPLVGALAFFAAN
PVTE

>P.sativum-Q9SSU7

KSILFFQGQRSGKLP SNQRISW

RRDSGLSDGSALHVLDLVGGYYDAGDNLKFGFPMAFTTTMLSWSVIEFGGLMKSEL PNAKKAVRWATDYLL
KATAHPNIIYVQVGD AKKDHACWERPEDMDTPRSVFKVDANAPGSEVAAETAALAAASLVFRKSDPTYA
KILVRRAIRVFQFADKHRRSYSNALKPFVCPFYCSYSGYQDGLLWGAAWLHKATKNP MYLKYIQ TNGQIL
GAAEFDNTFGWDNKHVGARILLSKEFLVQNVKSLH DYKGHSDNFVCSLIPGAGSSSAQYTPGGLLFKMSD
SNMQYVTSTTFLLVTYAKYLTKSHSVVNCGGTTVTPKRLRTLAKRQVDYLLGDNPLKMSYMVGYGPRYPQ
RIHHRGSSLPSMAVHPGKIQCSAGFGVMNSKSPNPNIILMGAVVGGPDQHDFPDQRSDYEQSEPATYVNA
PLVGTLAYLAHSFGQL

>P.vulgaris-AAC78504.1

KAILFFEGQRSGKLPSSQRVKWRE

DSALSDGKLQNVNLI GGGYYDAGDNLKFGWPMAFSTSLLSWA AVEYESEISSVNQLGYLQSAIRWGADFML
RAHTSPTTLYTQVGDGNADHNCWERPEDMDTPRTVYKIDANSPGTEVAAEYAAALSAASIVFKKIDAKYS
STLLSHSKSLDFADKNRGSYSGSCP FYCSYSGYQDELLWAAAWLYKASGESKYL SYIIISNQGWSQTVSE
FSWDNKFVGAQTLTLEEFYGGKDLAKIKTDAESFICAVMPGSNSRQIKTTPGGLLFTRDSSNLQYTTSS
TMVLFIFSRILNRNHINGINCGSSHFTASQIRGFAKTQVEYILGNNPMKMSYMVGF GSKYPKQLHHRGSS
IPSIKVHPAKVGCNAGLSDY YNSANPNPNTHVGAIVGGPDSNDRFNDARS DYSHAEPPTYINAAFVASIS

ALLAKT

>S.nigra-CAA52343.1

KAILFFEGQRSGLPTNQRVKWRGDSALSDG
KPHNVNLTGGYYDAGDNVKGFWPMAYTVSLLSWAAVEYKQEISPTNQLRYLQTAIRWGTNYILRAHTSST
TLYTQVGDGNSDHQCWERPEDMDTPRTLYKITSTSPGTEVAADNAAALAAASIVFQEVDNSYSAKLLRHS
KLLFQFADQYRGSYQASCPFYCSYSGYQDELLWAAAWLYKASGDATYLNIVLGNQGWSHAVSEFSWDNKF
AGAQTLLAKEFFGGKTNLGFKSDSESFICALMPGSSSVQIQTTGGLLYTRDSSNLQYVTSASMVFLIY
SKILNAANIKGVQCGSVNFPTSQIKAFKASQVDYILGNPMKMSYVGFSGSKYPLQLHHRGASIPSMQIH
PARVGCNEGYSAWYSSSKSNPNTHVGAIVGGPNSNDQFNDVRSYSHLETTTYMNAAFVGSVAALV

>T.aestivum-AAM13693.1

KALMFFNAQRSGHLPKHNGVXGRG
NSGMKDGLSDSTVVKSLVGGFYDAGDAIKFNYPMAWSMNMLSWTVIEYRAKYEAIGELDHVKEIIKWGTD
YMLKTFNNSADTIDRIVAQVGVGDTSKGPMNDHYCWMRPEDIDYKRPVIECHSCSDLAAGMAAALAAAS
IVFKDSKAYSDKLVHGAKALYKFGRLQRGRYSPNGSDQSLFCNSTSYWDEFVWGGAWMYFATGNTSYLTI
ATAPGMAKHAGAFWIGSPNYGVFTWDDKLPQSQVLLSRLRFLSPGYPYEEILRTFHNQTDNVMCSYLPV
FNSFNFTKGGLIQLNHGGPQPLQYVVNAAFSLASYADYLDTADTPRWYCRPNFYTTDVLKRFKAKSOLDYI
LGKNPQKMSYVVGFGKYPKRVHHRGASIPHNGVKYCKGGFKWREFKKNPNILVGMVAGPDKHDFK
DIRTNYNYTEPTLAANAGLVAALISLAD

>P.communis-BAC22690.1

KSLMFFNAQRSGKLPKHNNVSWR
GNSCLRDGNDPSTTFKDLAGGFYDAGDAIKFNFPASFAMTMLSWSVIEYSAKYEAAGELSHVKEIIKWGS
DYFLKTFNHSADSIDRLVAQVGVGSTAGGSTTPNDHYCWMRPEDIDYQRPVSQCHSCSDLAEMAALAA
SSIVFKDNKAYSQKLVHGAKTLFRFSREQRGRYSAGGSTDAATFYNSTSYWDEFIWGGAWMYATGNSSY
LQLATTPGLAKHAGAFWGGPDYGVLSWDNKLGAQVLLSRLXLFLSPGYPYEEILRTFHNQTSIIMCSYL
PVFTTFNRTKGGLIQLNHGRPQPLQYVVNAAFSLATLYSEYLDAAADTPGWYCGPNFYSTDVLRFAKTQID
YILGKNPRKMSYVVGFGNHYPKHVHHRGASIPKNKIKYSCKGGWKWRDTPKANPNTIDGAMVAGPDKHDG
FRDVRSNYNYTEPTLAGNAGLVAALVALS

>P.persica-CAA65597.1

KSILFFEGQRSGKLPANQRATWRANSGLSDGS
SYHVDLVGGYYDAGDNVKGFLPMAFTTTLLAWSVIEFGDSMHNQIENAKDAIRWSTDYLLKAATSTPGAL
YVQVADPNADHQCWERPEDMDTPRNVYKVSTQNPNGSDVAAETAALAAASIVFKDSDPSYSGKLLHTAMK
VFDFADRYRGSYSDSIGSVVCPFYCSYSGYHDELLWGASWIHRASQNSSYLAYIKSNGHILGADDDGFSF
SWDDKRPGTKVLLSKNFLEKNNEEFQLYKAHSDNYICSLLPGTSNFAQQYTPGGLLYKASESNLQYVTST
TLLLLTYAKYLRTNGGVATCGSSKVTAETLISEAKKQVDYILGNNPAKISYMGVFGKKYPLHIHHRGSSL
PSVHEHPERISCNNGFQYLNSGSPNPVNLVGAIVGGPDSKDSFSDDRNNYQQSEPATYINAPIVGALAFF
SANTNPN

