

No.	NT or AA	Name
1.	Nucleotide	Nucleotide sequence of Fv3A, a GH3 enzyme from <i>F. verticilliioides</i>
2.	Amino acid	Protein sequence of Fv3A
3.	Nucleotide	Nucleotide sequence of Pf43A, a GH43 enzyme from <i>P. funiculosum</i>
4.	Amino acid	Protein sequence of Pf43A
5.	Nucleotide	Nucleotide sequence of Fv43E, a GH43 enzyme from <i>F. verticilliioides</i>
6.	Amino acid	Protein sequence of Fv43E
7.	Nucleotide	Nucleotide sequence of Fv39A, a GH39 enzyme from <i>F. verticilliioides</i>
8.	Amino acid	Protein sequence of Fv39A
9.	Nucleotide	Nucleotide sequence of Fv43A, a GH43 enzyme from <i>F. verticilliioides</i>
10.	Amino acid	Protein sequence of Fv43A
11.	Nucleotide	Nucleotide sequence of Fv43B, a GH43 enzyme from <i>F. verticilliioides</i>
12.	Amino acid	Protein sequence of Fv43B
13.	Nucleotide	Nucleotide sequence of Pa51A, a GH51 enzyme from <i>P. anserina</i>
14.	Amino acid	Protein sequence of Pa51A
15.	Nucleotide	Nucleotide sequence of Gz43A, a GH43 enzyme from <i>G. zeae</i>
16.	Amino acid	Protein sequence of Gz43A
17.	Nucleotide	Nucleotide sequence of Fo43A, a GH43 enzyme from <i>F. oxysporum</i>
18.	Amino acid	Protein sequence of Fo43A
19.	Nucleotide	Nucleotide sequence of Af43A, a GH43 enzyme from <i>A. fumigatus</i>
20.	Amino acid	Protein sequence of Af43A
21.	Nucleotide	Nucleotide sequence of Pf51A, a GH51 enzyme from <i>P. funiculosum</i>
22.	Amino acid	Protein sequence of Pf51A
23.	Nucleotide	Nucleotide sequence of AfuXyn2, a GH11 enzyme from <i>A. fumigatus</i>
24.	Amino acid	Protein sequence of AfuXyn2
25.	Nucleotide	Nucleotide sequence of AfuXyn5, a GH11 enzyme from <i>A. fumigatus</i>
26.	Amino acid	Protein sequence of AfuXyn5

FIG. 1A

No.	NT or AA	Name
27.	Nucleotide	Nucleotide sequence of Fv43D, a GH43 enzyme from <i>F. verticillioides</i>
28.	Amino acid	Protein sequence of Fv43D
29.	Nucleotide	Nucleotide sequence of Pf43B, a GH43 enzyme from <i>P. funiculosum</i>
30.	Amino acid	Protein sequence of Pf43B
31.	Nucleotide	Nucleotide sequence of Fv51A, a GH51 enzyme <i>F. verticillioides</i>
32.	Amino acid	Protein sequence of Fv51A
33.	Nucleotide	Nucleotide sequence of Cg51B, a GH51 enzyme from <i>C. globosum</i>
34.	Amino acid	Protein sequence of Cg51B
35.	Nucleotide	Nucleotide sequence of Fv43C, a GH43 enzyme from <i>F. verticillioides</i>
36.	Amino acid	Fv43C protein sequence
37.	Nucleotide	Nucleotide sequence of Fv30A, a GH30 enzyme from <i>F. verticillioides</i>
38.	Amino acid	Fv30A protein sequence
39.	Nucleotide	Nucleotide sequence of Fv43F, a GH43 enzyme from <i>F. verticillioides</i>
40.	Amino acid	Fv43F protein sequence
41.	Nucleotide	Nucleotide sequence of Xyn3, a GH10 xylanase from <i>T. reesei</i>
42.	Amino acid	Xyn3 protein sequence
43.	Amino acid	Protein sequence of Xyn2, a GH11 xylanase from <i>Trichoderma reesei</i>
44.	Amino acid	Protein sequence of Bxl1, a GH3 β -xylosidase from <i>Trichoderma reesei</i>
45.	Amino acid	Protein sequence of Bgl1, a GH3 β -glucosidase from <i>T. reesei</i>
46.	Nucleotide	Deduced cDNA of Pa51A.
47.	Nucleotide	Codon optimized cDNA for Pa51A.
48.	Nucleotide	Coding sequence of CBH1 signal sequence upstream of genomic DNA encoding mature Gz43A.
49.	Nucleotide	Coding sequence of CBH1 signal sequence upstream of genomic DNA encoding mature Fo43A.
50.	Nucleotide	Nucleotide sequence of CBH1 signal sequence upstream of codon optimized DNA encoding Pf51A
51.	Nucleotide	Nucleotide sequence of Eg4, an endoglucanase from <i>Trichoderma reesei</i>

FIG. 1B

No.	NT or AA	Name
52.	Amino acid	Protein sequence of Eg4
53.	Nucleotide	Nucleotide sequence of Pa3D, a GH3 β -glucosidase from <i>P. anserina</i>
54.	Amino acid	Protein sequence of Pa3D
55.	Nucleotide <i>verticillioides</i>	Nucleotide sequence of Fv3G, a GH3 β -glucosidase from <i>F.</i>
56.	Amino acid	Protein sequence of Fv3G
57.	Nucleotide <i>verticillioides</i>	Nucleotide sequence of Fv3D, a GH3 β -glucosidase from <i>F.</i>
58.	Amino acid	Protein sequence of Fv3D
59.	Nucleotide <i>verticillioides</i>	Nucleotide sequence of Fv3C, a GH3 β -glucosidase from <i>F.</i>
60.	Amino acid	Protein sequence of Fv3C
61.	Nucleotide	Nucleotide sequence of Tr3A, a GH3 β -glucosidase from <i>T. reesei</i>
62.	Amino acid	Protein sequence of Tr3A
63.	Nucleotide	Nucleotide sequence of Tr3B, a GH3 β -glucosidase from <i>T. reesei</i>
64.	Amino acid	Protein sequence of Tr3B
65.	Nucleotide	Nucleotide sequence of Te3A, a GH3 β -glucosidase from <i>Talaromyces emersonii</i> , codon-optimized for expression in <i>T. reesei</i>
66.	Amino acid	Protein sequence of Te3A
67.	Nucleotide <i>niger</i>	Nucleotide sequence of An3A, a GH3 β -glucosidase from <i>A.</i>
68.	Amino acid	Protein sequence of An3A
69.	Nucleotide <i>oxysporum</i>	Nucleotide sequence of Fo3A, a GH3 β -glucosidase from <i>F.</i>
70.	Amino acid	Protein sequence of Fo3A
71.	Nucleotide <i>zeae</i>	Nucleotide sequence of Gz3A, a GH3 β -glucosidase from <i>G.</i>
72.	Amino acid	Protein sequence of Gz3A
73.	Nucleotide <i>haematococca</i>	Nucleotide sequence of Nh3A, a GH3 β -glucosidase from <i>N.</i>
74.	Amino acid	Protein sequence of Nh3A
75.	Nucleotide <i>dahliae</i>	Nucleotide sequence of Vd3A, a GH3 β -glucosidase from <i>V.</i>
76.	Amino acid	Protein sequence of Vd3A

FIG. 1C

No.	NT or AA	Name
77.	Nucleotide	Nucleotide sequence of Pa3G, a GH3 β -glucosidase from <i>P. anserina</i>
78.	Amino acid	Protein sequence of Pa3G
79.	Amino acid	Protein sequence of Tn3B, a GH3 β -glucosidase from <i>T. neapolitana</i>
80.	Amino acid	Protein sequence of Pa3C, a GH3 enzyme from <i>P. anserina</i>
81.	Nucleotide	Nucleotide sequence of Pa3C, from <i>Podospira anserina</i>
82.	Nucleotide	Nucleotide sequence of Fv3C/ <i>T. reesei</i> Bgl3 fusion/chimera
83.	Nucleotide	Nucleotide sequence of Fv3C/Te3A/ <i>T. reesei</i> Bgl3 fusion chimera
84.	Amino acid	Protein sequence motif 1 of GH61 family endoglucanases
85.	Amino acid	Protein sequence motif 2 of GH61 family endoglucanases
86.	Amino acid	Protein sequence motif 3 of GH61 family endoglucanases
87.	Amino acid	Protein sequence motif 4 of GH61 family endoglucanases
88.	Amino acid	Protein sequence motif 5 of GH61 family endoglucanases
89.	Amino acid	Protein sequence motif 6 of GH61 family endoglucanases
90.	Amino acid	Protein sequence motif 7 of GH61 family endoglucanases
91.	Amino acid	Protein sequence motif 8 of GH61 family endoglucanases
135.	Amino acid	Protein sequence of the Fv3C/Te3A/Bgl3 (FAB) chimera
159.	Amino acid	Protein sequence of the Fv3C/Bgl3 (FB) chimera
162.	Nucleotide	Nucleotide sequence of <i>T. reesei</i> Xyn2
163.	Nucleotide	Nucleotide sequence of <i>T. reesei</i> Bxl1

FIG. 1D

Enzyme	Tn3B	Fv3G	Fv3D	Tr3A	Pa3D	Te3A	An3A	Tr3B	Nh3A	Gz3A	Fv3C	Fo3A	Pa3G	Vd3A
Substrate interaction														
	D58	D101	D111	D92	D87	D92	D92	D99	D106	D106	D119	D119	D101	D107
	R64	R107	R117	R98	R93	R98	R98	R105	R112	R112	R125	R125	R107	R113
	L116	L150	L160	L141	L136	L141	L141	L148	L155	L155	L168	L168	L150	L156
	R130	R165	R175	R156	R151	R156	R156	R163	R170	R170	R183	R183	R165	R171
	K163	K198	K208	K189	K184	K189	K189	K196	K203	K203	K216	K216	K198	K204
	H164	H199	H209	H190	H185	H190	H190	H197	H204	H204	H217	H217	K199	H205
	R174	R209	R219	R200	R195	R200	R200	R207	R214	R214	R227	R227	R209	R215
	M207	M237	M266	M232	M227	M242	M245	M252	M259	M259	M272	M272	M254	M260
	Y210	Y240	Y269	Y235	Y230	Y245	Y248	Y255	Y262	Y262	Y275	Y275	Y257	Y263
Nucleophile	D242	D272	D301	D267	D262	D277	D277	D287	D294	D294	D307	D307	D289	D295
Substrate interaction														
	W243	W273	W302	W268	W263	W278	W278	W288	W295	W295	W308	W308	W290	W296
	S370	S455	S472	S415	S406	S447	S451	S457	S464	S464	S477	S477	S458	S465
Acid/Base	E458	E509	E534	E472	E463	E505	E509	E516	E523	E523	E536	E536	E517	E524

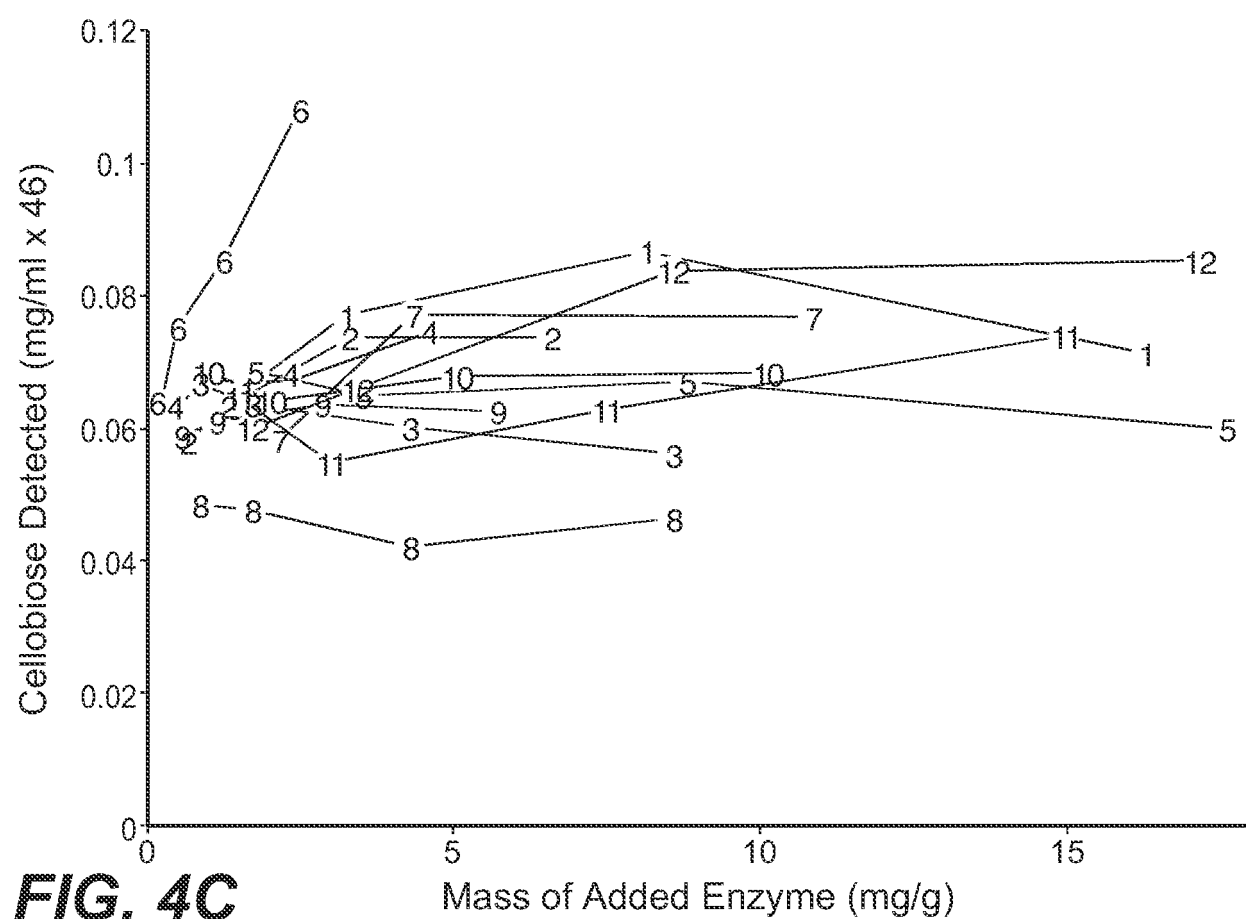
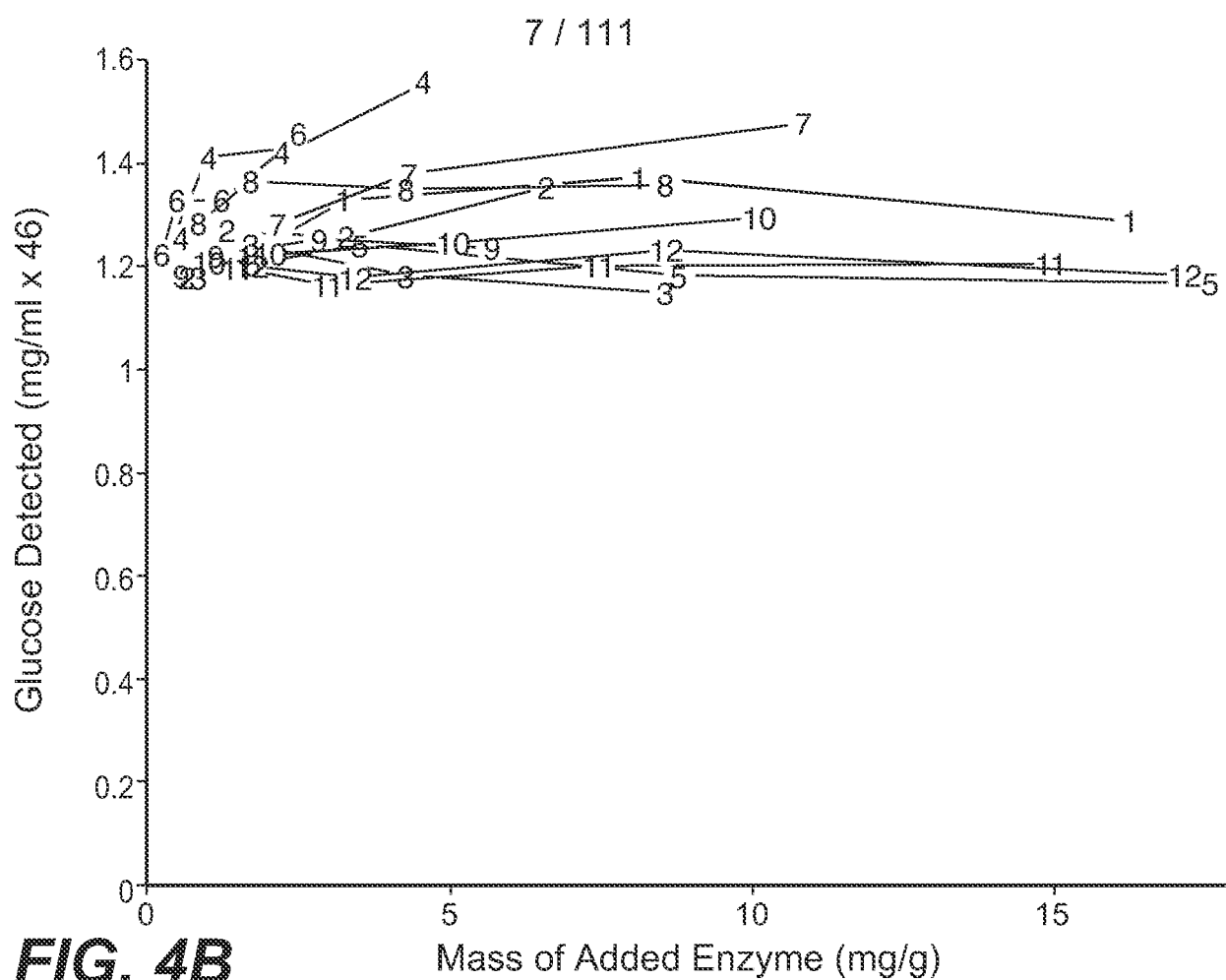
FIG. 2

Protein composition of <i>T.reesei</i> Integrated strain H3A	
Protein	% of Total Area
Fv3A	9.6
Fv51A+Fv43D	14.8
Xyn 3	12.6
Bgl 1	7.5
CBH1	36.4
EGLs	5.6
CBH2	9.5
Other	4.0

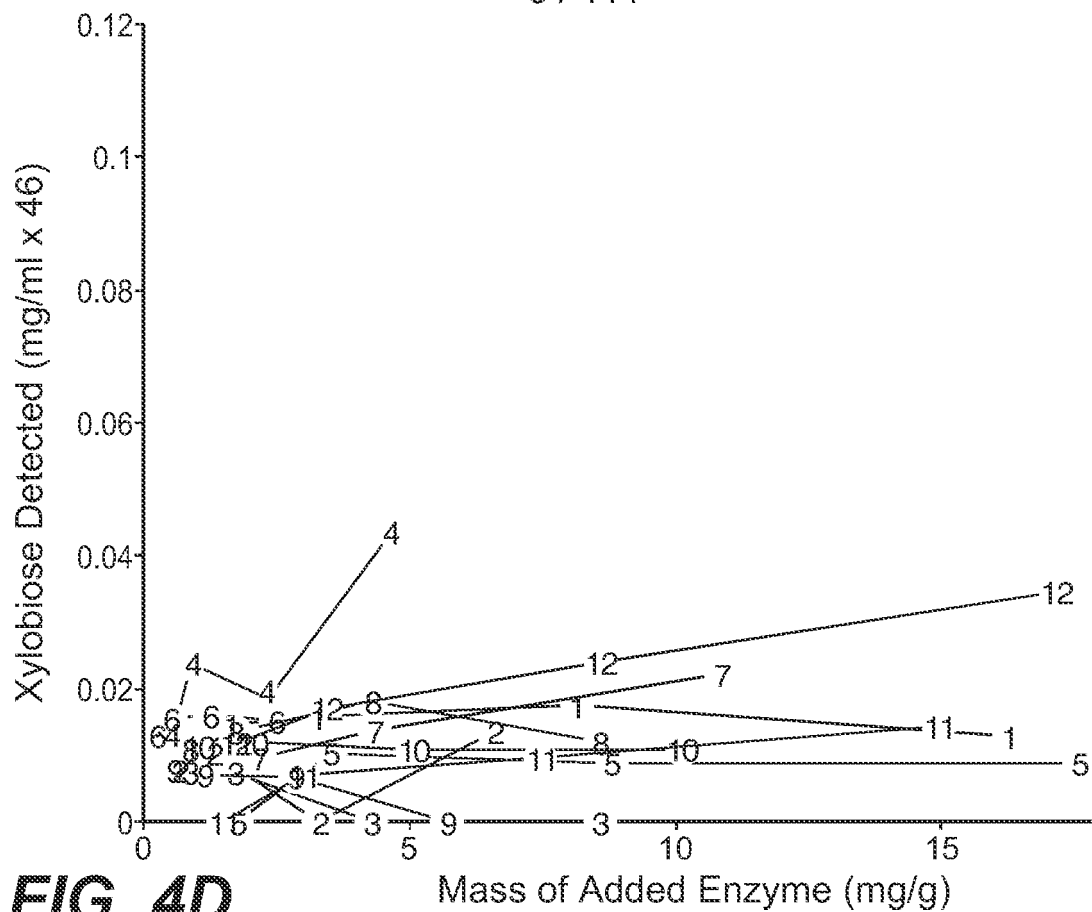
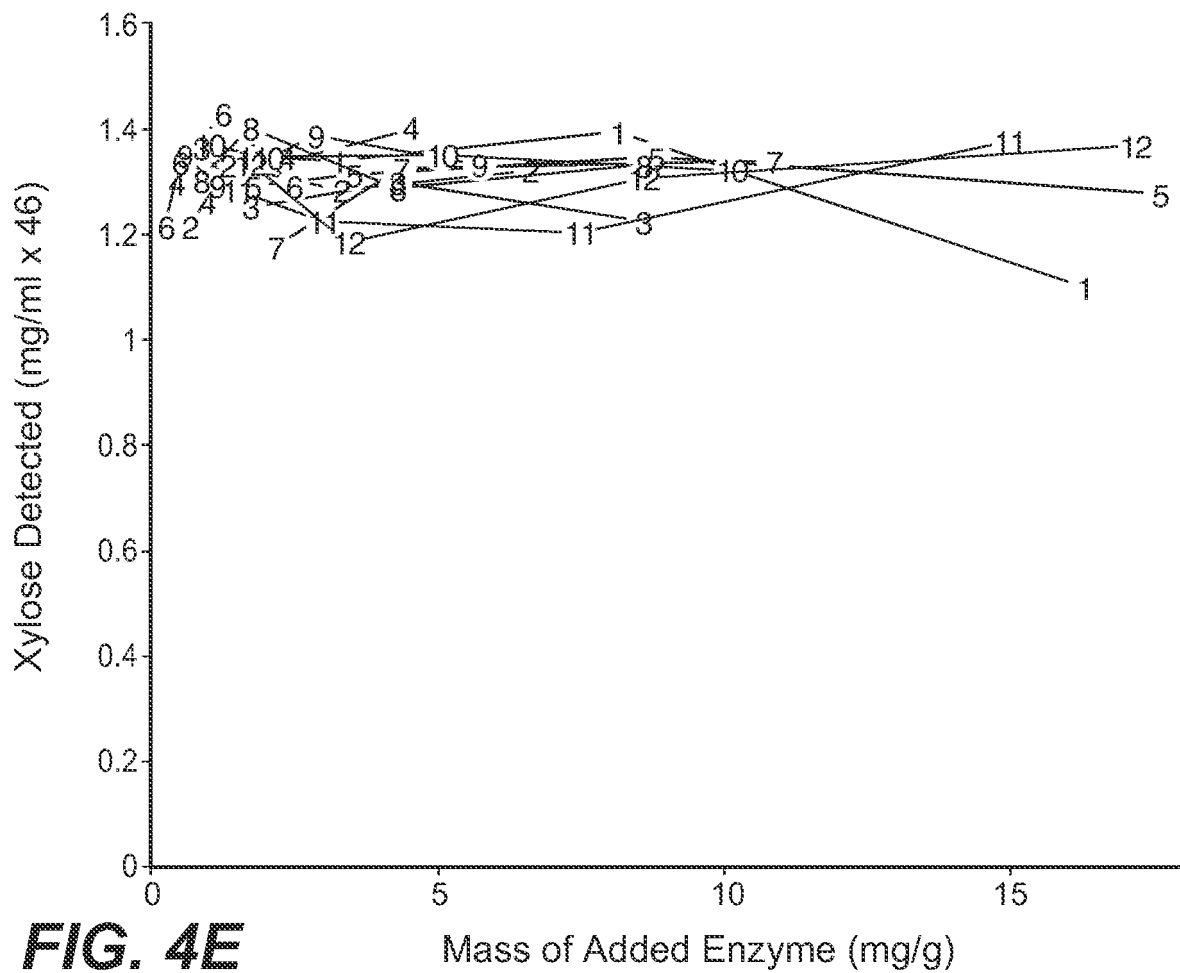
FIG. 3

Proteins added to <i>T. reesei</i> integrated strain H3A		
	Protein	Stock Protein Concentration (mg/ml)
1	Purified <i>T. reesei</i> CBH1	7.4
2	Purified <i>T. reesei</i> CBH2	3.0
3	Purified <i>T. reesei</i> EGI	3.9
4	Unpurified Fv3C	2.1
5	Water	
6	Purified <i>T. reesei</i> EG4	1.1
7	H3A UF concentrate	102.8
8	Purified <i>T. reesei</i> Bgl1	3.9
9	Purified <i>T. reesei</i> Xyn2	2.6
10	Purified <i>T. reesei</i> Xyn3	4.6
11	Purified <i>F. verticillioides</i> Fv43D	6.8
12	Purified <i>F. verticillioides</i> Fv51A	7.8

FIG. 4A



8 / 111

**FIG. 4D****FIG. 4E**

Enzyme	Concentration (mg/ml)	Cellobiase Activity		CNPG nM CNP/sec/mg Protein
		U/ml	U/mg	
<i>T. reesei</i> Bglu1, Purified	2.3	19.4	8.4	1242
Fv3C Shake Flask	2.4	42.7	18	1156
Fv3D Shake Flask	2.9	0.0	0.0	6221
Pa3C Shake Flask	1.9	0.0	0.0	2
<i>A. niger</i> Bglu1, Purified	2.4	244	102	168

FIG. 5A

Enzyme	Cellobiase activity relative to <i>T. reesei</i> Bgl1	CNPG activity relative to <i>T. reesei</i> Bgl1
<i>T. reesei</i> Bgl1, purified	1	1
Fv3C, purified	1.8	1
Fv3D, unpurified	0	5
Pa3C, unpurified	0	0
<i>A. niger</i> Bglu, purified	12.1	0.1
FAB, purified	1.3	1
FB, purified	2.4	1.3
<i>T. reesei</i> Bgl3, purified	5.6	1.5
Te3A, purified	0.7-1.4	4.2-7.7