>P.patens-XP_001781646.1

MFLFLCLFLFSSGKLPADFPKWRGDSNLLDGSVNVSLSGGIYDAGDSVKFGFPMAFTATILSWSVLEY
GPAMEKAGQLASAKNSIKWITDYLIKAAHPNVLYFQVGNASTDHKCWYRPEDGGSIAARPSLVLNNTTLPG
SEVAAETAAMAAASMVFRSTDATYADTLVAHAQQLFNFSPTYQASYSETIPEFQDYNSTGYGDELLWG
ATWLYYATGDNTYLAYVTGANGEKFADWGVFPSWFSWDSKRPVAVQVLLARLQMLKPPTNAVNTVSKGLTD
YKTTADGLMCAFLPGSPTASTDRTKGGYIWLNEWSALQHGINALLASFYSYDYLVAAKSSGITCSGKSFT
HAQLRAFASSQANYVLGNNPLSTSFMVGYGEKHPKYLHHRGASIPVDQIKTDCAHSWGWDYDSKEPNPNIA
YGAVVGGPFKNETYTDARTNIMQNEASVYTSAAFAGLSAGLVGSSNSVPISWI

>M.polymorpha-0030s0120

KTFLFYEAQRSGKLPDSQRVKWRKDSGLSDGETVNVDLGGYHDAGDNVKGFPMAYSITLLAWSVVEYGDF
LQKAEELQNAHEAIRWGTDLFLKAHTGPNELWVQVGDANADHMCWERPEDMDTPRTAYKVDKDNPGSDVAGE
TAAALAASSIVFRDADPAYAKRLLASAQQLFEFADNYRGRYSDAVPAACPFYCSYSGYKDELLWAATWLYKA
TNDEAYLRYILNSADDFGGYKSYSASTWTLDWDNKFAGAQILLAQTYLLGNTKFKAQKNWADKFVCSTLPGL
STTEVTITPGLLFTKPNASNFQYVTSTAFLLMIYAKYLRSQSSQLYCNHMPVSTHTLSSFSKQQVDYILGTN
PSNMSYMGVFGSKFKRLHHRASSIPSIHVHPANISCRDQWQFFAETTENPNILTALVGGPDIYQDAR
WNFEQSEPTNYINAPLVGLLAELYGVNAVPCK

>S.fallax-0051s0090

LSILFYDVQRSGVLPNWQRVWRVWNSAIYDGTQSKARLSGGYYDAGDNMKGFPMAFSMTLLSWSAVDFREEL
KQAGQLGHTLNAIRWGTDYLLKAYTAPNELWVQVGDPNSDHACWERPEDMDTPRPAFQVNTNRPGSDVAAETA
AALAAASLAFRDLDSIYSARLLTSAIQVFNFNANNYRGKYSDFSFGVCPFYCSYSGYNDELVWGAAWLYKATR

DVTYLQYLI SNGATLGGTTESVNSFDWDNKYAGA QVLLSAFVLGENDGGLHGYKARAENFICSILPRSVSPVT
QTAFTPGGLLFRSGQSNLQYVTTAAFLATVYGNYSNSRSTVSCGAIITPLQLASFAKSQVDYILGGNRLGM
SYMVGFGPKYPQQVHHRAASLPSKRVYPGMIYCQQGFSWFQTAKPNPNQATGAVIGGPDQSDNLNDVRSNYAQ
MEPTTYINAPLVGVLASLAEGSKGYK

>G.biloba-gbalocus47775

KSILFFEAQRSGKLPNQR

VSWRRDSALSDGSSQHVDLVGGYYDAGDNIKFGFPMAFTTTLLSWSVLEFGDHMGSELAN
AKAAIRWATDYLLKATAHPDTLYVQVGEPNMDHRCWERPEDMDTPRTVYKIDAQNPGSDV
AAETAALAAASMV FQVSDASYSHRLLQTAMRVDFADKHRGAYSDSLKSAVCPFYCSYS
GYQDELLWGAAWLHTASRNPSYLSYIHTNGQTLGADSDNSFSWDNKHVGTRVLLTKEFL
LQKVQLLESYKAHADNFICSLLPGTSTSQAEYTPGGLLYKLSDSNMQYVTATSFILLTYA
KYLSSSSQV VSCGSSTATPERLQSI AKRQVDYILGN NPMKMSYMGYGP KFPQH VHHRGS
SIPSVVQHPQVIGCDNGFN YFHSNDPNPNILV GAVVGGPDNKDQFSDDRSEYAQSEPSTY
MNAPLVGALAALLHMH A

>C.zofingiensi-Cz08g28050

LSNLFYFAQRSGRLPADNPIKWRGNAGLNHKAPDGRDVTGGWYDAGDNVKFNLPMAWTAAV
LSWSVDFDFREGYRKAGTLPETLANIRWANDYFIKCVGDGNTIVAQVGNQDHDHSGWTRPEDV
TGAVPVYVVTPSKPGSDVVGAMAASLAAASVI FTSTDYAYSVKLLAAALKAYKFATTYLGSY
SASIPDAAQFYKSSNYDDLAWAAIWLNVRTGKPEYKTA AVEFYK KHWNMENGAQVWNNFDW
DSNSWADVMI LHRMFPNDAFYKKRMLTFIDDWLTGRGPPNYVTYTPKGLAFSGDWGSLRHVG
NALFLMQSFVHTSKDQALNRRINCFTHRQLRYILGSTGRSFVVGF GNNPPQPHHRAASCTP
GQPCSWDALNPNP NPNVLYGALVGGPNVQDVYSDNRNNFVQNEVACDYNAGFQGALAAMVT
SNVNW PSCSAQYTQYQEMGF

>K.fedtschenkoi-Kaladp0098s0155

KSILFFEGQRSGKLP SGQRLKWRASALSDGSADHVDLVGGYYDAGDNVKFGLPMAFTTTMLA
WSVIEFGSSMG SQADHARDAVKWSTDYLLKAATAAPDTLYVQVADPNKDHQCWERPEDMDTPR
GVYKVTAQNPGSDVAGETAALAAASIVFRDADPSYSSKLLQTSKKVFEFADKHRGSYSDSLG
SVVCPFYCSYSGYQDELLWGASWLYRASQEETYRSYIQ TNGQTAGATDDDYSFSWDDK RAGTK
ILLSQEFLEKDTQEF EYVYKAHSDNFVCSLMPGTPTSQAQYTPGGLLYKLSGSNLQYVTSSTFL
MLTYAKYLESKGAASISCGSAAVTPDKLIAQAKSQVDYILGQNPAKMSYMGFGANYPKHIIH

RGSSLPSVRDHPDRIGCNDGFRYLYSSSPNPNVLVGAVVGGPDSNDRFADDRNNYQQSEPATY
INAPFVGALAYFSG

>O.thomaeum-Oropetium2015010523527

KSIIFFEGQRSGKLPNGRMPWRGDSGLRDGAQHNVDLVGGYYDAGDNVKFGLPMAFTTTMLAW
SVADFGKFMGADQLPHARAAVRWGADYLLKAATATPGTLYVQVGDPNQDHRCWERPEDMDTPRS
VYAVTRDRPGSDVAAETAALAASAVVFRSDPAYSSRLLRAAMETFEFADRHRGSYSSDSALS
SAVCPFYCSYSGYEDELLWAAAWLHRASNNASFMSYVQLNGAQLGAEEDDYSFSWDDKRVGTKV
LLARGFLRRKKTRLQGLLQLYKAHSDSYVCSLVPGTSSFQQSQYTPGGLIYKEGASNMQYVTTA
TFLLLAYAKYLRSYGACVVCGRDVPAPAEALVALAKRQVDYVLGKNPAGTSYMGVFGARYPRRLH
HRGASMPSVRDHPGRIGCDEGFRYMHSADADRNVLVGAVVGGPDARDAFADQRDSYGQSEPATY
INAPLVGALAFFAGTVKR

>S.polyrhiza-Spipo3G0031200



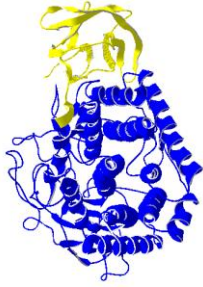

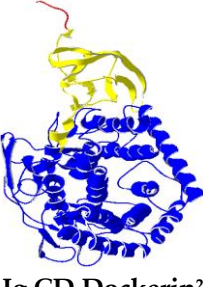
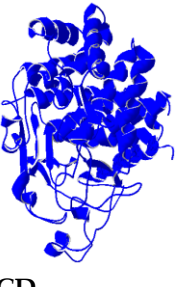

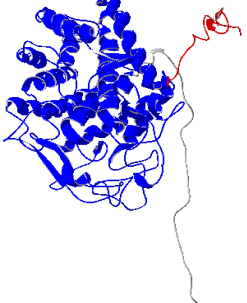

KSIIFFEGQRSGRLPASQRLKWRDGLSDGASMHVDLVGGYYDAGDNVKFGFPMAFTTTMLAWS
VVEFGGVMKGELQNAREAIRWASDYLLKATAHPNTVYVQVGDANKDHECWERPEDMDTPRTVFKV
DPSNPGSDVAAETAALAASLVFQKTDPAYSKLLRRRAISVFEFADKHRGPYSNGLKSAVCPFY
CSYSGYQDELLWGAAWLHRATRDPAYLSYIQVNGQTLGADESDFGWDNKHVVGARILLSKAFLV
QNVKSLYEYKGHADTFICSLVPGTFFSQTQYTPGGLLFFKMSDSNMQYVTSTSFLLLYAKYLYA
GKVVSCGGTTVTPKTLRRIAKRQVDYILGDNPLKMSYMGYGSRYPERIHHRGSSLPSVAAHPAK
IPCSAGFSLMNSGAPNPNVLVGAVVGGPDANDRFPDQRSYEQSEPATYINAPLVGALAYLAHSS
GQL

>Z.marina-Zosma196g00530

KSILFFEGQRSGKLPPEQRQAWRKDSGIRDGFDGVDLSGGYYDAGDNVKFGFPMAFTVTMLSWSV
VEFGSNMPSDEIRNAVAIRWGTDYLLKTI SQPNRIFVQVGDVEDHNCWERPEDMDTARTVYSVT
PDNPGSDVAGETAALAAASMVFRDIDNNYSDTLLHGAFKAFQFADTYRGAYSDDPAIKPGVCPFY
CDFDGYQDELLWGAAWLRRASGKDDYLNITTINGKILGAEDTVNEFGWDNKHAGINVLI SKEFLEQ
GKLYSLQSYKASADSFMCTLIPESSPHVGYTPGGLIYKPGGSNMQHVTSAIFLLLYADYLSNSS
QTFNCGGVTVGPESLRLQAKRQVDYLLGSNPKNMSYMGYGDHGNYPQRIHHRGSSLPSVSDHPEH
IRCKEGSPYFNSSEPNRNVLVGAVVGGPGKDDVYEDDRADFRKSEPTYINAPLVGLAYFAANS
AGADATLAKHTNYIK

```
>I.tegetiformans-PKOXscaffold2001883
KSILFYEGMRSGKLPPEQRMHWRCD SGLTDGHSQNVDLTGGYYDSGDNIKFGFPMAFTTTMLSWSI
IEYGSQLSKAGELGHAQA AVRWATDYFLKAYTSPT ELWVQVGD P NSDHQCWERPEDMDTPRTAYKV
TAENPGSDVASETAAALAAAS MVFRQCDPSYSNRLLQTARQMFEFADKFRGSYSDVLRSAVSPFYT
SYSGFQDELLWGATWLYKASRDGKYLQYIYTNGDSLGGPTRSFSALSWDNKYAGVDILLTQAFVFG
KQNKLG VYKARADEYIC SILPGRGQITPGGLIYHDGATNMQYVTTAAFLFTYSNYLAKSSQTVTC
GGTNLGA EHLSAFAKKQVDYILGENPSKMSY MVGFGSNFPRKVHHRGSSLPSFKESNAHIACSEGF
TWFHTNDPNPNLLMGAVVGGPDMSDRYS DERSRYTEAEPATYINSGLVGALALLSS
```

Supplementary Figure 2. FASTA sequences of the truncated cellulases comprising only CD regions used to build the phylogenetic tree of Figure 2 in the main text.

<p><i>Thermobifida</i>: 1JS4/4TF4 (Exo/endo)</p>  <p>CD→CBM/Fn3→Fn3.CBM</p>	<p><i>Clostridium cellulolyticum</i>: 1KFG/1GA2 (Exo/endo)</p>  <p>CD.→.CBM</p>	<p><i>Ruminiclostridium</i>: 1UT9 (Exo)</p>  <p>CBM.Ig.CD.Fn3.CBM→Dockerin²</p>
<p><i>Ruminiclostridium</i>: 2YIK (Endo)</p>  <p>?CD→Dockerin²</p>	<p><i>Ruminiclostridium</i>: 1CLC (Endo)</p>  <p>Ig.CD.Dockerin²</p>	<p>Termite: 1KS8 (Endo)</p>  <p>CD</p>
<p>(N-terminal)</p>  <p>CD→ CD→CBM</p>	<p>Spinach:KNA09089:</p> <p>(C-terminal)</p> 	<p>Abalone: BAD01504</p>  <p>CBM→CD</p>

Supplementary Figure 3. X-ray structures and models of selected family GH9 cellulases. Blue, CD; pink, CBM; turquoise, Fn3-like domain; pink/turquoise, Fn3-like domain within CBM; grey, linker; yellow, Ig-like domain. Organism names, accession/PDB codes, cellulase types are given alongside the structures. The threading templates used by I-TASSER for generating homology models are given in the top row and the I-TASSER statistics are given in Supplementary Table 1. The domain arrangement is given below the structure with dots depicting separation between domains. CD, catalytic domain; CBM, carbohydrate-binding domain; arrow, linker; /, overlapping domains; superscript, two consecutive domains; ?, unknown domain. Only 1JS4/4TF4 and 1KFG/1GA2 have X-ray structures available for the full-length sequence.