FIG. 5B

Enzyme	w/w%
Xyn 3	45.0
Fv3A	15.0
Fv43D	5.0
Fv51A	35.0

FIG. 6

Enzyme Mix	Dose (mg protein /g cellulose) for Glucan Conversion:		
	70%	80%	90%
Accellerase 1500 + Multifect Xylanase	38	-	-
whole cellulase from <i>T. reesei</i> integrated strain (H3A)	21	28	36
75% whole cellulase from <i>T. reesei</i> integrated strain (H3A) / 25% Fv3C	12	15	19

FIG. 7

10 / 111

SEQ ID NO:1**Nucleotide sequence for Fv3A, a GH3 family enzyme from *Fusarium verticillioides***

atgctgctcaatcttcaggctcgctgccagcgctttgtcgctttctcttttaggtggattggctgaggctg
ctacgccatatacccttcggactgtaccaaaggacctttgagcaagaatggaatctgcgatacttcgtt
atctccagctaaaagagcggtgctctagttgctgctctgacgcccgaagagaaggtgggcaatctggctc
aggtaaaatataccccccccccataatcactattcggagattggagctgacttaacgcagcaatgcaactg
gtgcaccaagaatcggaacttccaaggtacaaactggtggaacgaagcccttcattggcctcgctggatctcc
agggtgctcgctttgcccgaactcctccctacgaacggccacatcatttcccatgcctcttctcatggcc
gctgctttcgacgatgatctgatccacgatatcggcaacgtcgctggcaccgaagcgcgctgcttcaacta
acggcggttggcgcgaggctgacttctggacacccaacgtcaacccttttaagatcctcgctggggctcg
tggctccgaaactccagggtgaagatgcccttcattgtcagccgggtatgctcgctatatacgctcaggggtctc
gaaggcgataaggagcaacgacgtattgttgctacctgcaagcactatgctggaaacgactttgaggact
ggggaggcttcacgcgtcacgactttgatgccaagattactcctcaggacttggctgagtactacgtcag
gcctttccaggagtgcacccgtgatgcaaaggttgggttccatcatgtgcgcctacaatgccgtgaacggc
attcccgcatgcgcaaacctcgatatctgcaggagacgatcctcagagggcactggaactggacgcgcgata
acaactggatcactagtgattgtggcgccatgcaggatatctggcagaatcacaagtatgtcaagaccaa
cgctgaagggtgccaggtagcttttgagaacggcatggattctagctgcgagtatactactaccagcgat
gtctccgattcgtacaagcaaggcctcttgactgagaagctcatggatcggttcgttgaagcgcttttcg
aagggttgttcatactggtttctttgacggtgccaaagcgcaatggaactcgctcagttttgaggatgt
caacaccaaggaagctcaggatcttgcactcagatctgctgtggagggtgctgttcttcttaagaatgac
ggcactttgcctctgaagctcaagaagaaggatagtgttgcaatgatcggttctggggccaacgatactt
ccaagctgcagggtgggttacagtggacgtgctccgttccctccacagcccgctttatgcagctgagaagct
tggctcttgacaccaacgtggcttgggggtccgacactgcagaacagctcatctcatgataactggaccacc
aatgctgttgcgtgcggcgaagaagtctgattacattctctactttgggtggctcttgacgcctctgctgctg
gcgaggacagagatcgtgagaaccttgactggcctgagagccagctgacccttcttcagaagctctctag
tctcggaagccactgggttgttatccagcttgggtgatcaagctcgatgacacccgctcttttgaagaacaag
aagattaacagtatctctttgggtcaattaccctgggtcaggatggcgccactgcagtcattggacctgctca
ctggacgaaagagtctgctggccgactaccctgcacgcaatatccagtaaatcactgagcagattgg
catgactgacatggacctcagacctaccaagtcgttgccaggggagaacttatcgctggtactcaactcca
gttcttccctacggctttggcctccactacaccaagttccaagccaagttcaagtcacaacaagttgacgt
ttgacatccagaagcttctcaagggtgacgtgctcaatactccgataacttgccgcgctgccccccatcca
agttagtgtcaagaacacccggccgcattacctccgactttgtctctctgggtctttatcaagagtgaagtt
ggacctaaagccttaccctctcaagacccttgccgcttatggctcgcttgcatgatgtcgcgcccttcacga
cgaaggatatctcactggagtggaacgttgataacatttgccgcgacggggagagaatggtgattttggttgt
ttatcctgggaacttacactctgttgctggatgagcctacgcaagccaagatccagggttacgctgactgga
aagaaggctattttgataagtggcctcaagaccocaagctctgcgtaa

FIG. 8A**SEQ ID NO:2****Protein sequence of Fv3A**

mlnlqlvaasalslsllqqlaeatpytlpdctkgplskngicdtslspakraaalvaaltpeekvgnlv
snATGAPRIGLPRYNWNEALHGLAGSPGGRFADTPPYDAATSFPMPLLMAAAFDDDLIHDIGNVVGTEA
RAFTNGGWRGVDFWTPNVNPFKDPRWGRGSETPGEDALHVSRYARYIVRGLEGDKQRRIVATCKHYAGN
DFEDWGGFTRHDFDAKITPQDLAEYYVRPFQECTRDAKVGSIMCAYNAVNGIPACANSYLQETILRGHWN
WTRDNNWITSDCGAMQDIWQNHKYVKTNAEQAQVAFENGMDssceytttsdvdsdykqglltekldmrsl
krlfeglvhtgffdgakaqwnslsfadvntkeaqdlalrsavegAVLLKNDGTLPLKLKKKDSVAMIGFW
ANDTSKLQGGYSGRAPFLHSPLYAAEKLGLDTNVAVWGPTLQNSSSHDNWTTNAVAAAKKSDYILYFGGLD
ASAAGEDRDRENLDWPESQLTLLQKLSSLGKPLVVIQLGDQVDDTALLKNKKINSILWVNYPGQDGGTAV
MDLLTGRKSPAGRLPVTQYPSKYTEQIGMTDMDLRPTKSLPGRTYRWYSTPVLPGFGLHYTKfqakfks
nkltfdiqkllkgcsaqysdtcalppiqvsvkntgritsdfvslvfiksevqpkpyplktlaaygrlhdv
apsstkdlslewtldniarrgengdlvvypgtytllldeptqakiqvltltgkkailldkwpqdpksa

FIG. 8B

11 / 111

SEQ ID NO:3**Nucleotide sequence for Pf43A, a GH43 family enzyme from *Penicillium funiculosum***

atgcttcagcgatttgcttatatattttaccactggctctattgagtggttgagtgaaagccgacaaccct
ttgtgcagagcatctacacogctgatccggcaccgatgggtatacaatgacogcgctttatgtcttcattgga
ccatgacaacacccggagctacctactacaacatgacagactggcatctgttctcgtcagcagatatggcg
aattggcaagatcatggcattccaatgagcctggccaatttcacctggggccaacgcgaatgcgtggggccc
cgcaagtcattccctcgcaacggccaattctacttttatgtctcctgtccgacacaacgatggttctatggc
tatcgggtgtgggagtgagcagcaccatcacagggtccataccatgatgctatcggcaaaccgctagtagag
aacaacgagattgatccacccgtgttcacgcagatgacgggtcaggcataacctgtactggggaaatccag
acctgtgggtacgtcaaattgaaccaagatatgatatcgtacagcgggagccctactcagattccactcac
cacggctggatttggtactcgaacgggcaatgtcaacggccgaccacttttgaagaagctccatgggta
tacaacgcgaacggcatctactatatcgccatgacagccgattggtgttctgaggatattcgctactcca
cggaaccagtgccactgggtccgtggacttatcgaggcgtcatcatgcgcaccaaggtagcagcttcac
caatcacgaggggtattatcgacttccagaacaactcctactttttctatcacaacggcgctcttcccggc
ggaggcggctaccaacgatctgtatgtgtggagcaattcaaatacaatgcagatggaaccattccgacga
tcgaaatgaccaccgcgggtccagctcaaattgggactctcaacccttacgtgcgcacaggaagccgaaac
ggcggcatgggtcttcaggcatcactacggaggtttgtagcgaaggcgggaattgacgtcgggtttatcaac
aatggcgattacatcaaagttaaaggcgtagctttcggttcaggagcccattctttctcagcgcgggttg
cttctgcaaatagcggcgccactattgcaatacacctcggaagcacaactggtagcgtcgtgggcacttg
tactgtccccagcactggcggttggcagacttggaactaccgttacctgttctgtcagtggcgcactctggg
accaggatgtgtattttgttttcggtggttagcggaacaggataacctgttcaactttgattattggcagt
tcgcataa

FIG. 9A**SEQ ID NO:4****Protein sequence of Pf43A**

mlqrfayilplallsvqvkadnpfvqsiytadpapmvynrvyvmhdhntgatyynmtdwhlfssadma
nwqdhgipmslanftwananawapqviprngqfyfyapvrhndgsgmaigvgvsstitgpyhdaigkplve
nneidptvfiddgqaylywgnpdlwyvklndqmisysgsptqiplttagfgtrtgnagrpttfeeapwv
ykrngiyyiayaadccsedirystgtsatgpwtyrgvimptqgssftnhegiidfqnnsyffyhngalpg
gggyqrsvcveqfkynadgtiptiemttagpaqigtlnpyvrqEAETAAWSSGITTEVCSEGGIDVGFIN
NGDYIKVKGVAFGSGAHSFSARVASANSGGTIAIHLGSTTGTLVGTCTVPSTGGWQTWTTVTCVSGASG
TQDVYFVFGSGGTGYLFNFDYWQFa

FIG. 9B

12 / 111

SEQ ID NO:5**Nucleotide sequence for Fv43E, a GH43 family enzyme from *Fusarium verticillioides***

atgaaggtataactggctcgtggcgtgggccacttcttttgacgcccggcaactggctggcttgattggacacc
gtcgcgccaccaccttcaacaatcctatcatctactcagactttccagataacgatgtattcctcggtcc
agataactactactacttctctgcttccaacttccacttcagcccaggagcaccgcgttttgaagtctaaa
gatctgctaaactgggatctcatcggccattcaattccccgcctgaactttggcgacgggctatgatcttc
ctcctggctcacgttattaccgtggaggtacttgggcatcatccctcagatacagaaagagcaatggaca
gtggtaactggatcggctgcatcaacttctggcagacctgggtatacaactgcctcatcgccggaagggtcca
tggtaacaacaagggaaacttcgggtgataacaattgctactacgacaatggcatactgatcgaatgacgatg
ataccatgtatgtcgtatacgggttcgggtgaggtcaaagtatctcaactatctcaggacggattcagcca
gggtcaaactctcaggtagttttcaagaacactgatattgggggtccaagacttggagggtaaccgcgatgtac
aagatcaacgggctctactatatacctaaacgatagcccaagtggcagtcagacctggatttgaagtcga
aatcaccctggggcccttatgagtctaaaggtcctcgccgacaaagtcaccccgccctatctctgggtggtaa
ctcgcgcgatcagggtagtctcataaagactcccaatgggtggctggtaacttcatgtcattcacttgggcc
tactctgcccggcgtcttccgggttcttgcaccgattacgtggggtagcgatggtttccccattcttgtca
aggggtgctaattggcggtatggggatcatcttaccacaacacttccctggcacggatgggtgtgacaaagaattg
gacaaggactgataccttccgcggaacctcacttgctccgtcctgggagtggaaccataatccggacgtc
aactccttcaactgtcaacaacggcctgactctccgcactgctagcattacgaaggatatttaccaggcga
ggaacacgctatctcaccgaactcatggtgatcatccaacaggaatagtgaagattgatttctctccgat
gaaggacggcgaccggggccgggctttcagcgtttcgagaccaaagtgcatacatcggtattcatcgagat
aacggaaagttcacaaatcgctacgaagcatgggatgaatatggatgagtggaacggaacaacaacagacc
tgggacaaataaaaagccacagctaattgtgccttctggaaggaccaagatctggctgagacttcaacttga
taccaaccagcaggaactggcaacactatcttttcttacagttgggatggagtcaagtatgaaacactg
gggtcccaacttcaaactgtacaatggttgggcattctttattgcttaccgattcggcatcttcaacttcg
ccgagacggctttaggaggtcgcatacaggttgagttctttcacagctgcatag

FIG. 10A**SEQ ID NO:6****Protein sequence of Fv43E**

mkvywlvawatsltpalaglighrrattfnnpiiysdfpdndvflgpdnyyyfsasnfhfspgapvlksk
dllnwdlighsiprlnfgdgydlppgsryyrggtwasslryrksngqwywigcinfwqtwvytasspepp
wynkgnfgdnncyydngiliddddtmyvvygsgevkvsqlsqdgfsqvksqvfvkntdigvqdlegnrm
kinglyyilndspsgsqtwiwxskspwgpyskvladkvtppisggnspqhqsliktpnggwyfmsftwa
ypagrlpvlapitwgsdgfpilvkganggwssyptlpgtgdvtnkwttrtdtfrgtslapswewnhnpdv
nsftvnngltlrtasitkdiyqarntlshrthqdhptgivkidfspmkgddraglsafrdqsayigihrd
ngkftiatkhgmmndewngttdlgqikatanvpsgrtkiwlrlqltdtnpagtgntifsyswdgvkyetl
gpnfklyngwaffiayrfgifnfaetalggsikvesftaa

FIG. 10B

SEQ ID NO:7**Nucleotide sequence for Fv39A, a GH39 family enzyme from *Fusarium verticillioides***

atgcactacgctaccctcaccacttttggtgctggctctgaaccaccaacgctcgctgcacagcaaggcacag
caactgtcgacctctccaaaaatcatggaccggcggaaggcccttggttcaggcttcatatacggctggcc
tgacaacggaacaagcgtcgacacctccataaccagatttcttggttaactgacatcaaattcaactcaaac
cgcgggcggtggcgcccaaatcccatcactgggttggggccagaggtggctatgaaggatacctcggccgct
tcaactcaaccttatccaaactatcgcaccacgcgcaagtataacgctgactttatcttggtgcctcatga
cctctgggggtgcggatggcgggcaggggttcaaactccccgtttcctggcgacaatggcaattggactgag
atggagttattctggaatcagcttgtgtctgacttgaaggctcataatatgctggaaggctcttggtgattg
atgtttggaatgagcctgatattgatatcttttgggatcgccgctggctgcagtttcttgagtattacaa
tcgcgcgacccaaactacttcgggtgagtctactactgatccatacgtatttacagtgaagctgactggctga
attagaaaaacacttccaaaaactcttctcagtgggccagccatggcacattctccattctgtccgatg
ataaatggcatacctggcttcaatcagtagcgggtaacaagacagtcctgatatttactcctggcatca
gattggcgcttgggaacgtgagccggacagcactatccccgactttaccaccttgccgggcgcaatatggc
gttcccagagaagccaattgacgtcaatgagtaacgtgcacgcgatgagcaaaatccagccaactccgtct
actacctctctcaactagagcgtcataaccttagaggctcttcgcgcaaaactggggtagcggatctgacct
ccacaactggatgggcaacttgatttacagcactaccggtacctcggaggggacttactaccctaattggt
gaatggcaggcttacaagtactatgcggccatggcagggcagagacttgtgaccaaagcatcgteggact
tgaagtttgatgtctttgccactaagcaaggccgtaagattaagattatagccggcacgaggaccgttca
agcaaagtataacatcaaaatcagcggtttggaagtagcaggacttcctaagatgggtacggtaaaggctc
cggacttatcggttcgactgggctgggcccgaatggaaagggttgacgggcctgttgatttgggggagaaga
agtatacttattcggccaatacggtgagcagccctctacttga

FIG. 11A**SEQ ID NO:8****Protein sequence of Fv39A**

mhyatllttlvlalttnvaaqqgtatvdlsknhgpakalgsgfiygwpdngtsvdtstipdfvltdikfnsn
rgggagipslgwarggyegylgrfnstlsnyrttrkynadfillphdlwgadggggsnspfpdngnnte
melfwnqlvsdlkahnmlleglvidvwnepdidifwdrpwsqfleyynratkllrktltpktllsgpamahs
pilsddkwhtwlqsvagnktvpdiyswhqigawerepdstipdfttlraqygvpekpidevneyaardeqn
pansvyyllsqlerhnlrglranwgsgsdlnhwmgnliysttgtsegtyypngewqaykyyaamagqrlvt
kassdlkfdvfatkqgrkikiiagtrtvqakynikisglevaglpkmgvtkvrtyrfdwagpngkvdgpn
dlgekkytysantvsspst

FIG. 11B

SEQ ID NO:9**Nucleotide sequence for Fv43A, a GH43 family enzyme from *Fusarium verticillioides***

atgtggctgacctccccattgctgttcgccagcaccctcctgggcctcactggcggttgccttagcagaca
accccatcggtccaagacatctacaccgcagaccagcaccaatgggtctacaatggccggtctacctctt
cacaggccatgacaacgacggctctaccgacttcaacatgacagactggcggtctcttctcgtcagcagac
atgggtcaactggcagcaccatgggtgtcccatgagcttaaagaccttcagctgggccaacagcagagcct
gggctgggtcaagtcgttgccgaaacggaaagttttacttctatgttcctgtccgtaatgccaagacggg
tggaatggctattgggtgtcgggtgttagtaccacatccttgggccctacactgatgcccttggaaagcca
ttgggtcgagaacaatgagatcgacccaactgtctacatcgacactgatggccaggcctatctctactggg
gcaacctgtgattgtaactacgtcaagctcaaccaagacatgctctcctacagtggtagcatcaacaaagt
atcgctcacaacagctggattcggcagccgcgccgaacaacgcgcagcgctcctactactttcgaggaagga
ccgtgggtgttacaagcgtggaaatctctactacatgatctacgcagccaactgctgttcgaggacattc
gctactcaactggaccagcgccactggaccttggacttaccgcgggtgtcgtgatgaacaaggcgggtcg
aagcttcaccaaccatcctggcatcatcgactttgagaacaactcgtacttcttttaccacaatggcgct
cttgatggaggtagcgggtatactcgggtctgtgggtgtcgagagcttcaagtatggttcggacgggtctga
tccccgagatcaagatgactacgcaaggcccagcgcagctcaagtctctgaacccatatgtcaagcagga
ggccgagactatcgctctggtctgaggggtatcgagactgaggtctgcagcgaaggtgggtctcaacgttgct
ttcatcgacaatgggtgactacatcaagggtcaagggtgagtcgactttggcagcaccgggtgcaaagacgttca
gcgcccgtgttgcttccaacagcagcggaggcaagattgagcttcgacttggttagcaagaccggtaagtt
ggttggtaacctgcacggtaacgactacgggaaactggcagacttataagactgtggattgccccgtcagt
gggtgctactgggtacgagcgatctattctttgtcttcacgggctctgggtctggtctctctgttcaacttca
actggtggcagtttagctaa

FIG. 12A**SEQ ID NO:10****Protein sequence of Fv43A**

mwltspllfastllqltgvaladnpivqdiytadpapmvyngrvylftghdndgstdfnmtdwrlfssad
mvnwqhhgvpmslktfswansrawagqvvarngkfyfyvpvrnaktggmaigvgvstnilgpytdalgkp
lvenneidptvyidtdgqaylywgnpglyyvklngdmlsysgsinkvslttagfgsrpnnaqrpttfeeg
pwlykrgnlyymiyaanccsedirystgpsatgpwtyrgvmmnkagrsftnhpgiidfennsyffyhnga
ldggsgytrsvavesfkygsdgl~~ipeikmttgpaqlks~~INPYVKQEAETIAWSEGIETEVCSEGGLNVA
FIDNGDYIKVKGVDVGSTGAKTFSARVASNSSGGKIELRLGSKTGKLVGTCTVTTTGNWQTYKTVDCPVS
GATGTSDLFFVFTGSGSGSLFNFNWWQF's

FIG. 12B

SEQ ID NO:11**Nucleotide sequence for Fv43B, a GH43 family enzyme from *Fusarium verticillioides***

atgogcttctcttggctattgtgcccccttctagcgatgggaagtgcctcttctgaaacgaagacgggatg
tttcgacatacaccaaccctgtccttccaggatggcactcggatccatcgtgtatccagaaagatggcct
ctttctctgogctcacttcaacattcatctccttccagggtcttcccgtctatgcctcaagggatctagtc
aactggcgctctcatcagccatgtctggaaccgcgagaaacagttgcctggcattagctggaagacggcag
gacagcaacagggaatgtatgcaccaaccattcgataccacaagggaacatactacgtcatctgccaata
cctgggcggttgagatattattggtgtcatcttcaagaccaccaatccgtgggacgagagtagctggagt
gacctgtttaccttcaagccaaatcacatcgaccccgatctgttctgggatgatgacggaaaggtttatt
gtgctacccatggcatcactctgcaggagattgatttggaaactggagagcttagccccggagcttaatat
ctggaacggcacaggaggtgtatggcctgaggggtcccatatctacaagcgcgacgggttactactatctc
atgattgcgaggggtggaactgccgaagaccacgctatcacaaatcgctcgggcccgaagatcacccggcc
cctatgaagcctacaataacaaccaatcttgaccaaccgcgggacatctgagtacttccagactgtcgg
tcacgggtgatctgttccaagataccaagggcaactggtgggggtctttgtcttgctactcgcatcacagca
cagggagttttacccatgggcccgtgaagctgttttgttcaatggcacatggaacaagggcggaatggccca
agttgcaaccagtagcagggtcgcatgcctggaaacctctccaaagccgacgcgaaacggttcccggaga
tgggcccttcaacgctgacccagacaactacaactgaagaagactaagaagatccctcctcactttgtg
caccatagagtcccaagagacgggtgccttctctttgtcttccaaggggtctgcacatcgtgcctagtcgaa
acaacgttaccggtagtgtgttgccaggagatgagattgagctatcaggacagcgaggtctagctttcat
cggaacgcgcgcaaaactcacactctgttcaaatatagtgttgatategacttcaagccccagtcgatgat
caggaagctggaatcaccgttttccgcacgcagttcgaccatatcgatcttggcattgttcgtcttcta
caaaccaaggcgagcaacaagaaatctaagcttgcttccgattccggggccacaggagctcagaatgttcc
tgcaccgaaggtagtaccgggtccccgatggctgggagaagggcgtaatcagtctacatatcgaggcagcc
aacgcgacgcactacaaccttgagcttcgagccacagaggcaagactctcgacatcgcgacagcatcag
caagtcttgtgagtgagggcacgggttcatttgttggtagtttgcctggaccttatgctacctgcaacgg
caaaggatctggagtggaatgtcccaagggaggtgatgtctatgtgaccaaatggacttataagcccggtg
gcacaagagattgatcatggtgtttttgtgaaatcagaattgtag

FIG. 13A**SEQ ID NO:12****Protein sequence of Fv43B**

mrfswwllcp1lamqsalpetktdvstytnpvlpgwhsdpsciqkdglflcvststfisfpglpvyasrdlv
nwrlshvwnrekqlpgiswktagqqqgmyaptiryhkgtyyviceylgvvgdiigvifktnpwwdessws
dpvtfknhidpdlfwdddgvycathgitlqeidlletgelspelniwngtggvwpegphiykrddgyyl
miaeggtaedhaitiararkitgpyeaynnnpiltnrgtseyfqtvgghgdlfqdtkgnwwglclatrita
qgvspmgreavlfngtwnkgewpklqpvrgrmpgnllpkptrnvpdgpfnadpndynlkktkkipphfv
hhrvprdgafslsskgllhivpsrnnvtgsvlpgdeielsgqrglafigrqrqthtlfkysvdidfkpsdd
qeagitvfrtqfdhidlgivrlptnqgsnkksklafrfratgaqnvapkvvpvdpdgwekgvislhieaa
nathynlgasshrkgtldiatasaslvsggtgsfvgsllgpyatcngksgsvecpkggdvvy
tqwtlykpvaqeidhgvfvksel

FIG. 13B

SEQ ID NO:13**Nucleotide sequence for Pa51A, a GH51 family enzyme from *Podospira anserina***

atgatccacotcaagccagccctcgcggcggttggtggcgctgtcgacgcaatgtgtggctattgatttgt
ttgtcaagtcttcgggggggaataagacgactgatatcatgtatgggtcttatgcaagaggtatgtgtttt
gcgagatctccctttttgttttttgcgcactgctgacatggagaactgcaaacaggatatcaacaactccggc
gaaggcgccatctacgccgagctaattctccaaccgcgcgttccaagggagtgagaagttccctccaacc
tcgacaactggagccccgctcgggtggcgctacccttacccttcagaagcttgccaagcccccttctctgc
gttgcccttactccgtcaatgttgccaacccccaaaggaggggcaaggggcaagggaacaccaagggggaag
aaggttggttggttgccaatgctgggttttgggggtatggatgtcaagaggcagaagtacactggtagcttcc
acgttactgggtgagtacaagggtgactttgaggttagcttgccgcagcgcgattaccggggagacctttgg
caagaaggtggtgaagggtgggagtaagaaggggaagtggaccgagaaggagtttgagttggtgcctttc
aaggatgcgccccaacagcaacaacacctttgttggtgcagtgggatgcccaggtatgtgcttctttgatat
tggtgagatagaagttgggttgacatgatgtggtgcagggcgcaaaggacggatctttggatctcaact
tgatcagcttggtccctccgacattcaagggaaggaagaatgggctgagaattgatcttgccgagacgat
ggttgagctcaagccggtaagtcctctctagtcagaaaagtagagcctttgttaacgcttgacagacctt
cttgccgttccccgggtggcaacatgctcaggggtaacaccttggtggaagtggtagagacc
attggccctctgaaggatcgcccggtatggctgggtgtctgggagtagaccgcaaacccttggttggtgc
tggtcgagtacatggagtggtggcgatgacatgaacttgagcccagtagtgatcccatcttctggagtgc
acttctcttgctaacgtatccacagttgtcgggtgtcttcgctggtcttgccctcgatggctcgttcgttc
ccgaatccgagatgggtatgggtcatccaacaggctctcgacgaaatcgagttcctcaactggcgatgctaa
gaccaccaaattgggtgcccgtccgcgcgaagcttggtcaccccaagccttggaagggtcaagtgggttgag
atcggtaaacgaggattgggttgccggacgccctgctggcttcgagtcgtacatcaactaccgcttcccca
tgatgatgaaggccttcaacgaaaagtaccccgacatcaagatcatcgccctcgccctccatcttcgacaa
catgacaatccccgcgggtgctgccggtgatccaccgccgtacctgactcccgatgagttcgttgagcga
ttcgccaagttcgataaacttgagcaaggataacgtgacgctcatcgccgaggtgctgcgtcgacgcaccta
acgggtggtatogcttgggaggggagatctcatgccttgcccttggtggggcggcagtggtgctgaggctat
cttcttgatcagcactgagagaaaacgggtgacaagatcatcggtgctacttacgcgcctggtcttcgcagc
ttggaccgctggcaatggagcatgacctgggtgcagcatgcgcgcgacccggccctcaccactcgctcga
ccagttggtatgtctggagaatcctcgccaccacatcatccgtgagacgctcccggtcgatgccccggc
cggcaagccccaaactttgacctctgttctacgttgccggaaagagcgagagtggaaccgggtatcttcaag
gctgcgctctacaactcgactgaatcgatcccggtgtcgttgaaagtttgatgggtctcaacgaggggagcgg
ttgccaacttgacgggtgcttactggggccggaggatccgtatggatacaacgaccccttactgggtatcaa
tgttgtcaaggagaagaccaccttcatcaaggccggaaagggcggaagttcaccttcaccctgcccgggc
ttgagtggtgctgtgttggtgagacggccgacgcgggtcaaggggtggcaagggaagggaagggaaggga
agggtaaactga