Cr9B: XP001701544 Top templates: 1JS4 /1tf4, 1ks8, 1kfg/1ga2 Model scores: C-score = 0.16 TM-score = 0.73 ±0.11 RMSD = 7.0 ± 4.1 Å	Cr9C: XP001701546 Top templates: 1tf4 , 1ut9, 1clc , 1ks8, 1kfg/1ga2 Model scores: C-score = 0.75 TM-score = 0.81 ±0.009 RMSD = 5.7 ± 3.6 Å	Cr9D: XP001696497 Top templates: 1tf4 , 1ut9, 1ks8, 1kfg/1ga2 Model scores: C-score = -2.0 TM-score = 0.47 ±0.15 RMSD = 13.8 ± 4.0 Å
Gp: KXZ51468 (N-terminal) Top templates: 1tf4/1js4 , 1ks8, 1kfg/1ga2 Model scores: C-score = 0.83 TM-score = 0.83 ±0.008 RMSD = 5.3 ± 3.4 Å	Gp: KXZ51468 (C-terminal) Top templates: 1tf4/1js4, 1ks8, 1kfg/1ga2 Model scores: C-score = 0.93 TM-score = 0.84 ±0.08 RMSD = 5.2 ± 3.4 Å	Gp: KXZ44756 Top templates: 1tf4 /1js4, 1ks8 Model scores: C-score = -0.94 TM-score = 0.84 ±0.08 RMSD = 4.2 ± 2.8 Å
Gp: KXZ51466 Top templates: 1tf4/ 1js4, 1ks8 Model scores: C-score = 0.25 TM-score = 0.75 ±0.11 RMSD = 7.2 ± 4.2 Å	Vc: XP002958622 Top templates: 1tf4/1js4 , 1ks8, 1kfg/1ga2 Model scores: C-score = 0.92 TM-score = 0.84 ±0.08 RMSD = 5.3 ± 3.4 Å	Vc: XP002952174 Top templates: 1tf4/1js4 , 1ks8, 2yik Model scores: C-score = -0.11 TM-score = 0.7 ±0.12 RMSD = 7.7 ± 4.4 Å

Supplementary Table 1. Modelling statistics of algal cellulases by I-TASSER.

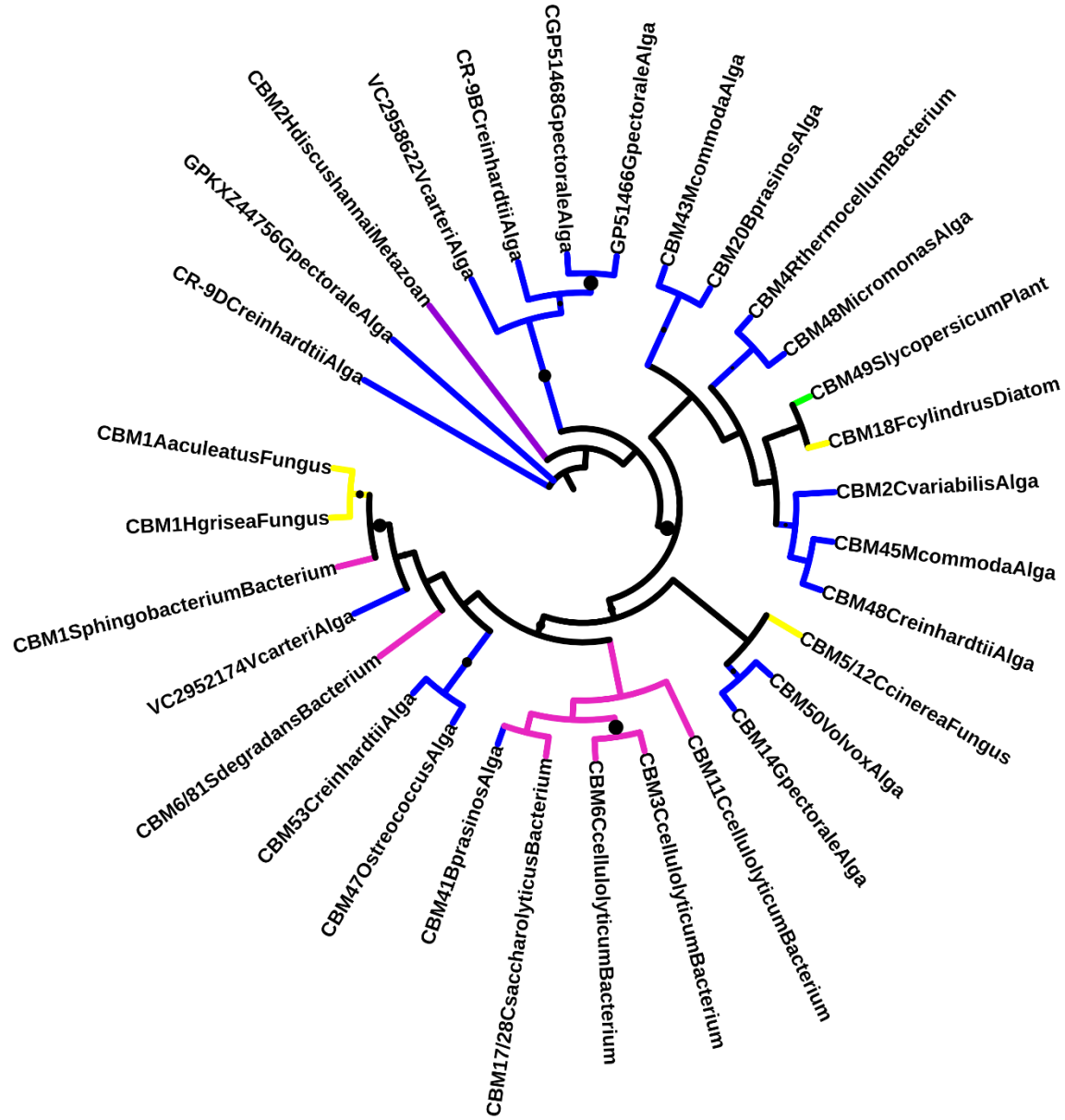
1KS8, termite; 1clc, *Clostridium thermocellum*; 1UT9, *Clostridium thermocellum*; 1JS4/1tf4, *Thermobifida fusca*; 1kfg/1ga2, *Clostridium cellulolyticum*.

All models have Z-score of between 2.0 - 7.4 (Z-score of > 1 means good alignment). C-score [-5 to 2], higher value indicates more accurate model; TM-score, >0.5 indicates a model of correct topology and < 0.17 means a random similarity.

Organism	ID/PBD	Taxonomic group	Glucanase type	Amino acids, mol.wt, pI, GRAVY
<i>Volvox carteri</i> (colony of 2000-6000 cells)	XP_002952174	Alga, this study	Putative exo/endo	758, 80.01, 5.89, -0.10
<i>Volvox carteri</i> (colony of 2000-6000 cells)	XP_002958622	Alga, this study	Putative exo/endo	732, 76.86, 7.36, -0.18
<i>Chlamydomonas reinhardtii</i> (single cell)	XP_001701544 (Cr9B)	Alga, this study	Putative exo/endo	619, 65.14, 6.47, -0.2
<i>Chlamydomonas reinhardtii</i> (single cell)	XP_001701546 (Cr9C)	Alga, this study	Putative exo/endo	606, 64.65, 8.35, -0.117
<i>Chlamydomonas reinhardtii</i> (single cell)	XP_001696497 (Cr9D)	Alga, this study	Putative exo/endo	888, 94.4, 5.18, -0.295
<i>Gonium pectorale</i> (colony of 4-16 cells)	KXZ51466, Gp51466	Alga, this study	Putative exo/endo	621, 65.62, 8.32, -0.24
<i>Gonium pectorale</i> (colony of 4-16 cells)	KXZ44756, Gp44756	Alga, this study	Putative exo/endo	644, 69.83, 5.48, -0.22
<i>Gonium pectorale</i> (colony of 4-16 cells)	KXZ51468, Gp51468	Alga, this study	Putative exo/endo	1148, 119.89, 7.4, -0.236
<i>Clostridium thermocellum</i>	2YIK	Bacterium [2]	Endo	611 68.51, 5.26, -0.45
<i>Thermomonospora fusca</i>	1JS4, 4TF4 WP061783773	Bacterium [3, 4]	Endo + Exo	834, 90.35, 4.44, -0.433
<i>Caldocellum saccharolyticum</i>	WP_011916637	Bacterium [5]	Endo	1719, 191.06, 5.58, -0.53
<i>Clostridium thermocellum/</i>	CAA56918 (1UT9)	Bacterium [6]	Exo	1230, 137.83, 4.83, 0.526
<i>Clostridium thermocellum/</i>	1CLC	Bacterium [6]	Endo	639, 71.20, 5.19, -0.36
<i>Neocallimastix patriciarum</i>	AEX92719	Fungus [7]	Putative exo/endo	770, 85.34, 4.95, -0.58
<i>Solanum lycopersicum</i> (Tomato)	NP001234172	Plant [8]	Endo	604, 66.77, 9.3, -0.393
<i>Spinacia oleracea</i> (Spinach)	KNA09089	Plant	Putative exo/endo	1145, 126.20, 5.49, -0.31
<i>Haliotis discus hannai</i> (Abalone)	BAD01504	Metazoan [9]	Endo	579, 63.21, 5.95, -0.51

<i>Nasutitermes takasagoensis</i> (Termite)	1KS8	Metazoan [10]	Endo	433, 47.80, 4.91, -0.458
---	------	---------------	------	--------------------------

Supplementary Table 2. Properties of the considered algal cellulases compared with other cellulases across different taxonomic groups.



Supplementary Figure 4. Maximum likelihood phylogenetic analysis (100 bootstraps) of truncated CBMs from algae and other organisms across various families and taxonomic groups (see Supplementary Fig. 5 for details). The circles refer to the bootstraps (range 0.6-1). The CBM and organism types are indicated in the tree. The different colors represent the different taxonomic groups, as in Figure 2.

```
>CBM1SphingobacteriumBacterium
KIQTkmnyALSHNTVYLNWGDnQQAMVTTSDNASLEIRKITGACFLMRFDNDKKEFEYQDEFGEKRNfYfKS
GAFYNKEDDQPFNKEWYKDLKIDQQDLFTIPEVYAVLDKGNLIPQSPRKIHLQnADKLIKAKSLALNNKLRQ
SKSTLMAVDAPPCNNYCRSGQSFHLSQIMACENATVEVNSGCCSNAYCIGCCSIIGCDcATVIGSYLAVCTA
VAKSCSGYGSPIATSPVWGQCGGNTWTGPTACTPGNKCVFINSNYSQCQPL
```

```
>CBM1AaculeatusFungus
ATASAYAQCgGNGWTGATVCFTGYTCTYSNAFYsQCVPS
```

```
>CBM1HgriseaFungus
AQQGAWQcGGVGFSGSTSCVSGYTCVYLNDWYSQCQ
```

```
>CBM2CvariabilisAlga
RLHFSLVgWSSFTWGPSDTDLKYAGTKTNAQVVLTpkEWLREIppGTTLSISFGGQGVAPSAIVFEQILPLLDp
DHDISLSTRGAFPQKLFAPFVDATLYPTPRLLDAYEATGQKWFTLAF
ITADLRTGARLGRVIPLWKQYFMDQIRDIRLLGGDCIVSFGGAAGQEQAQVRVDEdMLLKDYQTIVDLYKLRWI
DFDIEGGAVLEMASVQRRHRVLKRLQDANPGLVVSFTLPVLPVGLTADGVNLLRDAKAKGVRLDVLNIMTMDYg
DSAAPNPRGQMGDYAIQAAVNTRAQAQSVGYDDTKIGNTPMIGLNDVESEIFYLDDARKVGAWAKATPWLRTAF
WSVGRDKWNPAETYVSIHSSSIPQEPFEFTRIFKSFAS
```

```
>CBM2HdiscushannaiMetazoan
VDVTISNHWDGGFQAKACIAITTELHswKAHLKFSQAVDSLDCGTANVQKTNGGKEYILTNKQWNADEHAGDKL
CLDFVGHTSGDINPKTTLTIEGVAAGSSHTG
```

```
>CBM3CcellulolyticumBacterium
KMYKHSGGDPIPNFKAIEKITNDEVIIKAGLNSTGPNYTEIKAVVYNQTGWPARVTDKISFKYFMDLSEI
VAAGIDPLSLVTSSNYSEGKNTKvSGVLPWDVSNVYVNVDLTGENIYPGGQSACRREVQFRIAAPQGT
```


TYWNPKNDFSVDGLPTTSTVNTVTNIPVYDNGVKVFGNEPAGGSENPDPPEILYGDVNSDKNVDALDFAAL
KKYLLGGTSSIDVKAADTYKDGNI DAIDMATLKKYLLGTITQLPQG

>CBM4RthermocellumBacterium

NDLLYERTFDEGLCFPWHTCEDSGGKCDFAVVDVPGEPGNKAFRLTVIDKGQNKWSVQMRHRGITLE
QGHTYTVRFTIWSDKSCRVIYAKIGQMGEPEYTEYW
NNNWNPFNLTPGQKLTVEQNFTMNYPTDDTCEFTFHLGGELAAGTPYYVYLDDVSLYDP

>CBM5/12CcinereaFungus

APAYVSGTGYQSGAQVSYGGYIWQAKWFASQTPGSIVNGEWSAVSVCSGGGSPAPPPPPSSST
TTTTTTTRSSTTTTTRSTTSTSTTTTGSSTPAPPAPTGGLCAGVSAWSSSVAYDGGSKVVYSGRLWTAK
WWTQADI PGGLAGVVDNGPC

>CBM6CcellulolyticumBacterium

SRIEAEYSNQSGIQETETCSEGGEDVGFVENGDYTVYNNVDFGDGVGGFQARVAS
ATSGNIEIRLDSSTGTLTIGTCPVAGTGDWQTYTDAKCTVSGVTGKHDVYLVFKGDSGYLFNLNWFTFSE
KTVIGNLGDINSDGQVDAIDLQVLKKYLLQLGEIGDTKLADLDANGEINAIDFSLKQFLLGTIISFPGE
AL

>CBM6/81SdegradansBacterium

ARIEAENYDSAPVETTAGNSGSPNTCSYKMGVDVENSTEGACNIGWTAAGEKVTYNIGNADGTYDIALRVA
SMDAGKRISVHVNNSLADTVTTQGGGWQAWTTETISNVYIPSNV
ITVEFYDSGSNLNFLNITESSGT