FIG. 14A

SEQ ID NO:14**Protein sequence of Pa51A**

mihlkpalaallalstocvaidlfvkssggknkttdimyglmhedinnsgdggiaaelisnrafqgsekfp
snldnwspvggatltlqklakplssalpysvnnvanpkegkkgkdktkgkkvglanagfwgmdvkrqkytg
sfhvtgeykgdfevslrsaitgetfkgkvkvggskkgkwtekefelvpfkdapnsnntfvvqwdaeagkd
gsldlnlislfpptfkgrknglridlaqtmvelkptflrfpggnmlegntldtwkwyetigplkdrpgm
agvweyqqtllglglveymewaddmnlepivgvfaglalldgsfvpesemgwviqqaldeiefltgdahtk
wgavraklghpkpwkvkwveignedwlagrpagfesynyrfpmmmkafnekypdikiiaspsifdnmti
pagaagdhhpyltpdefverfakfdnlskdnvtligeaasthpnnggiawegdlmplpwggsvaeaifli
sterngdkiigatyapglrsldrwqwsmtwvqhaadpalttrstswyvrilahhiiretlpvdapagkp
nfdplfyvagksesgtgifkaavynstesipvslkfdglnegavanltvltgpedpygyndpftginvk
ekttfikagkggkftftlpglsavavletadavkggkkgkkgkkgkn

FIG. 14B**SEQ ID NO:15****Nucleotide sequence for Gz43A, a GH43 family enzyme from *Gibberella zeae***

atgaagtccaagttgttattcccactcctctcttttcgttgggtcaaagtcttgccaccaacgacgactgtc
ctctcatcactagtagatggactgcggtaccttcgggtcatgtctttaacgacaccttggtggtctatccc
gtctcatgacatcgatgctggtttgagaatgatcctgatggaggccagtagcccatgagagattaccat
gtctactctatcgacaagatctacggttcctgcggtcgatcacggtacggccctgtcagtgaggatg
tcccctgggcctctcgacagatgtgggtcctgacgctgccacaagaacggcaataactacctatactt
ccotgccaagacaaggatgatattcttcagaatcggcggttgcgtgtctcaccacccccggcggaaccattc
gtccccgacaagagttggatccctcacaactttcagcatcgaccccgccagtttcgtcgatgatgatgaca
gagcctacttggcatggggtggtatcatgggtggccagcttcaacgatggcaggataagaacaagtacaa

FIG. 15A

18 / 111

SEQ ID NO:16

Protein sequence of Gz43A

mksklfpllsfvvggslatnddcplitsrwtadpsahvfndtlwlypshdidagfendpdggqyamrdyh
vysidkiygslpvdhgtalsvedvpwasrqmwapdaahkngkyylyfpakdkddifrigvavsptpggpf
vpdkswiphtfsidpasfvddddraylawggimggqlqrwqdknkynesgtepgngtaalspqiaklskd
mhtlaekprdmliildpktgkpllsededrrffegpwihkrnkiiyltystgtthylvyatsktpygypty
qgrilepvdgwtthssivkyqgqwwlfyhdaktsgkdylrqvkakkiwydskgkiltkkp

FIG. 15B

SEQ ID NO:17

Nucleotide sequence for Fo43A, a GH43 family enzyme from *Fusarium oxysporum*

atgcagctcaagttttctgtcttcagcattgctgtttctctctgaccagcaaatgcgctgcgcaagacacta
atgacattccctccctgatcaccgacotctggctcgcagatccctcggetcatgttttcgaaggcaagct
ctgggtttaccatctcagcagatcgaagccaatgttgtaacggcacaggaggcgctcaatacgccatg
agggattaccatacctactccatgaagagcatctatggtaaagatcccggttgtegaccaaggcgctcgctc
tctcagtcgatgacgttccttgggcgaagcagcaaatgtgggctcctgacgcagctcataagaacggcaa
atattatctgtacttccccgcccaaggacaaggatgagatcttcagaattggagttgctgtctccaacaag
cccagcggtcctttcaaggccgacaagagctggatccctggcaagctacagtatcgatccctgctagctacg
tcgacactgataacgaggcctacctcatctggggcggtatctggggcgggccagctccaagcctggcagga
taaaaagaactttaacgagtcgtggattggagacaaggctgctcctaacggcaccaatgccctatctcct
cagatcgccaagctaagcaaggacatgcacaagatcacgaaacaccccgcatctcgtcattctcgccc
ccgagacaggcaagcctcttcaggctgaggacaacaagcgacgattcttcgagggcccttggtatccaaa
gcgcggaagctttaactacctcatgtactccaaccggtgatacccacttccttgctacgctacttccaag
aacatctacggctccttatacctaccggggcaagattcttgatcctggtgatgggtggactactcatggaa
gtattgttgagtataagggacagtggtggcttttcttctgtgatgcgcatacgtctggtaaggattacct
tcgacaggtgaaggcgaggaagatctggtatgacaagaacggcaagatcttgcttcaccgctccttag

FIG. 16A

SEQ ID NO:18

Protein sequence of Fo43A

mqlkflssallfsltskcaaqdtndipplitdlwsadpsahvfegklwvypshdieanvnngtggagqyam
rdyhtysmksiygdppvvdhgvalsvddvpwakqmwapdaahkngkyylyfpakdkdeifrigvavsnk
psgpfkadmkipgtysidpasyvdtneayliwgggiwggqlqawqdkknfneswigdkaapngtnalsp
qiaklskdmhkitetprdlvilapetgkplqaednkrrffegpwihkrklylmystgdthflvyatsk
niygyptyrgkildpvdgwtthgsiveykgqwwlffadahtsgkdylrqvkarkkiwydkngkillhrp

FIG. 16B

SEQ ID NO:19**Nucleotide sequence for Af43A, a GH43 family enzyme from *Aspergillus fumigatus***

atggcagctccaagttttatcctacccacaggtatccaatcgatataccaatcctctcttccctgggttggc
actccgatcccagctgtgcoctacgtagcggagcaagacacctttttctgcgtgacgtccacttttcattgc
cttccccgggtcttctctttatgcaagccgagatctgcagaactggaaactggcaagcaatattttcaat
cggcccagccagatccctgatcttcgcgtcacggatggacagcagtcgggtatctatgcgcccactctgc
gctatcatgagggccagttctacttgatcggttctgtacctgggcccgcagactaagggcttgcgtgttcac
ctcgtctgatccgtacgacgatgcgcgtggagcgatccgctcgaattcgcggtacatggcatcgaccgcg
gatatcttctgggatcacgacgggacggtctatgtcacgtccgcgaggaccagatgattaagcagtaca
cactcgatctgaagacgggggcgattggcccgggttgactacctctggaacggcaccggaggagtctggcc
cgagggcccgcacattttacaagagagacggatactactacctcatgatcgcagagggaggtaccgagctc
ggccactcggagaccatggcgcgatctagaacccggacaggtccctgggagccatacccgcacaaatccgc
tcttgctgaacaagggcacctcggagtacttccagactgtgggccatgcccacttgttccaggatgggaa
cggcaactgggtgggcggtggcgttgagcacccgatcagggcctgcatggaagaactatcccatgggtcgg
gagacgggtgctcgccccgcgcgttgggagaagggtagtgccctgtcattcagcctgtgagaggccaaa
tgcagggggcggtttccaccaccaataagcgagttcctcgcggcgagggcggtatggatcaagcaaccga
caaagtggatttcagggccggatcgaagataccggcgcacttccagtagtggcgatatcccaagacagag
gattttaccgtctccctcggggccaccgaataactcttcgggtcacaccctcctttttacaacctcaccg
gaactgcggacttcaagccggatgatggcctgtcgcttgttatgcgcaaacagaccgacacctgtttcac
gtacactgtggacgtgtcttttgaccccaagggttgccgatgaagaggcgggtgtgactgttttcccttacc
cagcagcagcacatcgatcttgggtattgtccttctccagacaaccgaggggctgtcgttgtccttccggt
tcgcgtggaaggccgcggtaactacgaaggtcctcttccagaagccaccgtgcctgttcccaaggaatg
gtgtggacagaccatccggcttgagattcaggccgtgagtgacaccgagtagtcttttgcggctgccccg
gctcggcaccctgcacagaggcaaatcatcagccgcgccaactcgttgattgtcagtggtgatacgggac
ggtttactggctcgcttgttggcgtgtatgccacgtcgaacgggggtgcggatccacgcccgcataat
cagcagatggagatacgaaggacggggccagatgattgatttttggtcagagtgggtcccgagctactga

FIG. 17A**SEQ ID NO:20****Protein sequence of Af43A**

maapslsyptgiqsytnplfpgwhsdpscayvaeqdtffcvststfiafpglplyasrdlqnwklaasnifn
rpsqipdlrvtdgqqsgiyaptlryheggfyilivsylygpqtkglftssdpyddaawsdplefavhgidp
difwdhdgtvyvtsaedqmikqytlldlktgaigpvdylwngtggvwpegphiykrdgyyylmiaeggte
ghsetmarsrtrtgpwepyphnpllsnkgtsyfqtvgadlfdgngnwwavalstrsgpawknypmgr
etvlapaawekgewpviqpvrqgmqgpfpppnkrvprgeggwikqpdkvdfprgskipahfqywrypkte
dftvsprghpntlrltspfyntltgtadfkpddglslvmrkqtdtlftytdvvsfdpkvadecagvtvflt
qqqhldlgivllqtteglslsfrfrvegrgnyegplpeatvpvpkewcggqtirleiqavsdteyvfaaap
arhpaqrqiisranslivsgdtgrftgslvgvyatsnggagstpayisrwrvegrgqmidfgrvpsy

FIG. 17B

SEQ ID NO:21

**Nucleotide sequence for Pf51A, a GH51 family enzyme from
*Penicillium funiculosum***

atgggaaagatgtggcattcgatcttgggtgtgttgggcttattgtctgtcgggcatgccatcactatca
acgtgtcccaaagtggcggcaataagaccagtcctttgcaatatgggtctgatgttcgaggtaatecttct
cttataccacatataaaaagttgcgtcatttctaagacaagtcaaggacataaatcacggcggtgatggcg
gtctgtatgcagagcttgttcgaaaccgagcattccaaggtagcacccgtctatccagcaaacctcgatgg
atacgactcgggtcaatggagcaatcctagcgcttcagaatttgacaaaacctctatcacccctccatgcct
agctctctcaacgtcgccaaggggtccaacaatggaagcatcgggttcgcaaatgaaggctggtggggga
tagaagtcaagccgcaaagatacgcgggctcattctacgtccagggggactatcaaggagatttcgacat
ctctcttcagtcgaaattgacacaagaagtcttcgcaacggcaaaaagtcagggtcctcgggcaaacacgag
gactgggttcaatacaagtagcaggttggtgccccaaaaggcagcatcaaaccaccaataacactctgacca
ttacttttgactcaaaggtatgttaaattttgggttttagttcgatgtctggcaattgtcttacgagaaac
gtagggttgaaagacggatccttgaaacttcaacttgatcagcctatttcccccaacttacaacaatcgg
cccaatggcctaagaatcgacctgggttgaaagctatggctgaactagagggggtaagctcttacaatatcaa
ctttatctttacgaagactaatgtgaaaacttagaaaatttctgcgggtttccaggcggttagcgatgtggaa
gggtgtacaagctccttactggtataagtggaaatgaaacggtaggagatctcaaggaccgttatagtaggc
ccagtgcatggacgtaogaagaagcaatggaattggcttgattgagtacatgaattgggtgtgatgacat
ggggcttgagccgagtgagtgattccattcagcgtcaaattccagtggtctaatcatcacatcagttct
tgccgtatgggatggacattacctttcgaacgaagtgatatcggaacacgatttgacgccatatatcgac
gacacctcaaccaactggaattcctgatgggtgcccagatacggcatatggtagttggcgtgcgtctc
tgggtatccgaagccgtggacgattaactacgtcgagattggaaacgaagacaatctatacgggggact
agaaacatacatcgccctaccggtttcaggcatattacgacgctataacagctaaatatccccatatgacg
gtcatggaatctttgacggagatgcctgggtccggcgccgctgcaagcgattaccatcaatattctactc
ctgatgggtttgtttccagttcaactactttgatcagatgccagtcactaatagaacactgaacgggtat
gaaaaccccccttttttaaatatgcttttaattggtattaaccatctttcataggagagattgcaaccgt
ttatccaaataatcctagtaattcgggtggcctgggggaagccattcccccttgatccttggtggattggg
tcgggtgcagaagctgttttccctaattggtgaagagaggaattcgccaaagataatcgggtgctagctacg
tacggaattctacttttcgagatttttaacattggataagaaggactaacctcaatacaggctccaatgtt
cagaaatatcaacaattggcagtggtctccaacactcatcgcttttgacgctgactcgtcgctacaagt
cgttcaacaagctggcatgtgatcaagggtatgctaattttcctcctcattcaaaccgcgagatgtgagct
aactttccgaagcttctctcgacaaaacaaaatcacgcaaaatttaccacagacttgagagtggcggtgaca
taggtccattatactgggtagctggacgaaacgacaatacaggatcgaacatatccaaggccgctgttta
caacagcacctcagacgtccctgtcaccgttcaatttgcaggatgcaacgcaaagagcgcaaatgtgacc
atcttgatccgacgatccgaacgcacgaactaccctggggggcccgaaagttgtgaagactgagatcc
agtctgtcactgcaaatgctcatggagcatttgagttcagtcctccgaacctaaagtgtggctgttctcaa
aacggagtaa

FIG. 18A

21 / 111

SEQ ID NO:22**Protein sequence of Pf51A**

mokmwhsilyvlgllsvghaitinvsqsggnktsplqyglmfedinhggdgglyaelvrnrafqgstvyp
 anldgydsvngailalqnltnplspmpsslnvakgsnngsigfanegwwgievkpqryagsfyvqgdyq
 gdfdislqskltqevfatakvrssgkhedwvqkyelvpkkaasntnltitfdskglkdgslnfnlis
 lfptynnrpnglridlveamaelegkflrfpggsdvegvpqpywykwnetvgdlkdrysrsawtyees
 ngiglieymnwcdmglepilavwdghylsnevisendlqpyiddtlnqleflmgapdtpygswraslgy
 pkpwtinyveignednlyggletyiayrfqayydaitakyphtvmeslttempgpaaaasdyhqystpdg
 fvsqfnfyfdqmpvtnrtnlgeiatvypnnpnsnvawgspfpflyp**wwigsvaeavfligeernspkiigas**
yapmfrninnwqwsptliafdadssrtsrstswhvikllstnkitqnlpttwsggdigplywvagrndnt
gsnifkaavynstdvpvtvqfagcnaksanltlssddpnasnypggpevvkteiqsvtanahgafefs
 lpnlsvavlkte

FIG. 18B**SEQ ID NO:23****Nucleotide sequence for AfuXyn2, a GH11 family enzyme from *Aspergillus fumigatus***

atggtttctttctcctacotgctgctggcgtgctccgccattggagctctggctgcccccgctcgaacccg
 agaccacotcgttcaatgagactgctcttcatgagttcgtgagcgcgcggcaccaccaagctccaccgg
 ctggaacaacggctactactactccttctggactgatggcggcgcgacgtgacctacaccaatggcgcc
 ggtggctcgtactccgctcaactggaggaacgtgggcaactttgtcggtggaaagggctggaaccctggaa
 gcgctaggtaccgagctttgtcaacgtcggatgtgcagacctgtggctgacagaagtagaaccatcaact
 acggaggcagcttcaacccagcggcaatggctacctggctgtctacggctggaccaccaacccttgat
 tgagtactacgttgttgagtcgtatggtacatacaaccccggcagcggcggtacctcaggggcactgtc
 aacaccgacgggtggcacttacaacatctacacggccgttcgctacaatgctccctccatcgaaggcacca
 agaccttcacccagtaactggtctgtgcgcacctccaagcgtaccggcggaactgtcaccatggccaacca
 cttcaacgcctggagcagactgggcatgaacctgggaactcacaactaccagattgtcgccactgagggg
 taccagagcagcgggatctgcttccatcactgtctactag

FIG. 19A**SEQ ID NO:24****Protein sequence of AfuXyn2**

mvsfsyllllacsaiqalaapvepettsfnetalhefaeragtpsstgwnngyyysfwtdgggdvtytnga
 ggsysvnrnrvgnfvvgkgwnpgsartinyggsfnpsgngylavygwtnplieyyvvesygtynpgsgg
 tfrgtvntdggtyniytavrynapsiegtktftqywsrvtskrtggvtvmanhfnawsrlgmnlgthnyq
 ivategyqssgsasitvy

FIG. 19B

SEQ ID NO:25**Nucleotide sequence for AfuXyn5, a GH11 family enzyme from *Aspergillus fumigatus***

atgatctccatttctctcgtcagctttggactcgccgctatcgccggcgcatatgctcttccgagtgaca
aatccgtcagcttagcggaacgtcagacgatcacgaccagccagacaggcacaaacaatggctactacta
ttccttctggaccaacggtgccggatcagtgc aaatatacaa atggtgctggtggcgaatatagtgtgacg
tgggcgaaccagaacggtggtgactttacctgtgggaagggctggaatccagggagtgaccagtaggcaa
cgcccgagaactatagaagaggacgcaaagaaagcactaaactctctactagtgcattaccttctctgg
cagcttcaatccttccggaaatgcttacctgtccgtgtatggatggactaccaacccccctagtcgaatac
tacatcctcgagaactatggcagttacaatcctggctcgggcacatgacgcacaagggcaccgtcaccagcg
atggatccacctacgacatctatgagcaccaacaggtcaaccagccttcgatcgtcggcacggccacctt
caaccaatactggtccatccgcca aacaagcgatccagcggcacagtcaccaccgcgaatcacttcaag
gcttgggctagtctggggatgaacctgggtaccataactatcagattgtttccactgagggatatgaga
gcagcgggtacctcgaccatcactgtctcgtctggtggttcttctctggtggaagtgggtggcagctcgtc
tactacttctcaggcagctccccactggtggctccggcagtgtaagtcttcttccatattggttggtggtc
tttatgtgtattctgactgtgatagtgtctgtcttgtggggccagtgcggtggaattggctggtctggt
cotacttgcgtgtcttccgggcacttgccaggtttcgaaactcgtactactccagtgcttgtagtaccttc
ttgcagggttatatccaagtga

FIG. 20A**SEQ ID NO:26****Protein sequence of AfuXyn5**

MISISSLSFGLAAIAGAYALPSDKSVSLAERQTITTSQTGTNNGYYSFWTNGAGSVQYTNGAGGEYSVT
WANQNGGDFTCGKGWNP GSDHDITFSGSFNPSGNAYLSVYGWTTNPLVEYYILENYGSYNPGSGMTHKGT
VTSDGSTYDIYEHQQVNQPSIVGTATFNQYWSIRQNKRSSGTVTTANHFKA WASLGMNLGTHNYQIVSTE
GYESSGTSTITVSSGGSSSGSGGSSSTSSGSSPTGGSGSCSALWGQCGGIGWSGPTCCSSGTCQVSNS
YYSQCL

FIG. 20B

SEQ ID NO:27**Nucleotide sequence for Fv43D, GH43 family enzyme from *Fusarium verticillioides***

atgcagctcaagtttctgtcttcagcattgttgctgtctttgaccggcaattgcgctgcgcaagacacta
atgatatccctcctctgatcaccgaacctctgggtctgcggatccctcggtcatgttttcgagggcaaact
ctgggtttaccatctcacgacatogaagccaatgtcgtaacggcacgggagggcgctcagtaagccatg
agagattatcacacctattccatgaagaccatctatggaaaagatcccgttatcgaccatggcgctcgctc
tgtcagtcgatgatgtcccatgggccaagcagcaaatgtggggtcctgacgcagcttacaagaacggcaa
atattatctctacttccccgcccaaggataaagatgagatcttcagaattggagttgctgtctccaacaag
ccagcggtcctttcaaggccgacaagagctggatccccgggtacttacagtatcgatcctgctagctatg
tcgacactaatggcgaggcatacctcatctggggcggtatctggggcgggccagcttcaggcctggcagga
tcacaagacctttaatgagtcgtggctcggcgacaaaagctgctcccaacggcaccaacgcctatctcct
cagatcgccaagctaagcaaggacatgcacaagatcaccgagacaccccgcatctcgtcacctcctggccc
ccgagacaggcaagccccttcaagcagaggacaataagegacgatttttcgagggggccctgggttcacaa
gcgcggcaagctgtactacctcatgtactctacggcgacacgcacttcctcgtctacgcgacttccaag
aacatctacggctccttatacctatcaggggcaagattctcgaccctgttgatgggtggactacgcattgaa
gtattgttgagtacaagggacagtggtggtgttctttcgggatgcgcatacttctggaaaggattatct
gagacaggttaaggcgaggaagatctggtatgacaaggatggcaagattttgcttactcgtcctaagatt
tag

FIG. 21A**SEQ ID NO:28****Protein sequence of Fv43D**

mglkflssalllsltoncaagqdtndipplitdlwsadpsahvfegklwvypshdieanvvngtggagqyam
rdyhtysmktiygkdpvidhgvalsvddvpwakqqmwapdaaykngkyylyfpakdkdeifrigvavsnk
psgpfkadmkipgtysidpasyvdtngayliwgggiwggqlqawgdhktfneswlgdkaapngtnalsp
qiaklskdmhkitetprdlvilapetgkplqaednkrrffegpwvhkrklylmystgdthflvyatsk
niygpytyqgkildpvdgwtthgsiveykgqwwlffadahtsgkdylrqvkarkiw ydkd gkilll trpki

FIG. 21B

SEQ ID NO:29**Nucleotide sequence for Pf43B, GH43 family enzyme from *Penicillium funiculosum***

atgagtcgcagcatccttcogtacgcctctgttttcgcctcctgggcggggctatcgccgaaccgttt
tggttctcaatagcgattttcccgatccagctctcatagagacatccagcggatactatgcattcggta
cacccgaaaacggagtcattgcgcaggttgcttcttcaccagactttaatacctggactttgctttccggc
acagatgcctcccgggaccatttcogtcatgggtagcttcgtctccacaaatctgggcggccagatgtt
tggttaagggtatgttcttatggaataacagttttaggagtaggtcagccaggatattgacaaaattataa
taggccgatgggtacctatgtcatgtacttttcggcatctgctgcgagtgactcgggcacaaactgcgttg
gtgccgcaactgcgacctcaccggaaggaccttacaccccggtcgatagcgctgttgccgtgtccattaga
ccaggaggagctattgatgccaatggattttattgacacccgacggcactatatacgttggtatacaaaatt
gatggaaacagctctagacgggtgatggaaccacacatcctaccccatcatgcttcaacaaatggaggcag
acggaacaaccccaacggcgagcccaatccaactcattgacccgatccgacctcgacggacctttgatcga
ggctcctagtttgctcctctccaatggaatctactacctcagtttctcttccaactactacaacactaat
tactacgacacttcatacgcctatgcctcgctcgattactggctccttggaacaaacaatctgcgccttatg
cacccttggttggttactggaaccgagactagcaatgacggcgccattgagcgccctgggtggtgccgattt
ctcgtcgatggcaccgaagatgttggttcacgcaaacctcaatggacaagatatctcgggcggacgcgcc
ttatttgctgcgtcaattactgaggccagcgatgtggttacattgcagtag

FIG. 22A**SEQ ID NO:30****Protein sequence of Pf43B**

msrsilpyasvfallqqaiaepflvlnsdfpdpslietssgyyafgttgngvnaqvasspdfntwtllsg
tdalpgpfpwvasspqiwapdvlvkadgtyvmyfsasaasdsghcvgaatatspegpytpvdsavacp
ldqggaidangfidtdgtiyvvykidgnsldgdgtthptpimlqqmeadgttptgspiqldrsdldgpl
ieapslllsngiyylsfssnyyntnyydtayassitgpwtkqsapyapllvtgtetsndgalsapgga
dfsvdgatkmlfhanlngqdisggralfaasiteasdvvtlq

FIG. 22B

25 / 111

SEQ ID NO:31**Nucleotide sequence of Fv51A, a GH51 family enzyme from *Fusarium verticillioides***

atgggttcgcttcagttcaatcctagcggctgcggccttgcttcgtggctggtgagtcagtcacatcaagg
tcgacagcaaggcggaacgctactagcggtcaccaatatggcttccttcacgaggttggtattgacac
accactggcgatgattgggatgctaacttggagctaggatatcaacaattccgggtgatggtggcatctac
gctgagctcatccgcaatcgtgctttccagtagcagcaagaaataccctgtttctctatctggtggagac
ccatcaacgatgctaagctctccctcaaccgtctcgacactcctctctccgacgctctccccgtttccat
gaacgtgaagcctggaaagggcaaggccaaggagattgggtttcctcaacgaggggttaactggggaatggat
gtcaagaagcaaaaagtacactggctctttctgggttaagggcgcttacaagggccactttacagcttctt
tgcgatctaacccttaccgacgatgtctttggcagcgtcaagggtcaaggtccaaggccaacaagaagcagtg
gggtgagcatgagtttggtgcttactcctaacaagaatgccctaacagcaacaacacttttgctatcacc
tacgatcccaaggtgagtaacaatcaaaactgggacgtgatgtatactgacaatttgtagggcgctgatg
gagctcttgacttcaacotcattagcttggttccctcccacctacaagggcgcgaagaacgggtcttcgagt
tgatcttgccgaggtctctgaaggtctccaccccgtaagggtttaccgtctcacgtgtatcgtgaacagtc
gctgacttgtagaaaagagcctgctgcgcttccccgggtggtaacatgctcgagggcaacaccaacaagac
ctgggtgggactggaaggataccctcggacctctccgcaaccgtcctgggttcgaggggtgtctggaactac
cagcagaccatgggtcttggaatcttgagtaacctccagtgggctgaggacatgaaccttgaaatcagta
ggttctataaaattcagtgacgggttatgtgcatgctaacagatttcagttgtcgggtgtctacgctggcct
ctccctcgacgggtccgtcaccctcccaaggaccaactccagccctcatcgacgacgcgctcgacgagatc
gaattcatccgaggtcccgctcacttcaaagtggggaaagaagcgcgctgagctcggccaccccaagcctt
tcagactctcctacgttgaagtcggaaacgaggactggctcgttggttatccactgggtggaactctta
caaggagtaccgcttccccatgttctcgaggctatcaagaaagctcaccocgatctcacgctcatctcc
totgggtgcttctattgaccccggttggttaagaaggatgctgggttcgatattcctgctcctggaatcggtg
actaccacccctaccgcgagcctgatgttcttggttgaggagttcaacctggttgataacaataagtatgg
tcacatcattgggtgaggttgcttctaccaccccaacgggtggaactgggtggagtggtaaccttatgctt
taccctgggtggatctctgggtgttggtgagggcgctcgtctctgcggttatgagcgcaacgccgatcgta
ttcccggaacattctacgctcctatcctcaagaacgagaaccgttggcagtgggctatcaccatgatcca
attcgccgcgactccgccatgaccacccgctccaccagctgggtatgtctggtcactcttcgcaggccac
cccatgaccatactctccccaccacgcgacttcgacccctctactacgtcgttggttaagaacgagg
acaagggaaactcttatctggaaggggtgctgctgataacaccaccaaggggtgctgacgttcccggtgtctt
gtccttcaaggggtgtaagcccggtgctcaagctgagcttactcttctgaccaacaaggagaaggatcct
tttgcttcaatgatcctcacaagggcaacaatggttggtgatactaagaagactgttctcaaggccgatg
gaaaggggtgcttcaacttcaagcttccctaacctgagcgtcgtggttcttgagaccctcaagaagggaaa
gccttactctagctag

FIG. 23A

26 / 111

SEQ ID NO:32

Protein sequence of Fv51A

mvrfssilaaaacfvavesvnikvdskggnatsghqygflhedinnsgdggiaelirnafrqyskkyppv
slsgwrpindaklslnrldtplsdaipvsmnvkpgkgkakeigflnegywgmdvkkqkytgsfwvkgayk
ghftaslrslntddvfgsvkvkskankkqwvehefvltpnknapsnntfaitydpkgadgaldfnlisl
fpptykgrknglrldlaealeghpsllrfpggnmlegntnktwwdwkdtlgplnrnpgfegvwnyqqth
glgileylqwaedmnleiiivgvyaglsldgsvtpkdqlqpliddaldeiefirgpvtskwgkkraelghp
kpfrlsyvevgnedwlagpytgwnsykeyrfpmfleaikkahpdltvissgasidpvgkkdagfdipapg
igdyhpyrepdvlveefnlfdnnkyghii**gevasthpnnggtgwsgnlmpypwwisgvgeavalcgyerna**
dripgtfyapilknenrwqwaitmiqfaadsamttrstswyvwslfaghpmthtlpttadfdplyyvagk
nedkgtliwkgaaynttkgadvpvslsfkgvkpgaqaeltlltnkekdppafndphkgnnvdtkkktvlk
adgkgafnflpnlsavavletlkkgkpyss

FIG. 23B

SEQ ID NO:41

Nucleotide sequence for Xyn3, a GH10 xylanase from *Trichoderma reesei*

atgaaagcaaacgtcatcttgtgctctctgccccccctggctgcgcgtctctccccacogaaaccatccacc
tcgacccccgagctcgccgctctccgcgccaacctcaccgagcgaacagccgacctctgggaccgccaagc
ctctcaaagcatcgaccagctcatcaagagaaaaaggcaagctctactttggcaccgccaccgaccgcggc
ctcctccaacgggaaaagaacgcggccatcatccaggcagacctcggccaggtgacgccggagaaacagca
tgaagtggcagtcgctcgagaacaaccaaggccagctgaactggggagacgccgactatctcgtaactt
tgcccagcaaaaacggcaagtcgatacgcggccacactctgatctggcactcgcagctgctgctgggtg
aacaatatcaacaacgcggatactctgcggcaagtcacccgacccatgtctctactgtggttgggcggt
acaagggcaagattcgtgcttgggtgagttttgaacaccacatgccccctttcttagtcgctcctcctc
ctcttggaaacttctcacagttatagccgtatacaacattcgacaggaaatttaggatgacaactactgac
tgacttgtgtgtgtgatggcgataggacgtgggtcaatgaaatcttcaacgaggatggaaacgctgcgctct
tcagctcttttccaggctcctcggcgaggagtttgtctcgattgcctttcgtgctgctcgagatgctgacc
cttctgcccgtctttacatcaacgactacaatctcgaccgcgccaaactatggcaaggtcaacgggttgaa
gacttacgtctccaagtggatctctcaaggagttccattgacgggtattggtgagccaacgacccctaaat
gtccccattagagttctcttcttagagccaaggcttgaagccattcagggactgacaacgagagccttctc
tacaggaagccagtcctcatctcagcggcgggcggaggtctctggtacgctgggtgcgctccagcagctggca
acgggtaccgcgtaccgagctggccattaccgagctggacattcagggggcaccgacgacggattacacc
aagttgttcaagcatgcctgagcgtctccaagtgcgtcggcatcacggtgtggggcatcagtgacaaggt
aagttgcttccccctgtctgtgcttataactgtaagcagcaacaactgatgctgtctgtctttacctagg
actcgtggcgtgccagcacaacctctctgtttgacgcaaaacttcaacccccagccggcatataacag
cattgttggcatcttacaatag

FIG. 24A

SEQ ID NO:42

Protein sequence for Xyn3

mkanvilcllaplvaalptetihldpelaalranlttertadlwdrqasqsidqlikrkgklyfgtatdrq
llqreknaaiiqadlgqvtpensmkwqslennqgqlnwgdadylvnfaqqngksirghtliwhsqlpaw
nninnadtlrqvirhvstvvgrykgkirawdvvneifnedgtlrssvfsrllgeefvsiafraardap
sarlyindynldranygkvnglktvyskwisqgvpidgigsqshlsgggsgtlgallqqlatvpvtelai
teldiqgaptttdytqvvgacslsvskcvgitvwgisdkdswrastnpllfanfnpkpaynsivgilq

FIG. 24B

SEQ ID NO:43**Protein sequence of Xyn2, a GH11 family xylanase from *Trichoderma reesei***

mvsftsl~~llaaspp~~srascrpaaevesvavekrqtiqpgtgynngyfysywndghggvtytngpgggqfsvn
 wsns~~gnfvggk~~gwqpgtknkvinfs~~gsynp~~ngnsylsvygwsrnp~~lieyy~~ivenfgtynpstgatk~~lgev~~
 tsdgs~~vydi~~yrtqrvnqpsiigtatfyqywsrrnrh~~rssg~~svntanhfnawaq~~qgl~~tlgtmdyqivaveg
 yfssgsasitvs

FIG. 25A**SEQ ID NO:162****Nucleotide sequence of Xyn2 from *Trichoderma reesei***

ATGGTCTCCTTCACCTCCCTCCTCGCCGGCGTCGCCGCCATCTCGGGCGTCTTGGCCGCTCCCCGCCGCCG
 AGGTCGAATCCGTGGCTGTGGAGAAGCGCCAGACGATTTCAGCCCCGGCACGGGCTACAACAACGGCTACTT
 CTA~~CTCGT~~ACTGGAACGATGGCCACGGCGGGCGTGACGTACACCAATGGTCCCGGGCGGGCAGTTCTCCGTC
 AACTGGTCCA~~ACTCGGG~~CAACTTTGTTCGGCGGCAAGGGATGGCAGCCCCGGGACCAAGAACAAGTAAGACT
 ACCTACTCTTACCCCCCTTTGACCAACACAGCACACAACAATACAACACATGTGACTACCAATCATGGAAT
 CGGATCTAACAGCTGTGTTTAAAAAAGGGTCATCAACTTCTCGGGAAGCTACAACCCCAACGGCAAC
 AGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCTGATCGAGTACTACATCGTCGAGA~~ACTTTGGCA~~
 CCTACAACCCGTCCACGGGCGCCACCAAGCTGGGGCAGGTCACCTCCGACGGCAGCGTCTACGACATTTA
 CCGCAGCAGCGCGTCAACCAGCCGTCCATCATCGGCACCGCCACCTTTTACCAGTACTGGTCCGTCCGC
 CGCAACCACCGCTCGAGCGGCTCCGTCAACACGGCGAACCACCTTCAACGCGTGGGCTCAGCAAGGCCTGA
 CGCTCGGGACGATGGATTACCAGATTGTTGCCGTGGAGGGTTACTTTAGCTCTGGCTCTGCTTCCATCAC
 CGTCAGCTAA

FIG. 25B**SEQ ID NO:44****Protein sequence of Bxl1, a GH3 family β -xylosidase from *Trichoderma reesei***

mvnnaallaalsallptalag~~nnq~~tyanysa~~qgq~~pdlypetlatltlsfpdcehgplknnlvcdssagyv
 eraqalislftleeli~~lntq~~ns~~gpgv~~prlglpnyqv~~wneal~~hgl~~dran~~fatkg~~gfew~~atsf~~mp~~piltta
 alnrtli~~hqi~~adiistqaraf~~sns~~grygl~~dv~~yapn~~vng~~frs~~plw~~grgqetpgeda~~ffl~~ssaytyeyitgi
 qggvdpehlk~~vaat~~vk~~hf~~agy~~dlen~~w~~nn~~qsr~~lgf~~daiitq~~qdl~~seyytpqflaaaryaksrslm~~cay~~ns~~v~~
 ngvps~~cans~~fflqtllresw~~gf~~pewgyvssdc~~dav~~ynvfn~~ph~~dyasnqssaa~~assl~~ragtdidcgqtypw
 hl~~nes~~fvagevsrgeiersvtrlyanlvrlgyfdkknqyrslgwkdv~~vkt~~dawnisyeaaveg~~iv~~llknd
 gtlplskkvrsialigpwanattqm~~qgn~~yygpapylispleaakkagyhvnfelgteiagnsttg~~fak~~ai
 aaak~~s~~daiiylggidntieqegad~~rtd~~iawp~~gn~~qldlikqlsevgkplvvlqm~~ggg~~qv~~dss~~slksnk~~kv~~
 nslvwggyp~~gq~~sggvalfdilsgkrapagrlvttqypaeyvhqfpqndmnlrpdgksnpgq~~tyi~~wytgkp
 vyefgsgl~~fy~~ttfketlashpkslkfntssilsaphpgy~~ty~~seqipvftfeaniknsgk~~tes~~pytamlfv
 rtsnagpapyp~~nk~~wlvgfdrladikpghssklsipipvsalarvdshgnrivypgkyela~~int~~desvkle
 felvgeevtienwpleeqqikdatpda

FIG. 26A

SEQ ID NO:163**Nucleotide sequence of Bxl1 from *T. reesei***

atggtgaataaocgcagctctttctcgccgcctgtcggtctctcctgcccacggccctggcgcagaacaatc
aaacatacgcacaactactctgtcagggccagcctgatctctaccccagacacttgccacgctcacact
ctcggttccccgactgcgaacatggccccctcaagaacaatctcgtctgtgactcatcgccggctatgta
gagcgagcccaggccctcatctcgtctcttcacctcgaggagctcattctcaacacgcaaaaactcggggc
ccggcgtgctcgcctgggtcttccgaactaccaagtctggaatgaggctctgcaaggcttggaaccgcgc
caacttcgccaccaaggcgccaggttcgaatggcgacactcggttccccatgccatcctcactacggcg
gcctcaaccgcacattgatccaccagattgccgacatcatctcgacccaagctcgagcattcagcaaca
gcggccggttacggctctcgacgtctatgcgccaaaacgtcaatggcttccgaagccccctctggggccgtgg
ccaggagacgcccggcggaagacgcctttttctcagctcgcctatacttaacgagtacatcacgggcac
caggggtggcgctcgacctgagcacctcaaggttgccgccacgggtgaagcacttttgccggatacgaacctg
agaactggaacaaccagtcctcggtctcggttccgacgccatcataactcagcaggacctctccgaatacta
cactccccagttcctcgtctgcggcccggttatgcaaagtcacgcagcttgatgtgcgcatacaactcgtc
aacggcgtgccagctgtgccaacagcttcttctcgcagacgcttttgccgcgagagctggggcttccccg
aatggggatacgtctcgtccgattgctgatgcctgtacaaacgttttcaacctcatgactacgccagcaa
ccagtcgtcagccgcgcagctcactgcgagccggcacccgatatcgactgcgggtcagacttacccgtgg
cacctcaacgagtcctttgtggccggcggaagtctcccgccggcgagatcgagcgggtccgtcacccgtctgt
acgccaacctcgtccgtctcggatacttcgacaagaagaaccagtaaccgctcgtcgggttggaaggatgt
cgtcaagactgatgcctggaacatctcgtacgaggctgctggtgagggcatcgtcctgctcaagaacgat
ggcactctccctctgtccaagaagggtgcgcagcattgctctgatcggaacctgggccaatgccacaacc
aaatgcaaggcaactactatggccctgccccatacctcatcagccctctggaagctgctaagaaggccgg
ctatcacgtcaactttgaaactcggcacagagatcgccggcaacagcaccactggctttgccaaaggccatt
gtgcccgaagaagtcggatgccatcatctacctcgggtggaattgacaacaccattgaacaggagggcg
ctgaccgcacggacattgcttgcccggtaatcagctggatctcatcaagcagctcagcgaggctcggcaa
accccttgctcctgcaaatggcggggtggtcaggtagactcatcctcgtcgaagagcaacaagaaggte
aactccctcgtctggggcggtatcccgccagtcgggaggcggtgcccctcttcgacattctctctggca
agcgtgctcctgcggccgactgggtcaccactcagtaccgggtgagtatgttcaccaattccccccagaa
tgacatgaacctccgaccgatggaaagtcaaaacctggacagacttacatctggtacaccggcaaaccc
gtctacgagtttggcagtggtctctttctacaccaccttcaaggagactctcgccagccacccccagagcc
tcaagttcaaacacctcatcgatcctctctgctcctcaccgccgatacaacttacagcgagcagattcccg
cttcaccttcgaggccaacatcaagaactcgggcaagacggagtcctccatatacggccatgctggttgtt
cgcacaagcaacgctggcccgagccccgtaccgcaacaagtggctcgtcggattcgaccgacttgccgaca
tcaagcctgggtcactcttccaagctcagcatccccatccctgtcagtgctctcgcccggtgttgattctca
cggaaaccggattgtataccccggcaagtatgagctagccttgaacaccgacgagctctgtgaagcttgag
tttgagttgggtgggagaagaggtaacgattgagaactggccggttgaggaggcaacagatcaaggatgcta
cacctgacgcataa

FIG. 26B

SEQ ID NO:45**Protein sequence of Bgl1, a GH3 family β -glucosidase from *Trichoderma reesei***

mryrtaaalalatgpfaradshstsgasaeavvppagtpwgtaydkakaaalaklnlqdkvgivsgvgwng
gpcvgnntspaskisypslclqdgplgvyrstgstafstpgvqaastwdvnlirergqffigeevkasgihvi
lgpvagplgktpqgggrnwefgvdpyltgiamgqtingiqsvgvqatakhyilneqelnretissnpddr
tlhelytwpfadavqanvasvmcsynkvnttwacedqytlqtlvldqldqgfpgyvmtwdnaqhttvqsans
gldmsmpgtdfngnnrlwgpaltnavnsnqvptsrddmvtrilaawyltgddqagypsfnisrnnvqgnh
ktnvraiardgivllkndanilplkkpasiavvgsaaaignharnspscndkgcddgalgmwgsagavny
pyfvapydaintrassqgtqvtlsntdntssgasaargkdvaivfitadsgegyitvegnagdrnnldpw
hngnalvqavagansnvivvvhsvgaiileqilalpqvkvavvwaglpesgnalvdvlwgdvpsgklv
ytiakspndyntrivsggsdsfseglfidykhfddanitpryefgyglsytkfnysrslsvlstaksgpat
gavvpggpsdlfqnvatvtvdiansgqvtagaevaqlitytpssaprtppkqlrgfaklnltpgqsgtatf
nirrrdlsywdtasqkwvvpssgsgfsgisvgassrdirltstlsva

FIG. 27A**SEQ ID NO:46:****Nucleotide sequence for Pa51A, a GH51 family enzyme from *P. anserina***

atgatccacctcaagccagccctcgcgcgcttggttggecgctgtcgacgcaatgtgtggctattgatttgt
ttgtcaagtcttcgggggggaataagacgactgatatcatgtatggtcttatgcacgaggatatcaacaa
ctccggcgacggcgccatctacgcgcgagctaattctcaaccgcgcgttccaagggagtgagaagttcccc
tccaacctcgacaactggagccccgtcggttggecgctacccttacccttcagaagcttgccaagcccttt
cctctgcgttgcccttactccgtcaatgttgccaaccccaaggagggaagggcaagggcaaggacacca
ggggaagaaggttggttggttgccaatgctgggttttggggatggtatggtcaagaggcagaagtacactggt
agcttccacgttactggtgagtacaagggtgactttgaggttagcttgcgcagcgcgattaccggggaga
cctttggcaagaaggtggtgaagggtgggagtaagaaggggaagtggaaccgagaaggagtttgagttggt
gcctttcaaggatgcgccccacagcaacaacaccttgttggtgcagtgggatgcccaggggcgcaaaggac
ggatctttggatctcaacttgatcagcttggtccctccgacattcaaggggaaggaagaatgggctgagaa
ttgatcttgcgcagacgatggttgagctcaagccgaccttcttgcgcttccccgggtggcaacatgctcga
gggtaacaccttggaacacttggtggaagtggtacgagaccattggccctctgaaggatgcccgggcatg
gctggtgtctgggagtaaccagcaaacccttggttggtgttggtcgagtagatggagtgggccgatgaca
tgaacttgagaccattgtcggtgtcttcgctggtcttgccctcgatggctcggttcggttccgaatccga
gatgggatgggtcatccaacaggctctcgacgaaatcgagttcctcactggcgatgctaagaccaccaa
tggggtgcccgtccgcgcgaagcttggtcaccccaagccttggaaggtcaagtggttgagatcggtaacg
aggattggcttgccggacgcctgctggcttcgagtcgtacatcaactaccgcttccccatgatgatgaa
ggccttcaacgaaaagtaccccgacatcaagatcatgcctcgccctccatcttcgacaacatgacaatc
ccgcgggtgctgcccgtgatcaccaccgctacctgactcccgatgagttcggttgagcgattecgcgaagt
tcgataacttgagcaaggataacgtgacgctcatcgccgaggctgcgtcgacgcacctaaccggtggtat
cgcttgggagggagatctcatgaccttgcttggtggggcgccagtggtgctgaggetatcttcttgatc
agcactgagagaaaagggtgacaagatcatcggtgctacttacgcgcctgggtcttcgcagcttggaaccgt
ggcaatggagcatgacctgggtgcagcatgcgcgcgaccggccctcaccactcgctcgaccagttggta
tgtctggagaatcctcgcccaccacatcctcggtgagacgctcccggtcgatgccccggccggcaagccc
aactttgacctctgttctacgttgccggaaagagcgagagtggaaccgggtatcttcaaggctgcccgtct
acaactcgactgaatcgatcccgtgtcggttgaaagtttgatgggtctcaacgagggagcggttgccaactt
gacgggtgcttactggggccggaggatccgtatggatacaacgaccccttcaactgggtatcaatgttgtaag
gagaagaccaccttcatcaaggccggaaagggcggaagttcaccttcaccctgcggggttgagtggtg
ctgtgttgagagacggccgacgcggtcaagggtggcaaggggaaagggcaagggcaaggggaaagggtaactga

FIG. 27B

atgategcaacctcaagcccgccctcgccgcccctcccgccctcagcaacccaatgcgctgcccategacctct
tcgtcaagagcagcggcgggcaacaagaccaccgacatcatgtacggcctcatgcacgaggacatcaacaa
cagcggcgacggcgggcatctacgccgagctgatcagcaaccgcgccctccagggcagcgagaagttcccc
agcaacctcgacaactggtcccccgtcggcgggcgccaccctcaccctccagaagctcgccaagccccctgt
cctctgccctccccctactccgtcaacgtcgccaaccccaaggagggttaagggttaagggtcaaggacaccaa
gggcaagaaggctcggcctcgccaacgcccggcttttggggcatggacgtcaagcgccagaaatacacgggc
agcttccacgtcacccggcgagtacaagggcgacttcgagggtcagcctccgcagcgccattacccggcgaga
ccttcgggaagaaggctcgtcaagggcggcagcaagaagggtcaagtgaccgagaaggagttcgagctggt
ccccctcaaggacgcccccaacagcaacaacaccttcgtcgtccagtgggacgcgcgagggcgcccaaggac
ggcagcctcgacctcaacctcatcagcctcttcccgcccaccttcaagggcgcaagaacggcctccgca
tcgacctcgcccagaccatggtcgagctgaagcccaccttcctccgctttcccgggcggaacatgctcga
gggcaacacctcgacacctggtggaagtgggtacgagaccatcggccccctgaaggaccgccttggtcatg
gcccgggtctgggagttaccagcagacgctgggcctcggcctgggtcgagtacatggagtgggccgacgaca
tgaacctcgagcccategtcggcgctttttgctggcctggccctggatggcagctttgtccccgagagcgga
gatggggtgggtcatccagcaggtcttcgatgagatcgagttcctcaccggcgacgcccaagaaccaccaag
tggggcgccgtccgcgcgaagctcgggccaccctaagccctggaagggtcaaattgggtcgagatcggaacg
aggactgggtcgcgcggccgacctgcccgttcgagagctacatcaactaccgcttccccatgatgatgaa
ggccttcaacgagaaataccccgacatcaagatcattgccagccccctccatcttcgacaacatgaccatt
ccagccgggtgctgcccgtgaccaccaccctacctcacccccagcgaatttgtcgagcgcttcgccaaagt
tcgacaacctcagcaaggacaacgtcacctcattggcgaggccgcacgacccaccaccaacggcggtcat
tgcttgggagggcgacctcatgcccctgcctggtggggcgggcagcgctcgccgaggccatcttcctcatc
agcacccgagcgcaacggcgacaagatcatcggcgccacctacgcccctggcctccgatctctcgaccgct
ggcagtgggagcatgacctgggtccagcacgcgcgcgaccctgccctcaccaccgcgacaccagctggta
cgtctggcgcatcctcgcccaccacatcattcgcgagacctccccgtcgacgcccccgccggcaagccc
aacttcgacccccctcttctacgtcgctggcaagtcggagagcggaaccggcatcttcaaggccgcgctct
acaacagcaccgagagcatccccgtcagcctcaagttcgacggcctcaacgagggcgccgtcgccaacct
cacgctcctcacccgcccccgaggacccttacgggtacaacgaccccttcaccggcatcaacgtcgtcaag
gaaaagaccaccttcatcaaggccggcaaggggcggaagttcacctttaccctccccggcctctctgtcg
ccgtcctcgagaccgcgcgacgcgctgaagggtggcaagggaagggaagggaagggttaagggttaacta
a

FIG. 27C

SEQ ID NO:48**Nucleotide sequence for Gz43A, a GH43 family enzyme from *Gibberella zeae***

atgtatcggaaagttggccggtcatctcggccttcttggccacagctcgtgctaccaaagcagactgtcctc
tcatcactagtagatggactgcggtatccttcgggtcatgtctttaacgacaccttgtggctctaccggtc
tcatgacatcgatgctggatttgagaatgatcctgatggaggccagtaacgccatgagagattaccatgtc
tactctatcgacaagatctacgggtccctgcccgtcgatcacgggtacggccctgtcagtgaggatgtcc
cctgggcctctcgacagatgtgggtcctgacgctgccacaagaacggcaaatactacctatacttccc
tgccaaagacaaggatgatatcttcagaatcggcggttgctgtctaccaacccccggcggaccattcgtc
cccgacaagagttggatccctcacactttcagcatcgaccccgccagtttcgtcgatgatgatgacagag
cctacttggcatggggtggtatcatgggtggccagcttcaacgatggcaggataagaacaagtacaacga
atctggcactgagccaggaaacggcacgcgtgccttgagccctcagattgccaaagctgagcaaggacatg
cacactctggcagagaagcctcgcgacatgctcattcttgacccaagactggcaagccgctcctttctg
aggatgaagaccgacgcttcttcgaaggaccctggattcacaaagcgcaacaagatttactacctcaccta
ctctactggcacaacccactatcttgtctatgcgacttcaaagacccctatggctccttacacctaccag
ggcagaattctggagccagttgatggctggactactcactctagtatcgtcaagtaccaggggtcagtggt
ggctatctttatcacgatgccaaagacatctggcaaggactatcttcgccaggtaaaggctaagaagatttg
gtacgatagcaaaggaaagatcttgacaaagaagccttga

FIG. 27D**SEQ ID NO:49****Nucleotide sequence for Fo43A, a GH43 family enzyme from *Fusarium oxysporum***

atgtatcggaaagttggccggtcatctcggccttcttggccacagctcgtgctcaagacactaatgacattc
ctcccctgatcaccgacctctgggtccgcagatccctcgggtcatgttttcgaaggcaagctctgggttta
cccatctcacgacatcgaagccaatgttggtcaacggcacaggaggcgctcaatacggccatgagggattac
catacctactccatgaagagcatctatggtaaagatcccggttgctgaccacggcgctcgctctctcagtcg
atgacgttccctgggcgaagcagcaaatgtgggtcctgacgcagctcataagaacggcaaatattatct
gtacttccccgccaaggacaaggatgagatcttcagaattggagttgctgtctccaacaagcccagcggt
cctttcaaggccgacaagagctggatccctggcacgtacagtatcgatcctgctagctacgtcgacactg
ataacgaggcctacctcatctggggcggtatctggggcgggccagctccaagcctggcaggataaaaagaa
ctttaacgagtcgtggattggagacaaggctgctcctaacggcaccaatgccctatctcctcagatcgcc
aagctaagcaaggacatgcacaagatcacgaaacaccccgcgatctcgctcattctcgcccccgagacag
gcaagcctcttcaggctgaggacaacaagcgacgattcttcgagggcccttggatccacaagcgcgga
gctttactacctcatgtactccacgggtgatacccacttcttgtctacgctacttccaagaacatctac
ggctccttatacctaccggggcaagattcttgatcctggtgatgggtggactactcatggaagtattgttg
agtataagggacagtggtggcttttcttctgtgatgcgcatacgtctggtaaggattaccttcgacaggt
gaaggcgaggaagatctggtatgacaagaacggcaagatcttgcttcaccgctccttag