>CBM11CcellulolyticumBacterium

AYGEQLIEDFEGAMQWAAYSVGVDATASCKISSGKSNNGLEITYAGSSNGYWGVDNEHRNQDWEKWQ
KISFDIKSSNTNEVRLLIAEQSKIEGEDGEHWTYVIKPSTSWTTIEIPFSSFTKRMDYQPPAQDGETFD
LYKVGSLHFMYSNSNSGTLNIDNIKLIIGLPEEQIGGK

>CBM14GpectoraleAlga

GLQYKLPAGVSCDNCTLQWWTTGNSCTPPCVPEDPDYVPGGAPNSCDKAGLGICGSSPAKYPEEFWNCADV
ITPAGSGASPTPSPSPHADGLHANPCDATCTTFINCGNVAYVQPCGAGLLFNAVAKYCDWPANVQCSGAGGAS
PSPSPSPSPSPPLPSPSPSPASCITTNFCSNRASGLYANPCDATCATFINCGNGIAYPKPQPCPGKAPPGGGIPG

ELAMVGAARCRVAPLGGPVRGRGATWAAGYNLGGSPPSLPAYAPKLTHINYAFASISYSPQLDSYLDFTDTWA
DIGACLTGSCPATCIVLNATCPGSNLAMAPTTKTPSAACPSSCFNGGGGGPGYPRACNTVAKDMSSPLRACGHYA
LVQRFIAEQAPNVRVLI SVGGWYDSNYFSMAASPAYRSRFVDSVLDLDFLDTFGFDGVDFDWEYPGFEHGGQPPYGA
APDYGSPDDVRDCASGSCTYSGRTADGANFVATLSELRSRLSAGRRSKRGEPYL

>CBM17/28CsaccharolyticusBacterium

WDISELSISGEYVRSRIKGIPIYQPIERTLKISQDQVACAPIGQPILPSEDFEDGTRQGDWDGPGSVKGA
LTIEEANGSNALSWEVEYPEKKLQDGWASAPRLILRNINTTRGDCKYLCDFYLPKQATKGELAI FLAF
APPSLNywaQAE DSFNIDL TNLSTLKKTPDDL YSFKISFDL DKIKEGKI IGP DTHLRDI IIVVADVNSDF
KGRMYLDNVRFT

>CBM18FcyllindrusDiatom

GLNSNTKVCGREGGTGINYDTWNDSLGNPMPVWTQGTYAIGGHVQIDILMTAHHLGHFVVKACAMGRDSTQ
GCFDEHPLEFVKDKVHGMPKDINYPERAMLFGDGVDSL SYKMKL PDDIAGQKVLLQIIYWTANSCSYLGYKE
YFTNNKTPSGNKPNWSPGLIDCPEDLPTLREGAEAVTPEIFVNCAEITIEGEPTPTAPIAPTAPSPTPAPA
PTPVAQEPVNA PVTSGLPVPVNPDI DGTCTGDTGNGICPAQTLCCSKFGYCGTIATKHCDSDPRFIPTPP
CVDLKGTVYKNKKNKGGKKKRTCKWVGENKCKNKKYEGEKLIKISCPVTCGMKICE

>CBM20BprasinosaAlga

MTTCPRHIACSSSSSVLMKTTTTTRTTTTTRTRTFSPSSNKISVAPSRPPRSNQSTFPSRRTRRGDLKIN
ASTQDYDDNKDQFMKMSSEGMNALKSISATDQKLTSSSSVNNNVISIDQSILKVPYKDALDMIGSR
TKSTPVNFSVQYDTKWGENL FVLGSHKKGAWDEAKAIPMHYKEGGHWSCEVDLQPGGIFFYKYLVR SIF
GTRWQEGANLLVLPEANDLPKNATYLVEDCFNGGPTQLTRTNQTL LAAKLIETQKEKVLyakELSKQQQ
MTKSALEELLIAREELASAQMQLARAI GDGRSYDVDTTTTTTTTTTNNDTSSKEEEEKKS GFWSSR

>CBM41BprasinosaAlga

PLGCTFMDEIIVVTLWAPSAIQVDFLLFDSPDFSHPKEELEMDFSSNGTWI
IHGRRKELYQMYNFRVTVFHPKENKVMTSIASDPYA

>CBM43McommodaAlga

AVSGRGRREESVPLLPRDVEAGADDAAGDARCGRSRGMIAGTSARDALDAGDGAAPRRLPRGVIALVSL LAV
AGCAGYSASVSGGRHGAALGAAGTRLRPDRWSFHQRSRPSALESVNPWRGRDTEGLKLATRRTAAPESRRGV
VMAGQWPGYGAAKKSRSRDDDEEEEEEEEEEDNGTLVPVLGDQVVTGESTPRRGAVTSGRRSRPCVLKDAVT

DEQAQAVLDFACAPESGVSCAPIGAGGALERPNTLLRDHAAWAIDRYFRLRSREPDAFFQRDCHFVGVASLD
APNNFYVSTTGALVRVNPVSDTIANKVTVPPIEGVVFSSGVGAVRGTLVSRGGGSSNGGGGFLRDDPLRPEAG
VKTTFFKFWAGSTATRSRGEPCVVETTUVYDFDGDGDADRTESEFELVQVPREPAMAPVETKIIGHSAKARGA
RFPRRVTDARVSLLVRSNPVWESSATYPSFLTVPYRE

>CBM45McommodaAlga

NELAAGLDVLFVAAAYLRWEQMGKPRVDEDEKHRIYSDAVNHITQRLNSGES
VEALETEFGVPPGLVRQTAALAAPPAAAPTQAKPTPPPFTPPAPPKAAAPAPAPSYGYDAAPAPAPANAV
KLMVIEGRRTAQGMLQMI VFGRS DQGI VLHWAGLDQPAGEWKNPPHGWSSMPENSWGTGGASWETEMEAL
TTARGWHAATIEAPCDRDGLVFWIRTADSAHWIKDDGQDFMCFADEATTLTDVRAIVKRRKEEERARRKA
EKEEQRRREREQQRSSPQKLKRGGLSTTTVKEVKMPARPEVIKRKDNHDEIKMHQ GALGHAGAAGNVAG
GSVDNICNSEEGATRSLMHRFNIA SDLI PQCKGEGEAGLVAMAVWFRFMALRQLVWNNDY

>CBM47OstreococcusAlga

DITMPLLPSPFDPGVTFVSN DAGLIGISVSKEIPGGDEPSGEFSVTKGRCVTPVCVKT DGNPCGEGQA AWS D
VGSHATAAVEAIKTDECIVAGAGVIEQNGGISVSREIRLPASGVNLLADAEANPTGMKNFKPSSVRIPEGK
FLLAFTGGDEAFKGETVIRSYKSKLNNRLYSMTSFVVS DIAAEFH EEPKSVGPEHAGSISKCKAMCAVK
KHCCNTDESIGSNQYLSCLQACVVRV RGT DERTCNSYCASATTSRHINGYMYNLATSCADV VASEGKLCST
RYGSDRSTCLYGCSIGRDPEQSLAVVKSTGFYMQLPAAHVTPRSTNNLRDRTLSSVIVRAGFVVKLYAGR D
LKGQYLT LGSSATLYGNHARFYSSLRGSFPNTKFAWANFNDRTRSIAILEAPVTLYTQPNFHGDHESKLEHA
FDYTS LGPTVGDRHVNSIFLREGSVVEVYEGRSFN GRGMQFISSVSDVRRATESIGDLSRPTWQRVYG