FIG. 27E

SEQ ID NO:50**Nucleotide sequence for Pf51A, a GH51 family enzyme from *Penicillium funiculosum***

atgtaccggaagctcgccgtgatacgcgccttccctggcgaactgctcgcgcgcacatcaccatcaacgtcagcc
agagcggcggcaacaagaccagcccgctccagtaacggcctcatgttcgaggacatcaaccacggcgggga
cggcggcctctacgcgcgagctgggtccggaaccgggccttccagggcagcaccgtctaccgggccaacctc
gacggctacgactcgggtgaacggcgcgattctcgcgcctccagaacctcaccaaccgcgtcagcccgagca
tgccctcgctcgctgaacgtcgccaagggctcgaaacaacggcagcatcggccttcgccaacgaggggtggtg
gggcatcgagggtcaagccgcagcggtaacgcgggcagccttctacgtccaggggcgactaccaggggcgacttc
gacatcagcctccagagcaagctcaccacaggaggtcttcgcgcagcggcgaagggtccgggtcgagcgggaagc
acgaggactgggtccagtaacaagtaacgagctgggtcccgaaagaaggccgcgcagcaacaccaacaacacct
caccatcaccttcgacagcaagggcctcaaggacggcagcctcaacttcaacctcatcagcctcttcccg
ccgacctacaacaaccggccgaacggcctccggatcgacctcgctcgaggccatggcggagctggagggga
agttcctccgcttccccggcggctcggacgtggagggcgctccaggccccgtactgggtacaagtggaaacga
gaccgtcggcgacctcaaggaccgctactcgcgcgcgcagcgcctggacctacgaggagagcaacggcctc
ggcctcatcgagtacatgaactgggtgcgacgacatgggcctcgagccgatcctcgcgcgtctgggacggcc
actacctcagcaacgagggtcatcagcgagaaacgacctccagcgcgtacatcgacgacacctcaaccagct
cgagttcctcatgggcgcgcccggaactccctacgggtcttggagggttagcctcgggtacccgaagccg
tggaaccatcaactacgtcgagatcggcaacgaggacaacctctacggcggcctcgagacctacatcgct
accggttcaggcctactacgacgccatcaccgccaagtaccgcacatgaccgtcatggagagcctcac
cgagatgcccggccccgctgccgcggcgtcggactaccaccagtaactcgacgcccgcagggcttcgtcagc
cagttcaactacttcgaccagatgccggtcaccaaccgcacgctgaacggcgagatcgccaccgtctacc
ccaacaacccgagcaactcgggtggcgtggggcagcccgcttcccgctctaccggtgggtggatcgggtccgt
ggctgaggccgtcttctcatcggcgaggagcggaaacagcccggaagatcatcggcgccagctacgcccc
atgttcgcaacattaacaactggcagtgaggcccgacctgatcgccttcgacgcccgcagcagccgga
cgtcgcgtctacttctggcacgtcatcaagctcctcagcaccaacaagatcaccagaacctgcccac
gacgtgggtctgggggggacatcggcccgctctactgggtcgcgggcgggaacgacaacaccggcgagcaac
atcttcaaggccgcgtctacaacagcaccagcgacgtcccggtcaccgtccagttcgccggctgcaacg
ccaagagcgccaacctcaccatcctctcgtcggacgaccccaacgccagcaactaccggggcgggccccga
ggtcgtcaagaccgagatccagagcgtcacccgccaacgcccacggcgcccttcgagttcagcctcccgaa
ctgtcgggtggctgtgctgaagacggagtag

FIG. 27F

SEQ ID NO:51**Nucleic acid sequence of Eg4, an endoglucanase from *Trichoderma reesei***

atgatccagaagctttccaaccttcttctcaccgcactagcgggtggcaacgggtgttggtggacacggac
 acatcaacaacattgtcgtcaacggagtgactaccagggatatgatcctacatcggtcccatatgaatc
 tgacccgcccatagtgggtgggctggacgggtgccgatcttgacaacgggttcgtctcaccgacgcataat
 cagagcccggacatcatctgccacaagaatgccaccaacgcaaaaggacacgcgtccgtcaaggccggag
 acaactattccctccagtggggtgccagttcccttggccgcacccaggccccatcgctcgactacctggccaa
 ctgcaacgggcgactgcgagaccgtggacaagaacgtcccttgagttcttcaagattgacggcgctcgggtctc
 atcagcggcggagatccgggcaactgggcctcggacgtgttgattgccaacaacaacacctgggttgtca
 agateccccgaggatctcgccccgggcaactacgtgcttcgccaagagatcatcgcttgccacagcgccgg
 gcaggcggaacggcgctcagaactacccctcagtgcttcaacctcgccgtcccaggctccggatctctgcag
 ccgagcggcggtcaagggaaccgcgctctaccactccgatgaccccggtgtcctcatcaacatctacacca
 gccctcttgcgtaacaccattcctggaccttccgtgggtatcaggccctccccacgagtgctcgcccaggggcag
 ctccgcgcgcagcgccactgccagcgccactgttccctggcggttagcggaccgggaaacccgaccagtaag
 actacgacgacggcgaggacgacacaggcctcctctagcagggccagctctactcctcctgctactacgt
 cggcacctgggtggaggcccaaccagactttgtacggccagtggtggtggcagcggtacagtggtcctac
 tcgatgcgcgcgcgcggccacttgcctctaccttgaaccatactacgcccgagtgcccttaactag

FIG. 28A**SEQ ID NO:52****Protein sequence of Eg4, an endoglucanase from *Trichoderma reesei***

MIQKLSNLLVTALAVATGVVGHghhindivingvwyqaydpttfpyesnp pivvgwtaadldngfvspday
 qnpdiichk natnakghasvkagdt ilfqwvpvpwphpgpivdylanengdcetvdkttleffkidgvgl
 lsggdpgt wasdvlisnnntwvkipdnlapgn yvlrheii alhsagqangaqnypqcfn iavsgsgslq
 psgvlgt dlyhatdpgvliniytsplnyiipgptvvs glpts vaqgssa atatasatvp gggsgptsrtt
 ttarttq assrpsstppattsapaggptqtlyggcggsgysgptrcappatcstlnpyyaqln

FIG. 28B

SEQ ID NO:53**Nucleic acid sequence of Pa3D, a GH3 family β -glucosidase from *Podospira anserina***

atggctcttcaaacccttcttctctgctggcggcgagccatgctggccaacgcagagacaacaggcgaaaagg
tctctcggcaagcacccgtctggcgtcaagcatgggcgcgcgccactcccaggctgcgcgcactctggc
cagaatgtcacagcaagacaagatcaacatgggtcacgggcattggctgggacagagggccttgcgtggga
aacacagctgccatcagctccatcaactatcctcaaatctgtcttcaggatggaccattgggcattcgct
toggcactggtaccaccgccttcacacctggcggtccaagctgcttcgacatgggacggttgatctgatccg
gcagcgcggtgcttaacctgggcgcgcgaagccaagggtgctgggcattcacatccttttggggcccggttgc
ggtgccctgggcaagattccccacggcggtcgcaactgggagggatttggcgccgacccctaccttgccg
gtattgccatgaaggagaccatcgagggtattcagtcagcaggcgtccaggccaacgccaaagcactacat
tgcaaacgaacaagagctcaaccgcgagaccatgagcagcaatgtggatgaccgcactcagcacagagctc
tacctctggcccttttgcgacgcgcgtgcacgccaacgtcgccagcgtcatgtgcagttacaacaagctca
atggcacgtgggcttgcgagaatgacaaggctctgaatcagatcttgaagaaggagctcggattccaggg
ctacgttctcagcgaactggaatgctcagcacagcactgctctgtctgctaacagtgggtctggacatgact
atgcccggtaccgatttcaacggcgcaatgtctactggggccctcaactgaacaacgctgtcaacgccg
gccaggttcagagatccagactagacgacatgtgcaagagaatcttggctggctggtaacttgcctcggtca
gaaccagggtatcccgccatcaacatcaggggccaacgttcaggggcaaccataaggagaacgtacgtgct
gttgccagagacggcatcgtcttgcgtgaagaacgatggaattctgcgcgtttccaagccgagaaagattg
ctgtcgtgggctcccactccgtcaacaatccccagggaatcaacgcctgtgttgacaagggtgcaatgt
tggcacccttggcatgggctggggttcaggcagcgtcaactaccctatctcgtgtccccgtacgatgct
ctccggactcgtgctcaggccgatggcacacaaatcagcctccacaacactgacagcaccaacgggtgtgt
caaacgttgtgtctgacgctgatgctgttgttgttgcacactgcccattctgggtgaagggtacatcac
tgtcgaggggccacgctggcgaccgcagccaccttgaccggtggcacaatggcaaccaacttgttcaggct
gccgcggctgccacaagaacgtcatcgttgttgtgcacagtgttggccagatcacccctggagactatcc
tcaacaccaatggagtcgcgcgattgtgtgggctggtcttccgggccaagagaatggcaacgctcttgt
tgatgttctctacggttgggttccgcatctggaaagcttccctacaccattggcaagagggagtcggac
tatggcacagccgttgttcgtggggatgataacttcaggagggcctttttgttgactaccgtcaacttg
acaatgccaggatcgagccgcgctatgagtttggcttgggtcttgaagtccagcggcgaggttgggt
ttgatttcaagctttcctaacctgataaaacagcttacaccaatttcaccttctccgacatcaagattac
ttccaatgtcaagccggggcccgctactggccagaccattcccgcggaacctgccgacctgtgggaggac
gttgcgacagtcactgcaaccatcaccaactcgggtgctgtcgagggcgctgaggttgccagctttaca
tcggcctgcgcgtcctcggtcctgcctctccccogaagcagctgctgtgattttccaagctgaagctggc
cccgggtgccagcggcactgccacattcaacctcagacgcagagatctcagctattgggatacccgcctc
cagaactgggtcgtgccagcggcaactttgtcgtcagcgtcggcgccagctcgagagatatccgcttga
cgggcaccatcacggcgtag

FIG. 29A

SEQ ID NO:54

Protein sequence of Pa3D, a GH3 family β -glucosidase from *Podospira anserina*

malqtffllaaamlanaettgekvsrqapsgagawaaahsqaaatlarmsqqdkinmvtgigwdrGPCVG
ntaaissinypqicldgplgirfgtgtaftpgvqaastwdvdlirrgaylgaeakgcgihillgpva
galgkiphggrnwefgdpylagiamketiegiqsagvqanakhyianeqelnretmssnvddrtqhel
ylwpfadavhanvasvmcsynklngtwacendkalnqilkkelgfggyvlsdwnaqhstalsansgldmt
mpgtdfnggrnvwywgpqlnnavnagqvqrsrlldmckrilagwyllgqnqgypainiranvqgnhkenvra
vardgivilkndgilplskprkiavvgshsvnnppginacvdkgcnvgtlmgwgsgsvnypylvspyda
lrtraqadgtqislnhtdstngvsnnvdsadavvvvitadsgegyitveghagdrshldpwhngnqlvqa
aaaanknvivvvhsvggitletilntngvraivwaglpqgengnalvdvlyglvspsgklpytigkresd
ygtavvrgddnfreglfvdyrhfdnarieryefgfglsytnftfsdikitsnvkpgpatggtipggpad
lwedvatvtatitnsgavegaevaqllyiglpssapasppkqlrgfsklklapgasgtatfnlrrrdlsyw
dtrlqnwvvpsgnfvsvvgassrdirltgtita

FIG. 29B

SEQ ID NO:55**Nucleotide sequence of Fv3G, a GH3 family β -glucosidase from *Fusarium verticillioides***

atgttttcttcttccatatcttgtttggcgccctgagttgatgagccaggggtctactagctcagagcc
aaccggaataatgtcatcacgatgatacctacttctacgggtcaatcgccaccagtgtatcctacacgtaa
gcactctctctgatttcccaacgaaagcaatactgatctcttgaccagcggaacaggtagacaccggctc
atgggctgcogetgtagccaaagccaagaacttgggtgtcccagttgactcttgaagagaaagtcaacttg
actacaggaggccagacgaccaccggctgctctggcttcatccctggcattccccgtgtaggctttccag
gactgtgttttagcagacgctggcaacgggtgtccgcaacacagattatgtgagctcgtttccctccgggat
tcatgtcgggtgcaagctggaatccggagttgacctacagccggagctactacatgggtgctgaggccaaa
gccaaagggcgtaacatccttctcgggtccagtatttggaccttggggcgagtagttgaaggtggacgca
actgggaggggttttccaatgatccctacctggcggttaaattagggcatgaagctgtcgcgggtatcca
agacgccggagttgttgcattgcccgaacatttccctgtctcaagagcaggagacccatagacttgcggcg
tctgtcactggggctgatgcaatctcatcaaatctcgatgacaagacactccatgaattatatctctgggt
aagcacatcatatcttgggtgagtagatgaaccttactaacacccgaactgggcttttctcgtgatgcagt
ccacgcccgaacttgccagtgatgtgtgcagctacaacagagcaaaccaattcacacgcctgccaaaactcg
aagcttctcaatggccttctcaagggcgagttaggattccagggttttgtcgtctcggactggggcgcac
agcaatctgggtatggcttcagcattggctggcctggatgtttgtcatgccagctcgatcttgtgggtgc
caaccttacccttgggtgtgaacaaacgggaactattcccagagtcacaggttgacaatatgggttacacggtac
gcgaagtctcagccttacttctcaattcttttgaaactgacaatcgtgttaggctccttgcaacttgggtatc
agttgaaccaggaccaagacaccgaagccccaggtcacggactcgtgcgaagctttgggagcctcacc
agtagtcgacgctcgcaacgcaagctccaagcctactatctgggaacgggtgcagtcgagggccatgttctt
gttaagaacaccaacaacgcactgccattcaagcccaacatgaaactcgtttctttgttcggatactctc
acaaagctcctgataagaacatcccagacccccgcccaaggcatgttctcogcttgggtctatcgggtgccca
atccgccaaacatcactgagctgaacctcggctttctcggaaatttgagtctcacatactccgccatcgcg
cccaacggaaccatcatctcgggtggaggtcgggtgccagcgttggactctgttcagctcacccttcg
atgcattcgttttctcgggcgaagaaagagggtactgcgcttttctgggattttgagagctgggatcctta
tgtgaacctacatctgaagcttgcattcgttgcgtggtaatgcatgggctagcgaaggctgggatagacct
gcaacctatgatgcctatactgatgagctcatcaataacgtcgtgacaagtgcgctaactattgttg
ttcttcacaatgctggaaacacgacttgtggatggcttctttgggtcaccccaacgtcaccgctattatcta
cgctcatctcccaggtcaggatagtgagatgctctggtatctttgctctatggcgatgagaacctatct
ggtcgcctcccttacaccggttgcgcgcaacgagacggattatgggtcactgctgaagccagacttgactc
tcgcccccaaccagttaccaacactttccccagtcgcgacttctccgaggggtattttcattgactaccgaca
tttcgatgctaagaacatcacgcctcgttccaggttgggtttcggttgagctacacaacctttgagtac
gctagtctccagatctcaaagtcaccaggcccagacaccggaatacccagctgggtgctcttaccgagggag
gcggttcagatttgtgggacgtcgttgcactgtcacagcaagcgtcaggaacactgggtctgtcgacgg
caaggaggttgacagctatacgttgggtgttccaggtgggtcctatgagacagctacgtggctttacgaaa
ccagctattaaggctggagagacggctacagtgacctttgagcttactcgccgcgacttgagtgtctggg
atgttaatgcccaggagtggaacttcagcaaggcaactatgctatctacgttggccgaagtagtcgaga
tttgctctgcaaagttaccttgagcatctag

FIG. 30A

SEQ ID NO:56

Protein sequence of Fv3G, a GH3 family β -glucosidase from *Fusarium verticillioides*

mfpssisclaalslmsqgllaqsqpenvitddtyfyggspvpvpythtgswwaavakaknlvsqtleekv
nlttggqtttgcsgfipgiprvvgfpglcladagnvrntdyvssfpsgihvgaswnpeltysrsyymgae
akakgvnillgpvfgplgrvveggrnwegfsndpylagklgheavagiqdagvvacgkhflaqeqethrl
aasvtgadaissnlddkthelylcvmcsynrannshacqnsklngllkgelgfggfvsdwgaqqsgm
asalagldvmpssilwganltlgvnngtipesqvdmvtrllatwyqlnqddteapghglaaklweph
pvvdarnasskptiwdgaveghvlvkntnnalpfpkpmklvslfgyshkapdknipdpaggmfsawsiga
qsanitelnlgflgnlsitysaiapngtiisggsgasawtlfsspfdafvsrakkegtalfwdfeswdp
yvnptseacivagnawasegwdrrpatydaytdelinnvadkcantivvlhnagtrldvgffghpnvtaii
yahlpqgdsgdalvsllygdenpsgrlpytvarnetdyghllkpdltlapnqyqhfpqsdffsegifidyr
hfdaknitprfefgfglsyttfeyaslqisksqaqtpeypagaltegggrsdlwdvvtasvrntgsvd
gkevaqlyvgvpggpmrqlrgftkpaikagetatvtfeltrrdlsvwdvnaqewqlqqgnyaiyvgrssr
dlplqstlsi

FIG. 30B

SEQ ID NO:57**Nucleotide sequence of Fv3D, a GH3 family β -glucosidase from *Fusarium verticillioides***

atggctagcattcgatctgtgttgggtctcgggtcttttggcgcgggtgtcaatgcccaagcctacgatg
cgagtgatcgcgctgaagatgctttcagctgggtccagcccaagaacaccactattcttggacagtaagg
ccattcgccctcattaccctgccagtatgttcaccaactacaccaagtgcactgaggctgtactgacatt
ctagacaatgctactggcaagggctgggaagatgccttcgcccaaggctcaaaactttgtctcccaactaa
ccctcgaggaaaaggccgacatgggtcacaggaactccagggtccttgcgctcggcaacatcgctcgccattcc
cogtctcaacttcaacgggtctctgtcttcacgacggccccctcgccatccgagtagcagactaagccagt
gttttccccgctgggtgtatcagccgcttcacgtgggacaaggacctcctctaccagcgcggtctcggca
tggttcaagagttcaaggccaaggggtgctcacatcctcctcgcccccgctcgccgggtcctcttggccgctc
ggcatactctggtcgtaactgggaggggtttctcgccggacccttacctactgggtattgcatggaggag
actatcatgggacatcaagatgctgggtgttcagggtactgcgaagcactttatcggtaatgagcaggagg
tcattgcgaaccctacttttgtcaaggatgggtatattgggtgaggttgacaaggaggctctttcgtctaa
catggatgatcgaaccatgcacgagctttacctctggccctttgccaatgctgttcatgccaaaggcttcc
agcatgatgtgctcgtaaccagcgtctcaacgggtcctacgcctgccagaactcaaagggtcctcaacggaa
ttctgctgatgagcttgggttccagggtacgtcatgtcagattgggggtgccaccacgcgggtgttgc
tgccatcaacagcgggtctcgacatggacatgcccggtgggtatcggtgcctacggaacatactttaccaag
tccttcttcggcggcaacctcaccgcgcggtcaccaacggcaccctcgacgagaccgcgtcaacgaca
tgatcaccgcgatcatgactccttacttctgggtcggccaggacaaggactatcctcgcgcgacccctc
cagcgggtgatctcaacacottcagccccaagagctcctgggtccgcgagttcaacctcaccggcgagcgc
agcgtgacgtccgcggtaaccacggcgacttgatccgcaagcacggcgccgagttctaccgtccttctca
agaacgagaagaacgccttccctcaagaagcccaagtcctatcgctgtcttgggaacgatgctgggtga
tatcactgaggggtttctacaaccagaatgactacgaatttggcactcttgttgctgggtgggtcctgga
actggtcgtttgacataccttgtttcgctctagccgccatcaatgctcgtgctaagcaggacggtaactc
ttgttcagcagtggtatgaacaacactcttattgctaccaccaacgtcactgatctctggatccctgctac
tccgatgtctgcctcggttttctgaagacttgggtcaggagggtgctgatcgtagcacctctcgtt
gactgggacggtaatgatgttgttgagtctgttgccaagtactgcaataacactgtcgtcgtcactcact
cttctgggtatcaacactcttcttgggtgaccaccccaacgtcaccgctattctcgtgcccacttccc
cggtcaggaggtctggcaactcctcgttgacctcctctacggcgatgtcaaccctctggtcgtcttccc
tacaccatcgcttcaacggcaccgactacaacgctccccccaccactgccgtcaacaccacgggcaagg
aggactggcagttcttgggtcgacgagaagctcgagattgactaccgctacttcgacgcgcacaacatctc
cgctccgctacgaattcggtctcgtctctcctactccaccttcgaaatctccgacatctcgtgagcca
ctcgcatccgacattacctcccagcccgaggatctccccgtgcagcccgggcggaaccccgccctctggg
agaccgtctacaacgtgaccgtctcgtctccaaacacgggcaaggctcgacggcgccactgtccccagct
atacgtgacattccccgacagcgcgcctgcgggtacaccacccaagcagctccgtgggttcgacaaggctc
ttccttgagggtggcgagagcaagagtgtcagctttgagctgatgcgcgctgatctgagctactgggata
tcatttctcagaagtgggtcatcctgagggagagtttactattcgtgttggttcagcagtcgggactt
gaaggaggagacaaagggttactgttgggtgaggcgtaa

FIG. 31A

SEQ ID NO:58

Protein sequence of Fv3D, a GH3 family β -glucosidase from *Fusarium verticillioides*

masirsvlvsgllaaqvnaqaydasdraedafswvqpknttilgqyghsphypannatgkgwedafaka
qnfvsqtlleekadmvtgtpgpcvgnivaiprlnfnglclhdgplairvadyasvfpagvsaasswdkd
llyqrglamgqefkakgahillgpvagplgrsaysgrnwegfspdpyltgiameetinghqdagvqata
khfigneqevmrnptfvkdgyigevdkealssnmddrtmhelylwpfanavhakassmmcsyqrlngsy
acqnskvlngilrdelgfggyvmsdwgathagvaainsgldmdmpggigaygtyftksffggnltravt
ngtldetrvndmitrimtpyfwlggdkdypsdpssgdlnfospksswfrelnltgersrdvrnghgd
irkhgaestvllkneknalplkkpksiavfgndagditegfynqndyefgtlvagggsgtgrltylvsp
laainarakqdgltlvqqwmnntliattnvtdlwipatpdivclvflktwaeeaadrehlsvdwdgndvve
svakycnntvvvthssgintlpwadhpntailaahfpggesgnsldllygdvnpssgrlpytiafngt
dynappttavnttgkedwqswfdekleidyryfdahnisvryefgfglsystfeisdisaeplasdits
qpedlpvqpggnpalwetvynvtvsvsntgkvdgatvpqlyvtfpdsapagtppkqlrgfdkvfleage
sksvsfelmrrdlsywdiisqkwlipegeftirvgfssrdlkeetkvtvvea

FIG. 31B

SEQ ID NO:59

Nucleotide sequence of Fv3C, a GH3 family β -glucosidase from *Fusarium verticillioides*

atgaagctgaattgggtcgccgcagccctgtctataggtgctgctggcactgacagcgcagttgctcttg
cttctgcagttccagacactttggctgggtgtaaagggtcagtttttttaccatttctctcgtctaatctc
agccttgttgccatatacgcccttgttcgctcggacgccacgcaccagatcgcgatcatttccctcccttgc
agccttgggttctcttacgatcttccctccgcaattatcagcgccttagtctacacaaaaacccccgag
acagtttttcattgagtttgtcgacatcaagttgcttctcaactgtgcatttgcgtgggtgtctacttct
gcctctagacaaccaaactctgggcgcaattgaccgctcaaacccttgttcaaataacccttttttattcagag
acgcacattttataaatatgcgccctttcaataataccgacttttatgcgcgggcggtgctgtggcggttgat
cagaaagctgacgctcaaaagggttgctcagcagagatacactcgcatactcgccgcctcattatccttcac
catggatggaccctaattgctgttgggtgggaggaagcttacgccaaagccaagagctttgtgtcccaact
cactctcatggaaaagggtcaacttgaccactgggtgttgggtaagcagctccttgcaaacagggtatctca
atccctcagctaacaacttctcagatggcaaggcgaacgctgtgttaggaaacgtgggatcaattctctg
tctcggtatgcgaggtctctgtctccaggatgggtcctcttgggaattcgtctgtccgactacaacagcgct
tttcccgctggcaccacagctgggtgcttcttggagcaagttctctctgggtatgagagaggtctcctgatgg
gcactgagttcaaggagaagggtatcgatatacgctcttgggtcctgctactggacctcttgggtcgactgc
tgctgggtggacgaaactgggaaggcttcacggttgatccttatatggctggccacgccatggccgagggcc
gtcaagggtattcaagacgcaggtgtcatttgccttgtgctaagcattacatcgcaaacgagcagggtaagc
cacttgacgatttgaggaattgacagagaactgacctcttgtagagcacttccgacagagtgggcgagg
tccagtcctcgcaagtacaacatctccgagtctctctcctccaacctggatgacaagactatgcacgagct
ctacgcctggcccttcgctgacgcgctccgcgccggcgctcggttccgtcatgtgctcgtaaacaccagatc
aacaactcgctacgggttgccagaactccaagctcctcaacgggtatcctcaaggacgagatgggcttccagg
gtttcgtcatgagcgattgggcgggccagcataccgggtgcgcttctgccgtcgctgggtctcgatatgag
catgcctgggtgacactgccttcgacagcggatacagcttctggggcggaacttgactctgggtgtcctc
aacggaactgttcccgccctggcgagttgatgacatggctctgcgaatcatgtctgccttcttcaagggtg
gaaagacgatagaggatcttcccgacatcaacttctcctcctggaccgcgacaccttccggttccgtgca
tacatttgcctcaagagaaccgcgagcaggtcaacttggagtcacagtcacgaccacaagagccac
atccgtgagggcgcgtgccaaagggaagcgctcggtgctcaagaacacccgggtcccttccctcaagaacccaa
agttcctcgctgtcattgggtgaggacgcgggtcccaacctgctggaccaaatgggtgtggtgacogtgg
ttgcgataatggtaccctggctatggcttggggctcgggaacttcccaattcccttacttgatcaccctc
gatcaagggtctctctaatcgagctaactcaagacggaactcgatatgagagcatcttgaccaacaacgaat
gggcttcagtacaagctcttgtcagccagcctaacgtgacccgtatcgtttttcgccaatgccgactctgg
tgagggatacattgaagtcgacggaaactttgggtgatcgcaagaacctcaccctctggcagcagggagac
gagctcatcaagaacgtgtcgtccatatgccccaacaccattgtagtctgcacacccgtcgccctgtcc
tactcgccgactacgagaagaacccccaacatcactgccatcgctctgggtgttcccgcccaagagtc
aggcaatgccatcgctgatctcctctacggcaagggtcagccctggccgatctcccttcaacttggggccgc
accgcgagagctacggtaactgaggttctttatgaggcgaacaacggccgtggcgctcctcaggatgact
tctctgaggggtgtcttcatcgactaccgtcacttcgaccgaagatctccaagcaccgatggaaagagctc
tcccaacaacaccgctgtctctctctacgagttcggtcacgggtctatcttgggtccaccttggagtactct
gacctcaacatccagaagaacgtcgagaaccttactctcctcccgctggccagaccatccccgccccaa
cctttggcaacttcagcaagaacctcaacgactacgtgttccccaaggcgctccgatacatctacaagtt
catctacccttctcacaacctcctcatccgccagcgaggcatccaacgatgggtggccagtttggtaag
actgccgaagagttcctccctcccaacgcctcaacgggtcagcccagcctcgtcttcccgctctgggtg
ccccaggtggtaacctcaattgtgggacatcttgtacacccgtcacagccacaatcaccaacacaggcaa
cgccacctccgacgagattccccagctgtatgtcagcctcggtggcgagaaacgagcccatccgtgttctc
cgcggttttcgacggtatcgagaacattgtctcccgccagagcgccatcttcaacgctcaattgacctgtc
gcgatctgagtaactgggatacaaatgccagaactgggtcatcactgacctcccaagactgtctgggt
tggaagcagctctcgcaagctgcctctcagcgccaagttggagtaagaaagccaaacaagggttgtttt
tggactgcaattttttgggaggacatagtagccgcgcgccagttacgtc

FIG. 32A

SEQ ID NO:60

Protein sequence of Fv3C, a GH3 family β -glucosidase from *Fusarium verticillioides*

mklnwvaaalsigaagtdsavalasavpdtlagvkkadaqkvvtrdtlayspphyppspwmdpnavgw
yakaksfvsqtlmekvnlttgvgwqgercvgnvgsiprlgmrglclqdgplgirlsdynsafpagttag
aswskslwyergllmgtefkekgidialgpatgplgrtaaggrnwegftvdpymaghamaeavkgiqdag
viacakhyanegehfrqsgevqsrkyniseslssnlddktnhelayawpfadavragvgsvmcsynqinn
sygcqnsklngilkdemgfqgfvmstdwaaqhtgaasavagldmsmpgdtafdsgysfwggnltlaving
tvpawrvddmalrimsaaffkvgtiedlpdinfsswtrdtfgfvhtfaenreqvnfgvnmghdhkshir
eaaakgsvvlkntgslplknkflavigedagpnpagpnngcgdrgcdngtlamawsgtsqfpylitpdq
glsnratqdgtryesiltnewasvqalvsqpnvtaivfanadsgegyievdgnfgdrknltlwqqgdel
iknvssicpntivlhtvgpvlladyeknpnitaivwaglpqgesgnaiadllygkvspgrspftwgrtr
esygtevlyeannrgapqdddfsegvfidyrhfdrrspstdgksspnntaaplyefghglswstfeysdl
niqknvenpysppagqtipaptfgnfsknldyvfpkgvryiykfiypflntssaseasndggqfgkta
eeflppnalngsaqprlpasgapggnpqlwdilytvtatitntgnatsdeipqlyvslggenepirvlrg
fdrieniapggsaifnaqltrrdlsnwdtnaqnwvitdhpkvtvwgsssrklplsakle

FIG. 32B

SEQ ID NO:61

Nucleotide sequence of Tr3A, a GH3 family β -glucosidase from *Trichoderma reesei*

atgcggttaccgaacagcagctgcgctggcacttgccactgggcccctttgctagggcagacagtcaggtata
gctgggtcccatactgggatgtgatatgtatcctggagacaccatgctgactcttgaatcaaggtagctca
acatcgggggcctcggtgagggcagttgtacctcctgcagggactccatggggaaccgcgtacgacaagg
cgaaggccgcattggcacaagctcaatctccaagataaggctcgcatcgtgagcgggtgtcggctggaacgg
cggctccttgcggttggaacacatctccggcctccaagatcagctatccatcgctatgccttcaagacgga
cccctcgggtgttcgatactcgacaggcagcacagcctttacgcgcgggcgttcaagcggcctcgacgtggg
atgtcaatttgatccgcgaacgtggacagttcatcggtgaggaggtgaaggcctcggggattcatgtcat
acttggctcctgtggctgggcccgtgggaaagactccgcagggcggctcgcaactgggagggcttcgggtgtc
gatccatatctcacgggcattgccatgggtcaaaccatcaacggcatccagtcggtaggcgtgcaggcga
cagcgaagcactatatcctcaacgagcaggagctcaatcgagaaaccatttcgagcaaccagatgaccg
aactctccatgagctgtatacttggccatttgccgacgcgggttcaggccaatgtcgcttctgtcatgtgc
tcgtacaacaagggtcaataccacctgggcctgagaggtacgtacacgctgcagactgtgctgaaagacc
agctgggggttcccaggtatgtcatgacggactggaacgcacagcacacgactgtccaaagcgcgaatto
tgggcttgacatgtcaatgcctggcacagacttcaacggtaacaatcggctctgggggtccagctctcacc
aatgcggtaaatagcaatcaggtcccccagagcagagtcgacgatatggtgactcgtatcctcgcgcgat
ggtacttgacaggccaggaccaggcaggctatccgtcgttcaacatcagcagaaatgttcaaggaaacca
caagaccaatgtcagggcaattgccagggacggcatcgcttctgtcagaatgacgccaacatcctgccg
ctcaagaagcccgtatgcattgccgtcgttggatctgcgcgaatcattggtaaccacgccagaaactcgc
cctcgtgcaacgacaaaaggctgcgacgacggggccttgggcatgggttgggggttcgggcgcgcgtcaacta
tcctgacttcgtcgcgccttacgatgccatcaataccagagcgtcttcgcagggcaccaggttaccttg
agcaacaccgacaacacgtcctcaggcgcacgtcgcagcaagaggaaaggacgtcgccatcgtcttcatca
ccgccgactcgggtgaaggctacatcacctggaggggcaacgcgggcgatcgcaacaacctggatccgtg
gcacaacggcaatgccctgggtccaggcgggtggccgggtgccaaacagcaacgtcattgttgttgcactcc
gttggcgccatcattctggagcagattcttgcctctccgcagggtcaaggccgttgcctgtgggcgggtcttc
cttctcaggagagcggcaatgcgtcgtcgcagctgctgtggggagatgtcagcccttctggcaagctggt
gtacaccattgcgaagagccccaatgactataaacctcgcacgttctccggcggcagtgacagcttcagc
gagggactgttcatcgactataagcacttcgacgacgccaatatcacgcgcgggtacgagttcggctatg
gactgtgtaagtttgctaaactgaacaatctattagacaggttgactgacggatgactgtggaatgatag
cttacaccaagttcaactactcacgcctctccgtcttgcgcagcccaagtctgggtcctgcgactggggc
cgttgtgcgggaggcccgagtgatctgttcagaatgtcgcgacagtcaccgttgacatcgcaaacctc
ggccaagtgactggtgccgaggtagcccagctgtacatcacctacccatcttcagcaccagggacccctc
cgaagcagctgcgaggctttgccaaagctgaacctcacgcctgggtcagagcgggaacagcaacgttcaacat
ccgacgacgagatctcagctactgggacacggcttcgcagaaatgggtgggtgccgtcgggggtcgtttggc
atcagcgtgggagcagagcagccgggatatcaggctgacgagcactctgtcggtagcgtag

FIG. 33A

43 / 111

SEQ ID NO:62

Protein sequence of Tr3A, a GH3 family β -glucosidase from *Trichoderma reesei*

MRYRTAAALALATGPFARADSHSTSGASAEAVVPPAGTPWGTAYDKAKAALAKLNLQDKVGIVSGVGWNG
GPCVGNTSPASKISYPSSLCLQDGPLGVRYSTGSTAFTPGVQAASTWDVNLIRERGQFIGEEVKASGIHVI
LGPVAGPLGKTPQGGRNWEGFGVDPYLTGIAMGQTINGIQSVGVQATAKHYILNEQELNRETISSNPDDR
TLHELYTWPFADAVQANVASVMCSYNKVNTTWACEDQYTLQTVLKDQLGFPGYVMTDWNQAHTTVQSANS
GLDMSMPGTDENGNNRLWGPALTNAVNSNQVPTSRVDDMVTRILAAWYLTGQDQAGYPSFNI SRNVQGNH
KTNVRAIARDGIVLLKNDANILPLKKPASIAVVGSAAIIGNHARNSPSCNDKGCDDGALGMWGSGAVNY
PYFVAPYDAINTRASSQGTQVTLSTNDNTSSGASAARGKDVAIVFITADSGEGYITVEGNAGDRNNLDPW
HNGNALVQAVAGANSNVIVVHSGAIILEQILALPQVKAVVWAGLPSQESGNALVDVLWGDVSPSGKLV
YTIAKSPNDYNTRIVSGGSDSFSEGLFIDYKHFDDANITPRYEFYGLSYTKFNYSRLSVLSTAKSGPAT
GAVVPGGPSDLFQNVATVTVDIANSQVGTGA EVAQLYITYPSSAPRTPPKQLRGFAKLNLTPGQSGTATF
NIRRRDLSYWD TASQKWVPSGSFGISVGASSRDIRLTSTLSVA

FIG. 33B

SEQ ID NO:63**Nucleotide sequence of Tr3B, a GH3 family β -glucosidase from *Trichoderma reesei***

atgaagacgttgtcagtggttgcgtgccgcccttttggcgccgtagctgaggccaatccctaccgcctc
ctcactccaaccaggcgtaactcgcctcctttctacccttcgccatggatggaccccagtgctccaggctg
ggagcaagcctatgccccagctaaggagttcgtctcgggcttgactctcttgagaaaggtcaacctcacc
accggtggttggttgatgggtgagaagtgcgttggaacggttggtaccgtgcctcgtttggcatgcgaa
gtctttgcatgcaggacggccccctgggtctccgattcaacacgtacaacagcgctttcagcgttggctt
gacggccgcgcagctggagccgacacctttgggttgaccgcggtaccgctctgggtccgaggcaaaag
ggcaaggggtgctgatgttctctcggacccgtgggtggccctctcggtcgcaaccccaacggaggccgta
acgtcgaggggttcggctcggatccctatctggcggtttgggtctggccgataccgtgaccggaatcca
gaacgcgggcaccatcgcctgtgccaagcacttctcctcaacgagcaggagcatttccgccagggtcggc
gaagctaacgggttacggataccccatcaccgaggtctctgtcttccaacggttgatgacaagacgattcacg
agggtgacggctggcccttcaggatgctgtcaaggctgggtgctgggtccttcatgtgctcgtacaacca
ggtcaacaactcgtacgcttgccaaaactccaagctcatcaacggcttgctcaaggaggagtaagggtttc
caaggctttgtcatgagcgactggcaggcccagcacacgggtgtcgcgtctgctggttgccggtctcgata
tgaccatgcctgggtgacaccgccttcaacacggcgcatcctactttggaagcaacctgacgcttgctgt
tctcaacggcaccgctccccgagtggcgcatgacgacatgggtgatgcgtatcatggctccttcttcaag
gtgggcaagacgggttgacagcctcattgacaccaactttgattcttggaaccaatggcgagtaagggtacg
ttcaggccgcgctcaatgagaactgggagaaggtaactacggcgctcgatgtccgcgcccaacctatgcgaa
ccacatccgcgaggttgggcgccaagggaactgtcatcttcaagaacaacggcaccctgcccttaagaag
cccaagttcctgacgctcattgggtgaggatgctggcgccaacctgcccggcccaacggctgcggtgacc
goggctgtgacgacggcactcttgccatggagtggggatctgggtactaaccaacttccctacctcgtcac
ccccgacggcgccctgcagagccaggctctccaggacggcaccgcctacgagagcaccctgtccaactac
gccatctcgcagacccaggcgtcgtcagccagcccgatgccattgccattgtctttgccaactcggata
gcggcgaggggtacatcaacgtcgtatggcaacgagggcgacggcaagaacctgacgctgtggaagaacgg
cgacgatctgatcaagactggtgctgctgtcaaccccaagacgattgtcgtcatccactcgaccggcccc
gtgattctcaaggactacgccaaccaccccaacatctctgccattctgtgggcccgtgctcctggccagg
agtctggcaactcgtggctgacattctgtacggcaagcagagcccgggcgccactcccttcaactgggg
ccgctcgttgagagctacggagttagtgttatgaccacgccccacaacggcaacggcgctccccaggat
aacttcaacgagggcgcccttcacgactaccgctactttgacaagggtgggtcccggaagcctcgcagct
cggacaaggctcccacgtacgagtttggtctcggactgtcgtggctcgacgttcaagttctccaacctcca
catccagaagaacaatgtcggccccatgagccccgcccaacggcaagacgattgcggtcctctctgggc
agcttcagcaagaaccttaaggactatgggttcccccaagaacgttcgcgcacatcaaggagtttatctacc
cctacctgagcaccactacctctggcaaggaggcgtcgggtgacgctcactacggccagactgcgaagga
gttctctcccgccggtgccttggaacggcagccctcagcctcgtctcgggcctctggcgaaccggcggc
aacggccagctgtacgacattctctacaccgtgacggccaccattaccaacacgggctcggtcattggacg
acggcgttccccagctgtacctgagccacggcggtcccaacgagccgcccaaggtgctgctggtggttcga
ccgcatcgagcgcatgtctccggccagagcgctcacgttcaaggcagacctgacgcgcgctgacctgtcc
aactgggacacgaagaagcagcagtggtcattaccgactacccaagactgtgtacgtgggcagctcct
cgcgcgacctgccgctgagcgcccgccctgccatga

FIG. 34A

SEQ ID NO:64

Protein sequence of Tr3B, a GH3 family β -glucosidase from *Trichoderma reesei*

mktlsvfaaallaavaeanpyppphsnqaysppfyppspwmdpsapgwedayaqakefvsgltllekvnl
ttgvgwmgekcvgnvgtvprlgmrslcmqdgplglrftynsafsvgltaaaswsrhlwvdrgtalgse
akgkgvdvllgpvagplgrnpnggrnvegfgsdpylaglaladtvtgignagtiacakhflnegehfr
qvgeangygypitealssnvddktihevypgpfqdavkagvgsfmcsvynqvnsyqcqnsklngllke
eygfggfvmfmsdwqaghtgvasavagldmtmpgdtafntgasyfgsnltlavlngtvpewriddmvmrim
apffkvgtvdsldtnfdswtngeyygyvqaavnenwekvnygvdvranhanhirevgakgtvifknng
ilplkkpkfltvigedaggnpagpncgdrgcdgtlamewsgttnfpylvtpdaalqsqalqdgtry
esilsnyaisqtqalvsqpdaiaivfansdsgegyinvdgnegdrknltlwknngddliktvaavnpkti
vvihstgppvilkdyanhpnisailwagapggsgnslvdilygkqspgrtpftwgpslesygvsvmttp
nngngapqdnfnegafidyryfdkvapgkprssdkaptyefgfglswstfkfsnlhiqknnvgpmsppn
gktiaapslgsfsknlkdygfpknvrrikefiypylstttsgkeasgdahyggtakeflpagaldgspq
prsaasgepggnrqlydilytvtatitntgsvmdavpqlylshggpneppkvlgfdrieriapggsv
tfkadltrrdlsnwdtkkqqwvitdypktvyvgsssrldplsarl

FIG. 34B

SEQ ID NO:65

Nucleotide sequence of Te3A, a GH3 family β -glucosidase from *Talaromyces emersonii*, codon-optimized for expression in *T.reesei*

atgcgcaacggcctcctcaaggtcgccgccttagccgctgccagcgccgtcaacggcgagaacctcgct
acagcccccccttctaaccagccctgggccaacggccaggcgactgggcccaggcctaccagaaggc
cgctcagttcgtcagccagctcaccctcgccgagaaggtaaacctcaccaccggcaccggctgggagcag
gaccgctgcgtcgccagggtcggcagcatccccgcttaggcttccccggcctctgcatgcaggacagcc
ccctcgggctcgccgacaccgactacaacagcgcccttccctgccggcggttaacgtcgccgccacctggga
ccgcaacttagcctacgcagaggcgctcgccatgggcgaggaaacaccgcggaaggcgctgcagctccag
ttaggccccgctcgccggcccttagggcgctctcctgatgccggcgcaactgggagggcttcgccccg
accccgctcctcaccggcaacatgatggccagcaccatccagggcacccaggatgctggcgctcattgcctg
cgccaagcaacttcactctctacgagcaggaacacttcggccaggcgccagggaaggctacgacatcagc
gacagcatcagcgccaacgcgcgacgacaagaccatgcacgagttatacctctggcccttcgccgatgccg
tcggcgccgggtgctcggcagcgctcatgtgcagctacaaccagggtcaacaacagctacgcctgcagcaacag
ctacaccatgaacaagctcctcaagagcgagttaggcttcagggttcgctcatgaccgactggggcggc
caccacagcggcgtcggtctctgcccgcggcctcgacatgagcatgcccgcgacattgccttcgaca
ggggcagctcttctggggcaccacactcaccggtgcgctcctcaacgggtccatccccgagtgggcgct
cgacgacatggcgctcgcctcatgagcgccactacaagggtcgggcgcgaccgctacagcgctccccatc
aacttcgacagctggaccctcgacacctacggccccgagcactacgcgctcgccaggggccagaccaaga
tcaacgagcagctcgacgtccggcggaaccaacgcgcgagatcatccagagatcgggcgccgctccgcgct
cctcctcaagaacaaggcggcctccccctcactggcaccgagcgcttcgctcggtgtctttggcaaggat
gctggcagcaaccctggggcgtaacgggtgcagcgacgcggtgcgacaacggcaccctcgccatgg
gctggggcagcggcacgcgccaactttccctacctcgtaacccccgagcagggccatccagcgcgaggctct
cagccgcaacggcaccttcacggcatcaccgacaacggcgcccttagccgagatggccgctgccgctct
caggccgacacctgcctcgctctttgccaacgcgcgactccggcgagggtacatcaccgtcgatggcaacg
agggcgaccgcaagaacctcaccctctggcagggcgccgaccagggtcatccacaacgtcagcgccaactg
caacaacaccgtcgctcgctcttacacaccgtcgggccccgctcctcatcgacgactggtaacgaccaccccaac
gtcacccgcatcctctggggcggtttaccgggtcaggaaagcggaacagcctcgctcgacgtcctctacg
gcccgtcaacccccggcaagaccccccttcacctggggcagagcccgcgaacgactatggcgccccctctcat
cgtcaagcctaacaacggcaaggcgccccccagcaggacttcaccgagggcatcttcacgactaccgc
cgcttcgacaagtacaacatcaccacctctacgagttcggttcggcctcagctacaccaccttcgagt
tcagccagttaaacgtccagcccatcaacgccccctccctacacccccgcgagcggttttacgaaggccgc
ccagagcttcggccagccctccaatgccagcgacaacctctaccttagcgacatcgagcgcgctccccctc
tacatctacccctggctcaacagcaccgacctcaaggccagcgccaacgacccccgactacggcctcccca
ccgagaagtagctcccccccaacgccaccaacggcgacccccagcccattgacctgcggggcggtgcccc
tgggcggaacccccagcctctacgagcccgctcgcccgcgtaaccaccatcatcaccacacccggcaaggctc
accggcgacgaggtccccagctctatgtcagcttagggcgccctgacgacgcccccaaggctcctccgcg
gcttcgaccgcatcaccctcgccctggccagcagtaaccttggaaccacacctcactcgcccgacat
cagcaactgggacccccgtcaccagaactgggtcgtaaccaactacaccaagaccatctacgtcggcaac
agcagccgcaacctccccctcaggccccctcaagccctaccccggcattctgatga

FIG. 35A

SEQ ID NO:66

Protein sequence of Te3A, a GH3 family β -glucosidase from *Talaromyces emersonii*

mrnqllkvaalaaasavngenlaysppfypspwangggdwaeayqkavqfvsqltlaekvnlttgwgweq
drcvqqvgsiprlgfpqlcmqdsplgvrdtdynsafpagvnvaatwdrnlayrrgvamgeehrgkgvdvq
lgpvagplgrspdagrnwegfapdpvltgnmmastiqqiqdagviacakhfilyeqehfrqgaqdgdydis
dsisanaddktmhelylwpfadavragvgsvmcsynqvnnsyacsnsytmnkllkselgfggfvmtdwgg
hhsgvgasalagldmsmpgdiafdsgtsfwgtnltvavlngsipewrvddmavrimsayykvgvrdrysvpi
nfdswtldtygpehyavgggqtkinehvdvrgnhaeiiheigaasavllknkgglpltgterfvvgvfkgd
agsnpwgvngcsdrgcdngtllamgwsgtanfpylvtpeqaiqrevlsrngtftgitdngalaemaaaaas
qadtclvfanadsgegyitvdgnegdrknltlwggadqvihnvsancnntvvvlhtvgpvliddwydhp
vtailwaglpqgesgnsldvlygrvnpkgktpftwgrarddygaplivkpnnkggapqqdftgigidyr
rfdkynitpiyefgfglsyttfefsqlnvqipinappytpasgftkaaqsfgqpsnasdnlypsdiervpl
yiypwlinstdlkasandpdyglptekyvppnatngdpqpdpaggapgnpslyepvarvtiitntgkv
tgdevpqlyvslggpddapkvlgfdritlapggqylwtttlttrdisnwdpvtqnwvvtnytktiyvg
ssrnplqaplkpypgi

FIG. 35B

SEQ ID NO:67**Nucleotide sequence of An3A, a GH3 family β -glucosidase from *Aspergillus niger***

atgcgcttcaccagcatcgaggccgctcgccctcaccgccgctcagcctcgccagcgccgacgagttagcct
acagccccccctactaccccagcccctggggccaaacggccagggcgactggggccgaggcctaccagcgcg
cgctcgacatcgctcagccagatgaccctcgccgagaaggtcaacctcaccaccggcaccggctgggagtta
gagttatgcgtcgccagactggtggcgctccccgcctcggcacccccggcatgtgcgcccaggacagcc
ccctcggcgtccgacagcgactacaacagcgccctccctgcccggcgtaacgtcgccgccacctggga
caagaacctcgctacctccgcgccagggccatggggccaggaattcagcgacaagggcgccgacatccag
ttaggccccgctgcgggcccttttagggcgctctcccgacggcggcagaaactgggagggccttcagccccg
accccgctctcagcggcgtcctcttcgcccagactatcaagggcacccaggtgctggcgctcgccac
cgccaagcactacattgcctacgagcaggaacacttcgcccagggcccccgaggcccagggtacggcttc
aacatcaccgagagcgggcagcgccaaacctcgacgacaagaccatgcacgagttataacctctggcccttcg
cogacgccattagagctggcgctggtgctgtcatgtgcagctacaaccagatcaacaacagctacggctg
ccagaacagctacacctcaacaagctcctcaaggccgagttaggcttcaggggcttcgtcatgtccgac
tgggccgcccaccacgcggcgctcagcgggcgcccttagccggcctcgacatgagcatgcccggcgacgtcg
actacgacagcgccaccagctactggggcaccaacctcaccatcagcgctcctcaacggcaccgtccccca
gtggcgcgctcgacgacatggccgtccgcatcatggccgcctactacaaggctcgggcgcgaccgcctctgg
accccccccaacttcagcagctggaccccgacgagtagcggttcaagtactactacgtcagcgagggcc
cctatgagaaggtaaccagttcgtcaacgtccagcgcaaccacagcgagttaatccgcccgcacgcggcg
cgacagcaccgtcctcctcaagaacgacggcgccctccccctcaccggcaaggaacgcctcgctcgccctc
atcggcgaggacgcccgcagcaaccctacggcgccaacggctgcagcgaccggcgctgcgacaacggca
ccctcgccatgggctggggcagcgccaccgccaacttccttacctcgtaacccccgagcaggccatcag
caacgaggtcctcaagaacaagaacggcgctctttaccgccaccgacaactgggcatcgaccagatcgag
gccttagccaagaccgcctctgtcagcctcgtctttgtcaacgcgcgacagcgggcgagggctacatcaacg
tcgacggcaacctcgggcgaccgcgcgaacctcaccctctggcgcaacggcgacaacgtcatcaaggccgc
cgccagcaactgcaacaacaccatcgtaacacacagcgctcgggccccgctcctcgtaacgagtggtac
gacaacccccaacgtcaccgccaatcctctggggcggttaccggccaggaaagcgggcaacagcctcgccg
acgtcctctacggccgctcaacctggcgccaagagcccccttcacctggggcaagacccgcgaggccta
tcaggactacctctacaccgagcccaacaacggcaacggcgccccccagggaagatttcgtcgagggcgctc
tttatcgactaccgcggttttgacaagcgcaacgagactcccatctacgagttcggtacaggcctcagct
acaccaccttcaactacagcaacctccaggtcgaggtcctcagcgccccctgcctacgagcccgcagcgg
cgagactgagggcgccccccaccttcggcgaggtcgggcaacgcgcagcgactactataccccgacggcctc
cagcgcatcaccaagttcatctacccctgggtcaacagcaccgacctcgaggccagcagcgggcgacgcct
cttacggccaggacgcctccgactacctccccgaggggtgccaccgacggcgagcgtcagcccatcttacc
tgccggtggcggtgctggcggaacccccagactctacgacgagctgatccgcgtcagcgtaacccatcaag
aacaccggcaaggtcgctggtgacgaggtccccagctctacgtcagcttagggggccctaacgagccca
agatcgctcctccgccagttcgagcgcatcaccctccagcccagcaaggaaactcagtgagcaccacct
cactcgccgcgacctcgccaactggaacgtcgagactcaggactgggagatcaccagctaccccaagatg
gtctttgcccggcagcagcagccgcaagctccccctccgcgccagcctccccaccgtccactgatga

FIG. 36A

SEQ ID NO:68

Protein sequence of An3A, a GH3 family β -glucosidase from *Aspergillus niger*

mrftsieavaltavslasadelaysppyyppswangggdwaeayqravdivsqmtlaekvnlttgtgwel
elcvggtggvprlgipgmcaqdsplgvrdsdynsafpagvnvaatwdknlaylrgqamgqefsdkgadiq
lgpaagplgrspdgggrnwegfspdpalsgvlfaetikgiqdagvvatakhyaieqehfrqapeaaggygf
nitesgsanlddktmhelylwpfadairagagavmcsynqinnsygcqnsytlnklkkaelgfggfmsd
waahhagvsgalagldmsmpgdvdydsgtsywgtnltisvlngtvpqwrddmavrmaayykvgrdrwl
tppnfsswtrdeygfkyyyvsegpyekvnqfvnqgrnhselirrigadstvlkndgalpltgkerlval
igedagsnpygangcsdrgcdngt lamgwsgtanfpylvtpeqaisnevlknkngvftatdnwaidqie
alaktasvslvfvnadsgegyinvdgnlgdrnltlwrngdnvikaaasncntiviihsvgpvlvnewy
dnpnvtailwgglpqgesgnsladvlygrvnpgakspftwgktreayqdyltepnngngapqedfvegv
fidyrgfdkrnetpiyefgyglstyttfnysnlqvevlsapayepasgeteaaptfgevgnasdylypdgl
gritkfliypwlinstdleassgdasyggdasdylpegatdgsaqpilpagggaggnprlydelirvsvtik
ntgkvagdevpqlyvslggpnepkivlrqferitlqpsketqgsttlttrrdlanwnvetqdweitsypkm
vfagsssrklpiraslptvh