>CBM48CreinhardtiiAlga

MLLQAPGLAPGSARRQAACSVAREATNVRI VTPALTPGRAGVSGRRILPPSRVVSVELEAPTLSSSP
ATVSTKKLFCEPSGQPASTAYGPALTGRPAPLGASIDADTGAINFSVFSSSAESV

>CBM48MicromonasAlga

AIQSVGHFGLASDLFGWPETPTLVPAISWTQGG SIVEVEGSFDNWQSRQALHRSGTREFAIVKMLPPG
VYQYKFIVDGEWKYAPDQPAMYDEMGNVNNVLEVQEYIPEILDSLDSFLAPSSPTESYNNILFSPDDFA
KDPPACPPHLLTLLNMPQIPDAPNLLPRPQHVV LNHIYNDKNMTLAGTQVMGTTHRYRSKYVTVILVKPG

>CBM49SlycopersicumPlant

VTIQQRATSSWALNGKTYRYSAVVTNKSGKTVKNLKL SIVKLYGPLWGLTKYGNSFIFPAWLNSLPAGK

SLEFVYIHTASPAIVSVSSYTLV

>CBM50VolvoxAlga

AVAASAFIVDTCAADGDSSRRL LASGCTYTIQPGDTFWAIAQRRGTTVDVIQSLNPGVVPTRLQVGQVINV
PCSGGGGSTPTSTAPPARGCTYTIQPGDTFWAIAQRRGTTVDVIQSLNPGVNPRLQVGQVINVPCGSNGP
APQGGGSKVLYSGSGSGTYYYDLRRTTCPQNPGGFPENNGYPYCASYNPSAPTYKTLAQLNTNNVIAIDRNV
LSANRARLCGKKVLVFKNGVPVTAPNGGSFFVWDGCEACVGGGRIDFSLSLQRAASNACSLGVVPGISWQ
VVDEVVQQFVPP

>CBM53CreinhardtiiAlga

GLAVDQQLKQKITAPQAASASRSSAASSTGRFEAAAGGSGYGYGRSSVSVLVAEPPSAPPAAASPPSYGASGS
GGGGGSPKGGATAFEVSSRDYAKDMASLSVELDATIDDE
EEEAPPRQVPEASTRTQPYAAAASRFEALLSERRPAGATVNGAQAQMLEAREKKAASSSSSAGGVNGAAVNGA
AAADEQAAKEAARAAVAEVEGHRAVDVVAGREHWSIIT
VPEKPVAGAPLQMYFNRNQSEKLRNRPHIVMQYGFNHWELQPEAGNSLDLFPAPT PKSDVTDFTWTCRMQVPEE
TYELNFILHDKAGAYENNNGMDFTYPVEAGIDYDTWVDT
AAERIVAKELARREAEAKAAEEERKAAEAAMEEQAKEFGERKAAELKNNLGS LQEGGTAALLRNGVPVYKVT P
ALPVAGGKAVVQYNRRGGSFHAFPIPEGESVKLLLYGFNGWQE

>VC2952174VcarteriAlga

GLIEVESLLHEGGCSWEGYCVSTSCGTPGDRGVL PAVQICVVMVMVAVVVAVVRAAIIISRP
INTNDMSDNRI RGGPSQPPPQPPAPPPPPSPPLGLPSDPSKAPATCRPTDAACRSCLGNTNVTNTTACSACVAV
CAELSIIDHRIDMRGRKKVKPATRCLSDWRDARAQCFCVTS GVTDAVSCAECALPTAAARAACMTCQVRPLS
AQSAS

>CR9BCreinhardtiiAlga

GLAAVDAAIKAAGCTWTSYCALTCTGLDAGKCTNSCSGIATAALQTVCMGTCVPNSAAKGTDWGCNQYCGASSL
VGTDPARAQQCAACVAGWSNPWDCQNCIGV

>VC2958622VcarteriAlga

GLTDLEQGLQRS GPFPPSPSPSLSPPPSPPPRPSPPSPSPSPPPPLASCSPTDYACQQCSQSTYTAPDACRSC
VGAMRSIGQDPYRCFSCSNGVTDPTIQGICFTECVPTALKGADWSCS QYCSAPALVANDPTRARDCISCVKGV S
NPWDCYNCAV TASLSDSAAARATCFKCVTTTTLGGWSCGDCASRATPAERDSCIKSRGGRLLAGENF

```
>GP51466GpectoraleAlga
ACTNALITAQGACRSCVATLTSKGQDPWQCHSCGTKGYTSDATIQTACFTQCVPSAVAKGIAWACADYCEAQAN
VAGDPSRASQCMSCVTAGKVNNSGNVWGCQSCMTGTSSSTSRTATCMSCVASNLLPTWQCPQCANAGSCRRRQMRHSL
```

```
>CGP51468GpectoraleAlga
GLTALDQALRSTGCNLACTNALITAQGACRSCVATLTSKGQDPWQCHSCGTKGYTSDATIQTACFTQCVPSAVAKGI
AWACADYCEKPAVVAGDMTRVAQCFSCVTGSGATSANVWGCENCQKATSTTAARSACSSCVGSNLRPPSDCATCANS GSCTTR
```

```
>CR9DCreinhardtiiAlga
GLLQLGASTPDWNAYCGATPSPVPSPTPTPSPSPSPPTPTPSPSPSPAPIPSPSPSPPTPSPSPSPSATPSPSPSPSPSPSPS
PSPSPSPSGNPSCPPTEYDCQQCAANADAVQSLLPGMTAPCQTCAAIAIDGWPCYNCLATPLVSTNPSIMQGCDFCAAAGVN
GWACTQCTKGALSATDNANCATCYRRASSGNNWGCLECQTAGGSSEGRRAACLACVGNNSDAWACTQCASRYGTPCEAEKCV
ACLKASGNAWGCYTATYAAQCGGRRSLGTEF
```

```
>GPKXZ44756GpectoraleAlga
GLLQLSASTPDWDAYCGTAPTPTITCPWACSSCDSGTQPGSNLASQRSNCYSCVNARGVSKSWQCHACVGNATYVASQGQHC
LSCVSAGADAWACQSYCTDLSSDIAVLPCTSCVADPAVRSAGPWRCVCMAPSVLAKGAAAVEACMSCVRSCLKGPYACAVSV
```