FIG. 36B

SEQ ID NO:69

Nucleotide sequence of Fo3A, a GH3 family β -glucosidase from *Fusarium oxysporum*

atgaagctgaactgggtcgccgcagccctctctataggtgctgctggcactgatgggtgcagttgctcttg
cttctgaagttccaggcacttttggtggtgtaaaggctcggttttttaaccatttctcactaattctcag
ccttggttgccatatacgcccttattcgctcggaagctacgcaccaaatecgcatcatttctcccttgag
ccttggtttcttttttcgatcttccctccgcaatcgccagcacccttagcctacacaaaaacccccgaga
cagtctcattgagtttgctgacatcaagttgcttctcaagtggtgcatgttgctggctgtctacttctgcc
tctagaccaccaaattctgggcgcaattgatcgctcaaacccttggtcgaataagccttttattcgagacgt
ccaatttttacagagaatgtacctttcaataataccgacggttatgcgcggcggtggctgctgtgatgggt
gttgatcagaatactgacgctcaaaagggttgacagagagatacactcgacactcactcctcactatc
cttcaccatggatggatcctaattgccattggctgggaggaagcttacgccaagcaaagaactttgtgtc
ccagctcactctcctcgaaaagggtcaacttgaccactgggtgttggttaagtagctccttgcaaacagtgc
atctcgggtctccttgactaacgactctctcaggtggcaaggcgacgctgtgtaggaaacgtgggatcaa
ttcctcgtcttggtatgagaggtctttgtcttcaggatggctcctcttggaattcgtctgtccgattacaa
cagtgtctttcccgctggcaccacagctgggtgcttcttgagcaagttctctgtgatgagaggggtctt
ctgatgggaactgagttcaaggggaagggtatcgatatacgctcttgccctgctactggctcctcttgccc
gcactgctgctggtggacgaaactgggagggctttaccggtgatccttatatggctggccatgccatggc
cgaggccgtcaagggcatccaagacgcaggtgtcattgcttggtgctaagcattacatcgcaaacgagcaa
ggtaagccaattggacgggtttgggaaatcgacagagaactgaccccttgtagagcacttccgacagagt
ggcgaggtccagtcgccgaagtacaacatctccgagtcctctcctccaacctggacgacaagactttgc
acgagctctacgcctggccctttgctgatgcggtccgcgctggcgctcggttcagtcattgtctctttaa
tcagatcaacaactcgtagcggttgccagaactccaagctcctcaacgggtatcctcaaggacgagatgggt
ttccagggcttcgtcatgagcgattggggcgcccgacacacgggtgctgcttctgcgctcgctgggtcttg
atatgagcatgcttggtgacaccgcttcgacagtggtatagcttctgggggtggaaacctgactcttgcc
tgtcatcaacggaactgttcccgctggcgagttgatgacatggctctgcgaatcatgtcggccttcttc
aagggttggaagacggtagaggacctccccgacatcaacttctcctcctggacccgcgacaccttcggct
tcgtccaaacatttgctcaagagaacccgcaacaagtcaactttggagttaacgtccagcacgaccacaa
gaaccacatccgtgagttctgcgcgaagggaagcgtcatcctcaagaacacgggtcccttccccctcaac
aatcccaagttcctcgtctgctattgggtgaggacgcgggtcccaacctgctggacccaatgggtgoggcg
accgtgggttgcgacaatggtaccttggtatggcttggggctcgggaaacttctcaattccttacttgat
cacacccgaccaagggtctccagaacogagctgcccagaacggaactcgatatgagagcatcttgaccaac
aacgaatgggcccagacacaggctcttggcagccaaacccaacgtgacgctatcggtttttgccaacgccc
actctggtgaggggttacattgaagtcgacggaaacttcgggtgatcgcaagaacctcaccctctggcaaca
gggagacgagctcatcaagaacgtctcgtccatctgcccacacaccattgtcgttctgcataacgctcggc
cctgtcctgctgcgcgactacgagaagaacccccaacatcacccgcatcgctctgggtggtcttcccgccc
aagagtctggcaatgccatcgctgatctcctctacggcaaggtaagccctggccgatctccttcaacttg
gggcccgaacccgtgagagctacggtaccgaggttctttatgaggcgaacaacggcgtggcgctcctcag
gatgacttctcggagggtgtcttcattgactacogtcactttgatcgacgatctcccagcacccgatggca
agagcgctcccaacaacaccgctgctcctctctacgagttcgggtcatggtctgtcttggaactacctttga
gtattcagacctcaacatccagaagaacgttaactccacctactctcctcctgctgggtcagaccattcct
gccccaaacctttggcaacttcagcaagaacctcaacgactacgtgttccctaagggtgtccgatacatct
acaagttcatctaccttctctgaacacttctcctcctccgcagcgaggcatctaacgacggcgccagtt
tggttaagactgccgaagagttcctacctccaaacgcctcacaacggctcagcccagcctcgtcttccctct
tctgggtgccccaggcggttaacctcaatttggtggatctcctgtacacggtcacagccacaatcaccaaca
caggcaacgccacctccgacgagattccccagctgtatgtcagcctcgggtggcgagaacgaacccgttcg
tgtcctccgcggttttcgaccgtatcgagaacattgctcccgccagagcgccatcttcaacgctcaattg
accgctcgcgatctgagcaactgggatgtggatgccagaactgggttatcccgaccatccaaagacgg
tgtgggttggaagtagttctcgcaagctgcctctcagcgccaagttggaataa

FIG. 37A

SEQ ID NO:70

Protein sequence of Fo3A, a GH3 family β -glucosidase from *Fusarium oxysporum*

mklnwvaaalsigaagtdqavalasevpgtlagvkntdaqkvvtrdtlahspphypspwmdpnaigweea
yakaknfvsqtltlekvnlttgvwgqgercvgnvgsiprlgmrglclqdgplgirlsdynsafpagttag
aswskslwyergllmgtefkgkgidialgpatgplgrtaaggrnwegftvdpymaghamaeavkgiqdag
viacakhyanegehfrqsgdevqsrkyniseslssnlddktlhelayawpfadavragvgsvmcsynqinn
sygcqnsklngilkdemgfggfvmstdwaaqhtgaasavagldmsmpgdtafdsygysfwggnltlaving
tvpawrvddmalrimsaaffkvgtvedlpdinfsswtrdtfgfvqtfagenreqvnfgvvnqhdhknhir
esaakgsvilkntgslplnnpkflavigedagpnpagpncgdrgcdngtlamawgsgtsqfpylitpdq
glqnraaqdgtryesiltnewaqtqalvsqpnvtaivfanadsgegyievdgnfgdrknltlwqqgdel
iknvssicpntivvlhtvgpvlladyeknpnitaivwaglpqgesgnaiadllygkvspgrspftwgrtr
esygtevlyeannrgapqddfssegvfidyrhfdrrspstdgksapnntaaplyefghglswttfeysdl
niqknvnstysppagqtipaptfgnfsknldyvfpkgvryiykfiypflntssaseasndggqfgkta
eeflppnalngsaqprlpssgapggnpqlwdilytvtatitntgnatsdeipqlyvslggenepvrvlrg
fdrieniapggsaifnaqltrrdlsnwdvdagnwvitdhpkvtwvgsssrklplsakle

FIG. 37B

SEQ ID NO:71**Nucleotide sequence of Gz3A, a GH3 family β -glucosidase from *Gibberella zeae***

ATGAAGGCCAATTGGCTTGCCGCGGCCGTTTATTTGGCTGCTGGCACCGATGCTGCAGTCCCTGACACTT
TGGCAGGAGTCAATGTAAGCTACTCTTCAATTTTCATCTCATCTCAACTTTGCCAGGCCACAACAACCTTTT
CTTCACTCACGATCTTTTCACCATAAACGCAACAGTTTCACAAAAAATAAAGCCCAATCATGTCTCTGA
TCGTTGAACTCGCCATCTTCGTTTACATCGCGGTTGTCTTTTTCTTCTTGTACTTCTCATTCGTTGTTGT
TCTCTACATTTTCGACTGGCTGTTTAGCCTTGAGATTCTTCTCACTCCCCGTGATGCCTAGATCACTCTC
TGAGGCGTTTAATCTACTTGTAGAGATGCGCCTCTCATTTGTTGTGTGCTAGTCGCGATAGTTGCTGGA
ATTGCAGTCCTTGATCTTCCTACTGACACTCAAAGCTCGTTGCGCGGGACACACTCGCTCACTCTCCTC
CTCACTATCCCTCGCCATGGATGGACCTTAACGCTGTGCGCTGGGAGGACGCTACGCCAAGGCCAAGGA
CTTTGTCTCCCAGATGACTCTCCTAGAAAAGGTCAACTTGACCCTGGTGTGGGTAAGTAACGAGCGAC
AAGACGTCTACAATCCACTAACACGATCTCTAGATGGCAGGGCGAACGTTGTGTTGGAAACGTGGGATCT
ATCCCTCGTCTCGGTATGCGAGGCCTCTGTCTCCAGGATGGTCCCTCTCGGAATTCGCTTCTCCGACTACA
ACAGCGCTTTCCCTACTGGTGTACCGCTGGTGCTTCTTGGAGTAAGGCCCTTTGGTACGAGCGAGGACG
ATTGATGGGTACCGAGTTTAAGGAGAAGGGTATCGATATTGCTCTCGGCCCTGCAACTGGTCTCTCGGT
CGCCACGCTGCTGGTGGACGAACTGGGAAGGCTTCACTGTGACCCCTACGCCGCTGGCCATGCTATGG
CTGAGACTGTCAAGGGTATCCAAGATTCTGGAGTCATTGCTTGTGCTAAGCATTACATCGCAAACGAGCA
AGGTATGTACAGGCCCATTCATGGCTTCAGGAACGAAACTAACTCTTAATAGAACACTTCCGTCAACG
AGGCGATGTCATGTCTCAAAAGTTCAACATTTCCGAGTCTCTGTCTTCCAACCTTGACGATAAGACTATG
CACGAGCTCTACAACCTGGCCTTTTCGCCGACGCGCTCCGCGCCGGTGTGGCTCCATTATGTGCTCTTACA
ACCAGGTCAACAACCTCATATGCTTGCCAGAACTCCAAGCTCCTCAACGGCATCCTCAAGGACGAGATGGG
TTTCCAGGGTTTCGTCATGAGCGATTGGCAGGCTCAGCACACCGGTGCCGCTCCGCTGTTGCCGGTCTT
GACATGACCATGCCTGGTGACACCGAGTTCAACACTGGCTTCAGCTTCTGGGGTGGAAACCTGACCTCG
CTGTTATCAACGGTACTGTTCCCGCTGGAGAATCGACGACATGGCTACCCGAATTATGGCTGCTTTCTT
CAAGGTTGGCCGATCTGTTGAGGAGGAACCCGACATCAACTTCTCAGCTTGGACTCGTGATGAGTATGGC
TTCGTCCAGACCTACGCCCAAGAGAACCGAGAAAAGGTCAACTTTGCTGTAAATGTCCAGCACGACCACA
AGCGCCACATTGCGGAGGCTGGCGCAAAGGGATCCGTGCTCCTCAAGAACACTGGCTCACTTCCTCTTAA
GAAGCCCCAGTTCCTCGCTGTCATTGGAGAGGACGCTGGTTCCAACCTGCCGGACCCAACGGTTGCGCT
GACCGTGGATGCGACAACGGTACTCTTGCCATGGCATGGGGTTCCGGAACCTCTCAATCCCCTACCTTG
TCACCCCCGACCAAGGCATCTCGCTCCAGGCTATTCAAGGACGGTACTCGTTATGAGAGCATCCTCAACAA
CAACCAGTGGCCCCAGACACAAGCTCTTGTGAGCCAGCCCAACGTCACCGCCATTGTCTTTGCCAATGCC
GATTCCTGGTGAGGGCTACATCGAGGTTGACGGCAACTACGGCGACCGCAAGAACCTCACTCTGTGGAAGC
AAGGCGATGAGCTCATCAAGAACGTCTCTGCTATCTGCCCCAACACCATTGTGGTCTTTCACACCGTTGG
CCCCGTCTTCTAACCGAGTGGCACAACAACCCCAACATCACCGCCATTGTTTGGGCTGGTGTGCCTGGA
CAGGAGTCCGGTAACGCCATCGCCGACATCCTCTACGGCAAGACCAGCCCTGGACGTTCTCCCTTCACCT
GGGGTGCACCTTATGACAGCTATGGCACCAAGGTTCTCTACAAGGCCAACAATGGAGAGGGTGCCCCCTCA
AGAGGACTTTGTCGAGGGCAACTTCATCGACTACCGCCACTTTGACCGACAATCCCCCAGCACCAACGGA
AAGAGTGCCACCAACGACTCTTCTGCTCCTCTCTACGAGTTTCGGTTTCGGTCTGTCTGGACTACCTTTG
AGTACTCTGATCTCAAAGTCGAGTCTGTGAGCAACGCCTCTTACAGCCCCCTCTGTGCGAAACACCATTCC
TGCCCCCTACCTACGGCAACTTCAGCAAGAACCTGGACGATTACACATTCCCCTCAGGTGTCCGATACCTC
TACAAGTTTCATCTACCCCTACCTCAACACCTCTTCCCTCCGCTGAGAAGGCTTCCGGCGATGTCAAGGGCA
GATTTGGTGAGACCGGCGACGAGTTCCCTCCCTCCCAACGCTCTCAACGGTTCATCGCAGCCTCGTCTTCC
TTCCAGTGGTGTCCCGCGGTAACCTCAGCTCTGGGACATTATGTACACCGTCACTGCCACCATCACC
AACACTGGTGACGCTACCTCGGATGAGGTTCCCCAGCTGTACGTCAGCCTCGGTGGTGAGGGCGAGCCTG
TCCGTGTCTCCGTGGCTTCGAGCGTCTTGAAAACATTGCTCCTGGTGAGAGTGCCACATTACCGCTCA
GCTTACTCGCCGTGACCTGAGCAACTGGGACGTCAACGTCCAGAAGTGGGTCAACCGATCACGCCAAG
AAGATCTGGGTGCGCAGCAGCTCTCGCAATCTGCCCTCAGCGCCGACCTGTAG

FIG. 38A

SEQ ID NO:72

Protein sequence of Gz3A, a GH3 family β -glucosidase from *Gibberella zeae*

mkanwlaaavylaaqtddaavpdtlagvnlvardtlaahspphypspwmdpnavgwedayakakdfvsqmtl
lekvnlttgvgwggercvgnvgsiprlgmrglclqdgplgirfsdynsafptgvtagaswskalwyergr
lmgtefkekgidialgpatgplgrhaaggrnwegftvdpyaaghamaetvkgiqdsqviacakhyaneg
ehfrqrgdvmsqkfniseslssnlddktmhelynwpfadavragvgsimcsynqvnnsyacqnsklngi
lkdemgfqgfvmwdwqaqhtgaasavagldmtmpgdtefntgfsfwggnltlavingtvpawriddmatr
imaaffkvgrsveeepdinfawtrdeygvqtyagenrekvnfavnvqhdhkrhireagakgsvvknt
gslplkkpqflavigedagsnpagpncadrgcdngtlamawsgtsqfpylvtpdggislqaiqdgtry
esilnnnqwpqtqalvsqpnvtaixfanadsgegyievdgnygdrknltlwkggdeliknvsaicpntiv
vlhtvgpvlltewhnnpnitaiwagvpggesgnaiadilygktspgrspftwgrtydsygtkvlykann
gegapqedfvegnfidyrhfdrgspstngksatndssaplyefgfglswttefsdlkvesvsnasysps
vgntipptygnfsknlddytfpsgvrylykfiypylntsssaekasgdvkgrfgetgdeflppnalngs
sqprlpssgapggnpqlwdimytvtatitntgdatsdevpqlyvslggegepvrvlrgferleniapges
atftaqltrrdlsnwdvnnvqnwvitdhakkiwvgsssrnlplsadl

FIG. 38B

SEQ ID NO:73

Nucleotide sequence of Nh3A, a GH3 family β -glucosidase from *Nectria haematococca*

atgcggttcaccgtccttctcgcggcattttcggggccttgccccatgggttggttcgcaagctgaccaga
aaccactacagctcgggtgtgaacaataacactctggcgcattcacctcctcactatccttcgccatggat
ggatcctgctgctcctggctgggaggaagcctatctcaaggcgaaagattttgtttcacagcttacccctt
cttgaaaagggtcaacttgaccactgggtgttggtgagtcacttgttttctcctcctgacgtgacactt
tgctttggcctgcttctctatatcgtctactagcattgctaacactcgaggcagatggatggggaacgtt
gcgtcggcaacgtgggttcactcctcgttttggaatgcgtgggtctctgcatgcaggatggccccctcgg
catccgcttgctgactataactctgcctttcctactgggtattacagctgggtgctccttgaggccgtgcc
ctttgggtaccaacgtggcctcctgatgggcaaccgagcatcgtgaaaaaggcatcgacgttgcaacttgggc
ctgctactgggtcctcttggtcgtaactcctactggcgcccgcaactgggaggggtttctcggttgatcccta
cggttgctggcggttgccatggccgagactgttagcggcattcaagatgggtggtactatcgctgtgctaag
cactacatcggcaacgaacaaggatgacctcttcaacttctcctcgtgataaatctgctcacaacaacct
agagcaccatcgccaagccccgaatccattggccgcggctacaacatcaccgagtcctctgctcgaac
gttgatgacaagacctccacgagctctatctctggccgttcgcagatgccgtcaaggctgggtgttggtg
ctatcatgtgttctaccagcagctgaacaactcttacggttgccaaaactctaagcttctcaacggaat
tctcaaggacgagctaggattccagggtctcgtcatgagtgaactggcaagcccaacatgctggagctgct
accgctgttgcaaggccttgacatgacctgcccgtgacactttgttcaacaccggatacagcttctggg
gtggtaacctgacctcgtgtagtcaatggcactgttcccgactggcggtattgaacgacatggctatgag
aatcatggcagctttcttcaagggttggaagactgttgaggaccttccctgacatcaacttttcttcttg
tctcgagacacttttggtctacgttcaagccgctgcccgaagagaactgggaacagatcaacttcggagttg
atgttcgtcacgaccacagcgaaacacattcgactctcggcccgccaagggaaccgtcctccttaagaactc
tggtcatttgctctgaagaagcccaagttccttgccgtcgttgggcgaggacgcggcccgaaacctgct
ggccccaacggctgtaacgaccgcggtatgtaacaacggcactctggccatgtcctggggctcaggaacag
cccagttcccttacctcgttactcccgactcagcgctacagaaccaggctgtcctcgacggcactcgcta
cgagagtgtcttgcggaacaaccagtggggaacagacacgcagttctcattagccaacctaacgtgacggct
attgtgtttgccaatgccaatccggagagggatatactgatgttgacggcaacgaaggcgatcggaaga
atttgacctgttggaacgaggggtgatgacctaatgaagaacgtctcctcaatctgccccaacacctgtg
tgttctgcacactgttggccctgtcactcctgacgggaatgggtatgacaaccgaacattaccgccaatagt
tggtgtgtgtacctggacaggagtccggcaatgctcttgggtgacatcctttatggcaaaaacaagccctg
gtcgtctcctccttcacatgggggtcgcacccgaaagagttacggcactgatgtcctatacagacccaaca
tggtcaggggtgctcctcaagatgatttcacggagggagtctttatcgactatcgtcattttgaccaggtt
tctcctagcaccgacggcagcaagtctaattgatgagtccagtcctcctacagagtttgccatgggtctgt
cctggaccacgtttgagtactctgaactcaacattcaagctcacaacaagattcccttcgatcctcctat
tgggcgagacgattgccgctccggctccttggaactacagtaccgaccttgccgattacacgttccccgat
ggaattcgctacatctaccagttcatctatccttggttgataacttcttcttccggaagagaggcttctg
gcatcccgactacggaaagacggccgaagagttcctgcccccgagctctcgacgggtcagctcagcc
gacacctccatcctctgggtgctccaggtggaaaacctcatctttgggatgtgttgtagactgttagtgc
atcatcaccaacactggcaacgccacctcggaacgagatcccgagctctacgttagtctcggtggcgaga
acgagcccgctccgctccttcgcggttcgacccaattgagaacattgcgctggccagagtgtcagatt
cacaactgacatcactcgccgcgacctgagcaactgggaacgtcgtctctcagaactgggtcattacagac
tacgagaagaccgtatatgtcgggagcagctcccgcaacctgcctctcaaggcaacctgaagtaa

FIG. 39A

SEQ ID NO:74

Protein sequence of Nh3A, a GH3 family β -glucosidase from *Nectria haematococca*

mrftvllaafsglypmvgsqadqkplqlgvnnntlahspphyppwmdpaapgweeaylkakdfvsqtl
lekvnlttgvgwmgercvgnvgsiprfgmrglcmqdgplgirlsdynsafptgitagaswsralwyqrgl
lmgtehrekgidvalgpatgplgrtptggrnwegfsvdpyvagvamaetvsgiqdggtiacakhyigneq
ehhrqapesigrgyniteslssnvddkthelylwpfadavkagvgaimcsyqqlnnsygcqnsklngi
lkdelgfggfvmstdwqaqhagaatavagldmtmpgdthfntgysfwggnltlavvngtvpdwriddmamr
imaaffkvgtvedlpdinfswsrdtfgyvqaaagenweqinfgvdvrhdhsehirlsaakgtvllkns
gslplkkpkflavgedagpnpagpncndrgcnngtlamswgsgtaqfpylvtpdsalqnqavldgtry
esvlrnnqweqtrslisqpnvtaivfanansgegyidvdgnegdrknltlwnegddliknvssicpntiv
vlhtvgpviltewydnpnitaivwagvpggesgnalvdilygktsprspftwgrtrksygtadvlyepnn
gggapqddftegvfidyrhfdqvspstdgsksndesspiyefghglswttfeyselniqahnkipfdppi
getiaapvlgnystldadytfdgiryiygfypwlnntsssgreasgdpdygktaeeflppgaldgsagp
rppssgapggnphlwdvlytvsaiitntgnatsdeipqlyvslggenepvrvlrgfdrieniapgqsvrf
ttiditrrdlsnwdvvsqnwvitdyektvyvgsssrnlplk

FIG. 39B

SEQ ID NO:75**Nucleotide sequence of Vd3A, a GH3 family β -glucosidase from *Verticillium dahliae***

ATGAAGCTGACCCCTCGCTACTGCCTTACTGGCAGCCAGCGGGTGTGTCTCTGCGGGACAACCCAAGCTCA
AGGTACGTACTTGCCTCTTTTTTCAACAAGGAAACCAAACCCGCACCATAATGGTGATTGAGCAGTCGTGCT
TTCCCTCAACCCGAATCAAACCCATGCCGTGTTTCGCGCATGCCCTTTTCGATCGTCTGTTGTGTGTGAACCC
ACGCTCTTCAAGCATCGCACATAGCACCCTCCATCTTTCATTTTCGAGCAATTTCCGGCCGCAGAGAGCG
GTCTTTCACCTTACCACAATCGTTCATGCCTCGTGCCCCACTGCCATGTTTCTTCCCAGTATTCTACTTC
TGAGAGCCTTGACCACCGTTGTTCGACATCTCGTCGCCAAGGCTCGTTGACACGGACTCTGTTTCCCTTGG
AATTAATATTTCGAAACAATGCTGACCAGCATCCTCAGCGCCAGACTAACAGCTCTAGCGAGCTCGCCTTT
TCCCCTCCGCCTACCCCTTCTCCATGGATGAACCCCCAAGCGACTGGGTGGGAGGACGCCTACGCCCCTG
CCAGAGAGGTGGTAGAGCAGATGACTCTGCTCGAAAAGGTCAACCTGACGACAGGTGTCCGGTAAGCTTC
ACAGACCCCGTCTTGCCATCCAAAGTCATCTGACAGAATCCTAGCTGGAGCGGTGATCTCTGCGTCGGAA
ACGTCGGCTCGATCCCCCGAATCGGCTGGAGGGGGCTTTGTTTGCAGGATGGCCACAGGGTATCCGTTT
CGCGGACTACGTCTCGTACTTCACTTCGAGCCAGACAGCCGGCGCTACCTGGGACCGAGGGCTTCTGTAC
CAGCGCGCTCACGCCATTGGCGCCGAAGGAGTAGCCAAGGGCGTCGACGTCGTCCTCGGGCCCGCCATTG
GCCCTCTAGGTCGCCTTCCC GCCGGAGGTCTGTAACCTGGGAGGGTTTCGCCGTGGACCCCTACCTCAGTGG
CGTTGCTGTCCCGAATCCGTCAGGGGCATCCAGGATGCTGGTGCTATTGCCAACGTCAAGCACTACATC
GTCAATGAGCAGGAACATTTCCGCCAGGCTGGCGAGGCTCAAGGTTACGGCTACGATGTGACGAGGGCAT
TATCGTCGAACGTTGACGACAAGACCATGCATGAGCTTTACCTTTGGCCATTTGCAGACGCTGTCCGTGC
TGGAGCCGGCAGTGTCTATGTGTTCTTATCAACAGGTGGGGGCAATACCATTCTCTCCTCTTTCCTTGCAG
ACAGTGCCTGACCGACCTTTTTTGGCCCAAGATCAACAACAGTTACGGCTGTCAAACTCACATCTTCTG
AATGGGCTCCTCAAGGACGAACTCGGCTTTTCAAGGGGTTCTGTCCTCAGCGATTGGCAAGCGCAGCATGCTG
GTGCTGCCACTGCCGTTGCTGGACTTGACATGGCCATGCCCGGTGACACTCGCTTCAACACCGGAGTCGC
CTTCTGGGGCGCTAACCTTACCAATGCCATTTTGAACGGCACCGTTCCCGAATATCGGCTCGATGACATG
GCCATGCGTATTATGGCGGCCTTTTTTCAAAGTTGGAAAGACCCCTGGACGATGTTCTCTGACATCAACTTCT
CGTCTTGGACAAAAGACACCATCGGCCCCGCTGCACTGGGCGGGCCAGGACAATGTGCAGGTCATCAACCA
ACACGTTGATGTCCGTCAAGACCACGGCGCCCTCATTCGCACCATCGCTGCCCGCGGTACTGTCTTACTA
AAAAATGAGGGATCACTGCCTCTGAACAAGCCGAAATTTGTTGCTGTCAATTGGTGAAGATGCTGGCCCTC
GTCTGTGTTGGTCCCAATGGCTGCCCTGATCAGGGTTGCAATAACGGCACTCTGGCTGCTGGATGGGGATC
TGGCACCGCCAGTTTCCCTTATCTCATCACTCCTGATAGTGCTCTTCAGTTTCAAGCCGTTTCGGATGGC
TCGCGATACGAAAGCATCCTCAGCAACTGGGATTATGAGCGCACAGAGGCCCTTGGTTTCCCAGGCGGATG
CTACTGCTCTGGTTTTTCGTCAATGCAAACTCTGGCGAAGGATATATCAGCGTTGATGGAAACGAAGGTGA
TCGCAAGAACCTCACTCTCTGGAATGGAGGAGACGAGCTTATTCAACGAGTCGCTGCGGCCAACAAACAAC
ACCATCGTCATCATCCATTGCGTTGGTCCCCTTAGTCACTGACTGGTACGAGAATCCCAATATCACGG
CTATCATCTGGGCCGGCTTACCCGGACAGGAGTCTGGCAACTCTATCGCCGATATTCTTTACGGCCGCGT
GAACCTTGGTGGCAAGACACCTTTACCTGGGGTCCAACCTGTTGAGAGCTACGGCGTTGACGTCTTGAGA
GAGCCCAACAATGGCAATGGTGTCTCCCCAGAGCGATTTCGACGAGGGAGTCTTCATCGATTACCGTTGGT
TTGACCGGCAGTCGGGTGTTGATAACAATGCATCAGCGCCGAGGAACAGCAGCAGCAGCCACGCCCCAAT
CTTCGAGTTTGGCTATGGCCTTTTCGTACACAACCTTTGAATTCTCCAATCTTCAGATTGAGAGGCATGAC
GTTACAGATTACGTCCCTACCACTGGGCAGACGAGCCCTGCGCCGAGATTGTTGCTAACTACAGTACGA
ACTACGACGACTACGTCTTTCCCGAGGGCGAAATCCGTTACATCTATCAACACATCTACCCATACCTCAA
TTCCTCAGACCCAAAGGAGGCATTGGCTGATCCTAAATACGGCCAACTGCAGAAGAGTTCCTCCAGAG
GGCGTCTTTGATGCCTCACCGCAGCCTAGGCTCCCAGCTTCTGGAGGGCCCGGAGGCAACCCAATGCTTT
GGGACGTCATATTCACGGTCACCGCGACCGTGACCAACACGGGTAAGGTTGCTGGGGACGAAGTGGCACA
GCTTTACGTTTCTCTTGGTGGACCTGACGATCCGATTTCGAGTCTCCGTGGGTTTCGACCGCATTACATC
GCGCCTGGAGCCTCGAAACCTTCCGTGCGGAACTCACGCGCCGGGACCTCAGCAACTGGGATGTTGTCA
CGCAAAATTGGTTTCATCAGCCAGTACGAAAAGACGGTCTTTGTGCGGAGCTCATCCCGAAACCTCCCTCT
CAGCACTCGCCTCGAATAG