Supplementary Figure 5. FASTA sequences of the CBMs used to build the phylogenetic tree of Supplementary Figure 4. The selected sequences from the Cazy database (<http://www.cazy.org/Carbohydrate-Binding-Modules.html>) containing CBMs were then truncated to only CBM parts by subjecting these sequences to MotifScan (https://myhits.isb-sib.ch/cgi-bin/motif_scan). Full sequences were used for standalone CBMs especially from the algae and for those sequences where CBM motifs were not identified.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1: CBM18 <i>Fragilariopsis cylindrus</i> , diatom	100	19	28	14	15	14	14	14	15	13	14	18	18	19	13	19
2: CBM2 <i>Chlorella variabilis</i> , alga	19	100	13	15	15	17	10	9	17	11	6	16	10	8	23	10
3: CBM18 <i>Micromonas commode</i> , alga, chitinase	28	13	100	19	17	13	0	14	19	16	17	22	18	16	19	17
4: CBM47 <i>Ostreococcus lucimarinus</i> , alga	14	15	19	100	15	13	15	12	20	16	15	13	16	13	19	15
5: CBM50 Vc, alga, chitinase,	15	15	17	15	100	9	21	15	25	16	17	15	21	20	19	21
6: CBM20 <i>Bathycoccus prasinus</i> , alga	14	17	13	13	9	100	25	14	17	8	9	15	15	14	15	14
7: CBM48 Cr, alga, isoamylase	14	10	0	15	21	25	100	13	24	19	21	15	9	24	18	18
8: CBM1 <i>Sphingobacterium</i> , bacterium	14	9	14	12	15	14	13	100	22	16	15	15	24	23	22	17
9: CBM14 Gp, alga	15	17	19	20	25	17	24	22	100	23	18	27	21	18	16	23
10: Vc2952174	13	11	16	16	16	8	19	16	23	100	24	24	23	25	15	31
11: Gp44756	14	6	17	15	17	9	21	15	18	24	100	34	32	34	24	28
12: Cr9D	18	16	22	13	15	15	15	15	27	24	34	100	30	30	26	39
13: Gp51466	18	10	18	16	21	15	9	24	21	23	32	30	100	75	39	45
14: Gp51468	19	8	16	13	20	14	24	23	18	25	34	30	75	100	37	41
15: Cr9B	13	23	19	19	19	15	18	22	16	15	24	26	39	37	100	40
16: Vc2958622	19	10	17	15	21	14	18	17	23	31	28	39	45	41	40	100

Supplementary Figure 6. Percent identity matrix of algal CBMs with most similar CBMs selected from top hits in Supplementary Fig. 3. Cr, *Chlamydomonas reinhardtii*; Gp, *Gonium pectorale*; Vc, *Volvox carteri*.

Name	Sequence (5'→3')	Efficiency (%)	GenBank number
GpKXZ51468Fwd	TTACCTGCGACTGGAACAAC	66.3%	KXZ51468.1
GpKXZ51468 oligo	CAGCCCCAGCGTGCTGCTG		
GpKXZ51468Rev	TCGAGGTAGGAATCGTCCTG		
GpKXZ51466Fwd	TGGGACCAAGTCAAGAACAG	78%	KXZ51466.1
GpKXZ51466 oligo	AGTTACGACGTGGTGTGGGATCAGGT		
GpKXZ51466Rev	TGTTCTGGATGCTCTGGATG		
GpKXZ44756Fwd	AGGCATGGACTGGGACAAC	80%	KXZ44756.1
GpKXZ44756 oligo	TTCAACCAGGCGTCCGTCATGAT		
GpKXZ44756Rev	TGCCAGAGGTTGAGTTGTAG		
GpTubA1Fwd	TCAAGTGCGCCATCAACTAC	90.2%	KXZ42248.1
GpTubA1Rev	CATGAGGTCGAACTTGTGGTC		
GptbpAFwd	TGAAGTGGAGGCAGAGATGAC	90.3%	KXZ55925.1
GptbpARev	TGGGGTTGTATTCTGCGTTG		
Gprpl23Fwd	ACACGCTGGTCTTCATTGTG	86%	KXZ44903.1
Gprpl23Rev	TGTTGACCTTCTTCGTCTGG		
Gpeef1Fwd	AGCCCCTCATTGTGGAGTC	90.1%	KXZ43317.1
Gpeef1Rev	TTGAACTGCACATCGGTGAC		

Supplementary Table 3. Primer sequences used in this study, with details of **the primer amplification** efficiencies (in %) and the GenBank number.

Supplementary References

1. Zverlov, V.V.; Velikodvorskaya, G.V.; Schwarz, W.H.; Bronnenmeier, K.; Kellermann, J.; Staudenbauer, W.L. Multidomain structure and cellosomal localization of the *Clostridium thermocellum* cellobiohydrolase CbhA. *J Bacteriol* 1998, 180:3091-3099.
2. Kurokawa, J.; Hemjinda, E.; Arai, T.; Kimura, T.; Sakka, K.; Ohmiya, K. *Clostridium thermocellum* cellulase CelT, a family 9 endoglucanase without an Ig-like domain or family 3c carbohydrate-binding module. *Appl Microbiol Biotechnol* 2002, 59:455-461. DOI:10.1007/s00253-002-1048-y.
3. Sakon, J.; Irwin, D.; Wilson, D.B.; Karplus, P.A. Structure and mechanism of exo/endocellulase E4 from *Thermomonospora fusca*. *Nat Struct Biol* 1997, 4:810-818. DOI:10.1038/nsb1097-810.
4. Jung, E.D.; Lao, G.; Irwin, D.; Barr, B.K.; Benjamin, A.; Wilson, D.B. DNA sequences and expression in *Streptomyces lividans* of an exoglucanase gene and an endoglucanase gene from *Thermomonospora fusca*. *Appl Environ Microbiol* 1993, 59:3032-3043.
5. Te'o, V.S.; Saul, D.J.; Bergquist, P.L. CelA, another gene coding for a multidomain cellulase from the extreme thermophile *Caldocellum saccharolyticum*. *Appl Microbiol Biotechnol*. 1995, 43:291-296. DOI.org/10.1007/BF00172827
6. Bayer, E.A.; Shimon, L.J.; Shoham, Y.; Lamed, R. Cellosomes-structure and ultrastructure. *J Struct Biol* 1998, 124:221-134. DOI: 10.1006/jsbi.1998.4065.
7. Wang, T.Y.; Chen, H.L.; Lu, M.J.; Chen, Y.C.; Sung, H.M.; Mao, C.T.; Cho, H.Y.; Ke, H.M.; Hwa, T.Y.; Ruan, S.K.; Hung, K.Y.; Chen, C.K.; Li, J.Y.; Wu, Y.C.; Chen, Y.H.; Chou, S.P.; Tsai, Y.W.; Chu, T.C.; Shih, C.A.; Li, W.H.; Shih, M.C. Functional characterization of cellulases identified from the cow rumen fungus *Neocallimastix patriciarum* W5 by transcriptomic and secretomic analyses. *Biotechnol Biofuels* 2011, 4:24. DOI:10.1186/1754-6834-4-24.
8. Urbanowicz, B.R.; Catalá, C.; Irwin, D.; Wilson, D.B.; Ripoll, D.R.; Rose, J.K. A tomato endo-beta-1,4-glucanase, SlCel9C1, represents a distinct subclass with a new family of carbohydrate binding modules (CBM49). *J Biol Chem* 2007, 282:12066-12074. DOI:10.1074/jbc.M607925200.
9. Suzuki, K.; Ojima, T.; Nishita, K. Purification and cDNA cloning of a cellulase from abalone *Haliotis discus hannai*. *Eur J Biochem* 2003, 270:771-778.
10. Khademi, S.; Guarino, L.A.; Watanabe, H.; Tokuda, G.; Meyer, E.F. Structure of an endoglucanase from termite, *Nasutitermes takasagoensis*. *Acta Crystallogr D Biol Crystallogr* 2002, 58:653-659.