FIG. 40A

SEQ ID NO:76

Protein sequence of Vd3A, a GH3 family β -glucosidase from *Verticillium dahliae*

mkltlatalaasgcvsagqpkklkhpqrqtnssselafspphypspwmnpqatgwedayararevveqmt
llekvnlttgvgwsgdlcvgnvgsiprigwrglclqdgpggirqfadyvsyftssqtagatwdrgllyqra
haigaegvakgvdvvlgpaigplgrlpaggrnwegfavdpylsgvavaesvrgiqdagaiianvkhyivne
qehfrqageaaggygydvdealssnvddkthelylwpfadavragagsvmcsyqqinnnsygcqnshllng
llkdelgfqgfvlsdwqaghagaatavagldmampgdtrfntgvafwganltnailngtvpeyrlddmam
rimaaffkvgkltddvpdinfsstktigtigplhwaagdnvqvinqhvdvrgdhgalirtiaargtvllkn
egslplnkpkfvavigedagprpvpgngcpdggcnngtlaagwgsgtasfpylitpdsalqfqavsdgsr
yesilsnwdyertealvsqadatalvfvnansgegyisvdgnegdrknltlwnggdeliqrvaannnti
viihsvgpvlvtdwyenpnitaiiwaglpqgesgsniadilygrvnpggktpftwgptvesygvdlrep
nngngapqsdfddegvfidyrfdrqsgvdnnasaprnsssshapifefgyglsttfeftnlqierhdvh
dyvpttgqtspaprfganystnyddyvfpegeiriyqhiypylnssdpkealadpkyygqtaeeflpega
ldaspqprlpasggpggnpmlwdviftvtatvtntgkvagdevaqlvslggpddpirvlrgfdrihiap
gasqtfraeltrrdlsnwdvvtqnwfwisqyektvfvvgsssrnlplstrle

FIG. 40B

SEQ ID NO:77**Nucleotide sequence of Pa3G, a GH3 family β -glucosidase from *Podospira anserina***

ATGAAACTCAATAAGCCATTCCTGGCCATTTATTTGGCTTTCAACTTGGCCGAGGCTTCGAAAACCTCCGG
ATTGCATCAGTGGTCCGCTGGCAAAGACCTTGGCATGTGATACAACGGCGTCACCTCCTGCGCGAGCAGC
TGCTCTTGTGCAGGCTTTAAATATCACGGAAAAGCTTGTGAATCTAGTGGAGTATGTCAAGTCAAGAGAA
GCTCCTTTAGGGATTTCAATTACAGCTAATCACTCCTCATAGCATGAGCCTCGGTGCAGAAAGGATCGGCC
TTCCAGCTTATGCTTGGTGGAAACGAAGCTCTTCATGGTGTGCGCGCTCGCCTGGGGTCTCCTTCAATCA
GGCCGGACAAGAATTCTCACACGCTACTTCATTTGCGAATACTATTACGCTAGCAGCCGCCTTTGACAAT
GACCTGGTTTACGAGGTGGCGGATACCATCAGCACTGAAGCGCGAGCGTTTCAGCAATGCCGAGCTCGCTG
GACTGGATTACTGGACGCCAATCAACCCGTACAAAGATCCGAGATGGGGGAGGGGCCATGAGGTTTG
TTACCTTAGCCTTCTTTTCCGTGCCGTGCAGTTGCTGAGAACTCAAAGACACCCGGAGAAGATCCGGTA
CACATCAAAGGCTACGTCCAAGCACTTCTCGAGGGTCTAGAAGGGAGAGACAAGATCAGAAAGGTGATTG
CCACTTGTAACACTTTGCAGCCTATGATTTGGAGAGATGGCAAGGGGCTCTTAGATACAGGTTCAATGC
TGTTGTGACCTCGCAGGATCTTTCCGAGTACTACCTCCAACCGTTTCAACAATGCGCTCGAGACAGCAAG
GTCCGGTCTTTCATGTGCTCATATAATGCGCTCAACGGAACACCGGCATGTGCAAGCACGTATTTGATGG
ACGACATCCTTCGAAAACACTGGAATTGGACCGAGCACAACAACATATATAACGAGCGACTGTAATGCTAT
TCAGGACTTCCTCCCCAACTTTCACAACTTCAGCCAACTCCAGCTCAAGCCGCCGCTGATGCTTATAAC
GCCGGTACAGACACCGTCTGTGAGGTGCCTGGATACCCCCACTCACAGATGTAATCGGAGCATACAATC
AGTCTCTGCTGTCAGAGGAAATTATCGACCGAGCACTTCGCAGATTATACGAAGGCCTCATCCGAGCTGG
CTATCTCGACTCAGCCTCCCCACATCCATACACCAAAATCTCATGGTCCCAAGTAAACACCCCCAAAGCC
CAAGCCCTGGCTCTCCAGTCCGCCACCGACGGGATAGTCTTCTCAAAAACAACGGCTCCTTCCCCCTAG
ACCTCACCAACAAAACCATAGCCCTCATAGGCCACTGGGCCAATGCAACCCGCCAAATGCTAGGCGGCTA
CAGCGGTATCCCCCTTACTACGCCAACCCTAATCTATGCAGCCACCCAGCTCAACGTCACCTTTTCATCAC
GCCCCAGGACCGGTGAACCAGTCATCTCCCTCCACAAATGACACCTGGACCTCCCCCGCCCTCTCCGCGG
CTTCCAAATCGGATATCATCCTCTACCTCGGCGGCACCGACCTCTCCATCGCAGCCGAAGACCGAGACAG
AGACTCCATCGCCTGGCCATCCGCTCAACTTTCTTGTAACTCCCTCGCCAGATGGGAAAACCCACA
ATCGTAGCAAGACTAGGCGACCAAGTAGACGACACCCCCCTGCTCTCCAACCCAAACATCTCCTCCATCC
TATGGGTAGGCTACCCAGGCCAATCAGGCGGAACAGCCCTCTTGAACATCATCACCGGAGTCAGCTCCCC
CGCCGCTCGACTGCCCCTCACAGTCTACCCAGAACTTACACCTCCCTCATCCCCCTGACAGCCATGTCC
CTCCGCCCAACCTCCGCCCGCCAGGCCGGAATTACAGGTGGTACCCCTCCCCCGTGTCCCTTTCGGCC
ACGGCCTCCACTACACAACCTTTACCGCCAAATTCGGCGTCTTTGAGTCCCTCACCATCAACATTGCCGA
ACTCGTTTCCAACGTGAACGAACGATACCTCGACCTCTGCCGTTCCCGCAGGTGTCCGTCTGGGTGTCG
AATACGGGAGAACTCAAATCTGACTATGTCGCCCTTGTTTTTGTGAGGGGTGAGTACGGACCGGAGCCGT
ACCCGATCAAGACGCTGGTGGGGTACAAGCGGATAAGGGATATCGAGCCGGGGACTACGGGGGGCGGCC
GGTGGGGGTGGTGGTGGGGGATTTGGCTAGGGTGGATTTGGGGGGGAATAGGGTTTTGTTTCCGGGAAG
TATGAGTTTCTGCTGGATGTGGAGGGGGGAGGGATAGGGTTGTGATCGAGTTGGTTGGGGAGGAGGTGG
TGTTGGAGAAGTTCCTCAGCCGCTGCGGCGGGTTGA

FIG. 41A

59 / 111

SEQ ID NO:78**Protein sequence of Pa3G, a GH3 family β -glucosidase from *Podospira anserina***

mkl~~nk~~pflaiylafnlaeasktpdcisgplaktlacdtaspparaaalvqalniteklnlveyvksre
 aplgisiglithphmslgaeriglpayawnealhgvaaaspqvsfnqagqefshatsfantitlaaafdn
 dlvyevadtistearafснаelagldywtpninpykdprwgrghevacylsllfravqlirtqktggedpv
 hikgyvqalleglegrdkirkviatckhfaaydlerwqgalryrfnavvtsqdlseyylqpffqccardsk
 vgsfmcsynalngtpacastylmddilrkhnwtehnnyitsdcnaiqdfpfnfnfsqtpaqaaadayn
 agtdtvcvpgyppltdvigaynqslseeiidralrrlyeggliragyldsasphpytkiswsqvntpka
 qalalqsatdgivllknngllpldltnktialighwanatrqmlggysgippyanyapiyaatqlnvtfhh
 apgpvnqsspstndtwtpalsaaasksdililylggtldlsiaaedrdrdsiawpsaqlslitslaqmkgpt
 ivarlgdqvddtpll~~sn~~pnissilwvgypgqsggtallniitgvsspaarlptvypetytsliptams
 lrptsarpgrrtyrwyppspvlpfghglhyttftakfgvfesltiniaelvsnchneryldlcrfpqvsvwvs
 ntgelksdyvalvfvrgeygpeypiktlvgykri~~rd~~iepgttgaapvgvvvgdlarvdlggnrvlfp~~gk~~
 yeflldveggrdrvvielvgeevvlekfpqppaag

FIG. 41B**SEQ ID NO:79****Protein sequence of Tn3B, a GH3 family β -glucosidase from *Thermotoga neapolitana***

MEKVNEILSQLTLEEKVKLVVGVLPGLFGNPHSRVAGAAGETHPVPRVGLPAFVLADGPAGLRINPTRE
 NDENTYYTTAFPEIMLASTWNRELLLEVKGAMGEEVREYGV~~DL~~LAPAMNIHRNPLCGRNFEYYSEDPV
 LSGEMASSFVKGVQSQGVGACIKHEVANNQETNRMVVD~~T~~IVSERALREIYLRGFEI~~AV~~KKSKPWSVMSAY
 NK~~LN~~GKYCSQNEWLLKKVLREEWGFE~~GF~~VMSDWYAGDN~~PVE~~QLKAGNDLIMPGKAYQVNTERRDEIEEIM
 EALKEGKLSEEV~~LD~~ECVRN~~IL~~KVLVNAPSFKNYRYSNKP~~DL~~EKHAKVA~~YE~~AGAEGV~~LL~~RNEEALPLSEN
 SKIALFGTGQIETIKGGTGS~~GD~~THPRYAISILEGIKERGLN~~FDE~~ELAKTYEDYIKK~~RE~~TEEYKPRRDSW
 GTIIKPKLPENFLSEKEIHK~~LAK~~NDVAVIVISRISGEGYDRKPVKGDFYLS~~DE~~TDLIKTVSREFHEQG
 KKVIVLLNIGSPVEV~~VS~~WRDLVDGILLVWQAGQETGRIVADVLTGRINPSGKLPTTFPRDYS~~DP~~SWTFP
 GEPKDN~~PQ~~KVVEEDIIYVGYRYDTFGVEPAYEFGYGLSYTTFEYSDLNVS~~FD~~GETLRVQYRIENTGGRA
 GKEVSQVYIKAPKGKIDKPFQELKAFHKTRLLNPGESEEVVLEIPVRDLASFN~~GE~~EWVVEAGEYEVRVGA
 SSRNIKLKGTFSVGEERRFKP

FIG. 42

60 / 111

Alignment of amino acid sequences of Fv3C homologs. Alignment was made in Muscle (in accordance with Edgar R.C., BMC Bioinformatics, 2004, 5: 113) using default parameters.

	*	20	*	40	*	
Tn3B :	-----					-
Fv3G :	---MFPSSISCLA---	ALSLMSQGLLAQSQ	PENV-----	ITDDTY	:	34
Fv3D :	MASIRSVLVSGLL--	AAGVNAQAYDASDRAEDAF	SWVQP---	KNTTILGQ	:	45
Tr3A :	--MRYRTAAALAL--	ATGPFARADSHS-----		TSGASA	:	29
Pa3D :	---MALQTFLL--	AAAMLANAE-----		TTGEKV	:	24
Te3A :	--MRNGLLKVAAL--	AAASA-----		VNGENL	:	22
An3A :	--MRFTSIEAVAL--	TAVSL-----		ASADEL	:	22
Tr3B :	--MKTLSVFAAALL--	AAVAEANPYPPP-----		HSNQ	:	28
Nh3A :	--MRFTVLLAAAFSGLVPMVGSQADQKPLQLG-----			VNNNTL	:	35
Gz3A :	--MKANWLAAAVYL--	AAGTDAA-----	VPDTLAGV-----	NLVARDTL	:	35
Fv3C :	--MKLNWVAAAALSIGAAGTDSAVALASAVPDTLAGVKKADAQKVVTRDTL				:	48
Fo3A :	--MKLNWVAAAALSIGAAGTDGAVALASEVPDTLAGVKNNTDAQKVVTRDTL				:	48
Pa3G :	--MKFSVVVAAAL--	ASGALATPQYPPK-----		LIKRD	:	30
Vd3A :	--MKLTLATALLA--	ASGCVSAGQPKLKHPPQRT-----		NSSSEL	:	36
	60	*	80	*	100	
Tn3B :	-----		MEKVNEILS	QLTLEEKVKLVVGVGLP	:	26
Fv3G :	FYQGSPPVYP----		THTGSWAAAVAKAKNLVS	QLTLEEKVNLTG-GQT	:	78
Fv3D :	YG--HSPHYPAN---		NATGKGWEDAFKAQNFVS	QLTLEEKADMVTGT----	:	88
Tr3A :	EA--VVP-----		PAGTPWGTAYDKAKAALAKLNLQDKVGIVSGVGWN	:	69	
Pa3D :	SR---QAP-----		SGAQAWAAAHSQAAATLARMSQQDKINMVTGIGWD	:	64	
Te3A :	AY--SPPFYPSPWANGQGD--		WAEAYQKAVQFVS	QLTLAEKVNLTGTTGTGWE	:	69
An3A :	AY--SPPYYPSPWANGQGD--		WAEAYQRAVDIVSQMTLAEKVNLTGTTGTGWE	:	69	
Tr3B :	AY--SPPFYPSPWMDPSAPGWEQAYAQAQKEFVS		GLTLLEKVNLTGTVGWM	:	76	
Nh3A :	AH--SPPHYPSPWMDPAAPGWEEAYLKAKDFVS		QLTLLEKVNLTGTVGWM	:	83	
Gz3A :	AH--SPPHYPSPWMDPNAVGWEDAYAKAKDFVS		QMTLLEKVNLTGTVGWQ	:	83	
Fv3C :	AY--SPPHYPSPWMDPNAVGWEEAYAKAKSFVS		QLTLMEKVNLTGTVGWQ	:	96	
Fo3A :	AH--SPPHYPSPWMDPNAIGWEEAYAKAKNFVS		QLTLLEKVNLTGTVGWQ	:	96	
Pa3G :	AY--SPPVYPSPWMNPEADGWAEAYVKAREFVS		QMTLLEKVNLTGTTGTGWA	:	78	
Vd3A :	AF--SPPHYPSPWMNPQATGWEDAYARAREVVEQMTLLEKVNLTGTVGWS			:	84	
	*	120	*	140	*	
Tn3B :	GLFGNPHSRVAGAAGETHPVPRVGLPAFVLADGPAGLRINPTRENDENTY	:				76
Fv3G :	T-----	TGCSGFIPGIPRVGFPLCLADAGNGVRNTD-----	:			110
Fv3D :	P-----	GPCVGNIVAIPRLNFNGLCLHDGPLAIRVAD-----	:			120
Tr3A :	G-----	GPCVGNTSPASKISYPSLCLQDGPLGVRYST-----	:			101
Pa3D :	R-----	GPCVGNTAAISSINYPQICLQDGPLGIRFGT-----	:			96
Te3A :	Q-----	DRCVGQVGSIPRLGFPGLCMQDSPLGVRDSD-----	:			101
An3A :	L-----	ELCVGQTGGVPRLGIPGMCAQDSPLGVRDSD-----	:			101
Tr3B :	G-----	EKCVGNVGTVPRLGMRSLCMQDGPLGLRFNT-----	:			108
Nh3A :	G-----	ERCVGNVGSLPRFGMRGLCMQDGPLGIRLSD-----	:			115
Gz3A :	G-----	ERCVGNVGSIPLRGMRGLCLQDGPLGIRFSD-----	:			115
Fv3C :	G-----	ERCVGNVGSIPLRGMRGLCLQDGPLGIRLSD-----	:			128
Fo3A :	G-----	ERCVGNVGSIPLRGMRGLCLQDGPLGIRLSD-----	:			128
Pa3G :	S-----	EQCVGQVGAIPLRLGLRSLCMHDAPLGIRGTD-----	:			110
Vd3A :	G-----	DLCVGNVGSIPIRGWRGLCLODGPQIRFAD-----	:			116

FIG. 43A-1

61 / 111

	160	*	180	*	200	
Tn3B :	YTTAFPFVEIMLASTWNRELLEEVGKAMGEEVREYGV		DVLLAPAMN-IHRN		: 125	
Fv3G :	YVSSFPSGIHVGASWNPELTYSRSYYMGAEAKAKGV		NILLGPVFGPLGRV		: 160	
Fv3D :	YASVFPAGVSAASSWDKDLLYQRLAMGQEFKAKGAH		ILLGPVAGPLGRS		: 170	
Tr3A :	GSTAFTPGVQAASTWDVNLIRERGQFIGEEVKASGI		HVILGPVAGPLGKT		: 151	
Pa3D :	GTTAFTPGVQAASTWDVDLIRQRGAYLGAEAKGCGI		HILLGPVAGALGKI		: 146	
Te3A :	YNSAFPAGVNVAATWDRNLAYRRGVAMGEEHVRGK		GVQVQVAGPLGRS		: 151	
An3A :	YNSAFPAGVNVAATWDKNLAYLRGQAMGQEFSDKG		ADIQLGPAAGPLGRS		: 151	
Tr3B :	YNSAFSVGLTAAASWSRHLWVDRGTALGSEAKGKG		VQVAGPLGRN		: 158	
Nh3A :	YNSAFPTGITAGASWSRALWYQRLMGTEHREKGI		DVALGPATGPLGRT		: 165	
Gz3A :	YNSAFPTGVTAGASWSKALWYERGRMGTEFKEKG		IDIALGPATGPLGRH		: 165	
Fv3C :	YNSAFPAGTTAGASWSKSLWYERGLMGTEFKEKG		IDIALGPATGPLGRT		: 178	
Fo3A :	YNSAFPAGTTAGASWSKSLWYERGLMGTEFKEKG		IDIALGPATGPLGRT		: 178	
Pa3G :	YNSAFPQGQTAAATWDRQLMYRRGYAIGKEAKGK		GINVILGPVAGPLGRM		: 160	
Vd3A :	YVSYFTSSQTAGATWDRGLLYQRAHAIGAEGVAK		GVQVQVAGPLGRL		: 166	
	*	220	*	240	*	
Tn3B :	PLCGRNFEYYSEDPVLSGEMASSFVKGVQSQGVG		ACIKHFVANNQETNRM		: 175	
Fv3G :	VEGGRNWEGFSNDPYLAGKLGHEAVAGIQDAGV		VACGKHFLAQEQETHRL		: 210	
Fv3D :	AYSGRNWEGFSPDPYLTGIAMEETIMGHQDAGV		QATAKHFIGNEQEVMRN		: 220	
Tr3A :	PQGGRNWEGFGVDPYLTGIAMGQTINGIQSVGV		QATAKHFIILNEQELNR-		: 200	
Pa3D :	PHGGRNWEGFGADPYLAGIAMKETIEGIQSAGV		QANAKHYIANEQELNR-		: 195	
Te3A :	PDAGRNWEGFAPDPVLTGNMMASTIQGIQDAGV		IACAKHFILYEQEHFRQ		: 201	
An3A :	PDGGRNWEGFSPDPALSGVLFAETIKGIQDAGV		VATAKHIIAYEQEHFRQ		: 201	
Tr3B :	PNGGRNVEGFGSDPYLAGLALADTVTGIQNAGT		IACAKHFLNEQEHFRQ		: 208	
Nh3A :	PTGGRNWEGFSVDPYVAGVAMAETVSGIQDGGT		IACAKHYIGNEQEHHRQ		: 215	
Gz3A :	AAGGRNWEGFTVDPYAAGHAMAETVKGIQDSG		VIAKAKHYIANEQEHFRQ		: 215	
Fv3C :	AAGGRNWEGFTVDPYMAGHAMAEEAVKGIQDAG		VIAKAKHYIANEQEHFRQ		: 228	
Fo3A :	AAGGRNWEGFTVDPYMAGHAMAEEAVKGIQDAG		VIAKAKHYIANEQEHFRQ		: 228	
Pa3G :	PAAGRNWEGFSPDPVLTGVGMAETVKGHQDAGV		IACAKHFFIGNEQEHFRQ		: 210	
Vd3A :	PAGGRNWEGFAVDPYLSGVAVAESVRGIQDAGA		IANVKKHYIVNEQEHFRQ		: 216	
	260	*	280	*	300	
Tn3B :	V-----VDTIVSERALREIYLRGFEIAVKKSKP		WSVMSAY		: 210	
Fv3G :	AASVTG-----ADAISSNLDDKTLHELYL-----		CVMCSY		: 240	
Fv3D :	PTFVKDGYIGEVDKEALSSNMDDRTMHLYLWPF		FANAVHAKAS-SMMCSY		: 269	
Tr3A :	-----ETISSNPDDRTHLYLWPFADAVQANVA--		SVMCSY		: 235	
Pa3D :	-----ETMSSNVDDRTQHELYLWPFADAVHANVA--		SVMCSY		: 230	
Te3A :	GAQD-----GYDISDSISANADDKTMHLYLWPF		ADAVRAGVG--SVMCSY		: 245	
An3A :	APEAQG--YGFNITESGSANLDDKTMHLYLWPF		ADAIRAGAG-AVMCSY		: 248	
Tr3B :	VGEANG--YGYPIREALSSNVDDKTIHEVYGWPF		QDAVKAGVG-SFMCSY		: 255	
Nh3A :	APESIG--RGYNITESLSSNVDDKTLHELYLWPF		ADAVKAGVG-AIMCSY		: 262	
Gz3A :	RGDVMS--QKFNISESLSSNLDDKTMHLYLWPF		ADAVRAGVG-SIMCSY		: 262	
Fv3C :	SGEVQS--RKYNISESLSSNLDDKTMHLYLWPF		ADAVRAGVG-SVMCSY		: 275	
Fo3A :	SGEVQS--RKYNISESLSSNLDDKTLHELYLWPF		ADAVRAGVG-SVMCSY		: 275	
Pa3G :	VGEARG--YGFNISETLSSNIDDKTMHLYLWPF		ADAVRAGAG-SFMCSY		: 257	
Vd3A :	AGEAQG--YGYDVDEALSSNVDDKTMHLYLWPF		ADAVRAGAG-SVMCSY		: 263	

FIG. 43A-2

62 / 111

	*	320	*	340	*	
Tn3B :	NKLNGKYCSQNEWLLKKVLREEWGFEGFVMSDWYAGDNPVEQLKAGNDLI :	260				
Fv3G :	NRANNSHACQNSKLLNGLLKGELGFQGFVVS DWGAQQSGMASALAGLDVV :	290				
Fv3D :	QRLNGSYACQNSKVLNGLLRDELGFQGFVMSDWGATHAGVAAINSGLDMD :	319				
Tr3A :	NKVNTTWACEDQYTLQTVLKDQLGFPGYVMTDWN AQHTTVQSANSGLDMS :	285				
Pa3D :	NKLNGTWACENDKALNQILKKELGFQGFVLS DWNAQHSTALSANSGLDMT :	280				
Te3A :	NQVNNSYACSNSYTMNKLLKSELGFQGFVMTD WGGHHSVGVSALAGLDMS :	295				
An3A :	NQINNSYGCQNSYTLNKLKLAELGFQGFVMSD WAAHHAGVSGALAGLDMS :	298				
Tr3B :	NQVNNSYACQNSKLLINGLLKEEYGFQGFVMSD WQAQHTGVASAVAGLDMT :	305				
Nh3A :	QQLNNSYGCQNSKLLNGILKDELGFQGFVMSD WQAQHAGAATAVAGLDMT :	312				
Gz3A :	NQVNNSYACQNSKLLNGILKDEM GFQGFVMSDWQAQHTGAASAVAGLDMT :	312				
Fv3C :	NQINNSYGCQNSKLLNGILKDEM GFQGFVMSDWAAQHTGAASAVAGLDMS :	325				
Fo3A :	NQINNSYGCQNSKLLNGILKDEM GFQGFVMSDWAAQHTGAASAVAGLDMS :	325				
Pa3G :	QQVNNSYGCQNSKLMNGLLKDDELGFQGFVLS DWQAQHTGAAAAAAGLDMS :	307				
Vd3A :	QQINNSYGCQNSHLLNGLLKDDELGFQGFVLS DWQAQHAGAATAVAGLDMA :	313				

	360	*	380	*	400	
Tn3B :	MPGKAYQVNTERRDEI--EEIMEALKEGKLSEEVLDECVRN ILKVL----					304
Fv3G :	MPSS-----ILWGANLTLGVNNGTIPESQVDNMVTRLLATWYQLN :					330
Fv3D :	MPGGIGAYGT YFTKSFFGGNLTRA VTNGTLDETRVNDMITRIMTPYFWLG :					369
Tr3A :	MPG----TDFNGNRLWGPALTN AVNSNQVPTSRVDDMVTRILA AWYLTG :					331
Pa3D :	MPG----TDFNGRNVYWG PQLNNAVNA GQVQRSRLDDMCKRILAGWYLLG :					326
Te3A :	MPGD---IAFDSGTSFWGTNLTVAVLN GSIPEWRVDDMAVRIMSAYYKVG :					342
An3A :	MPGD---VDYDSGTSYWG TNLTISVLNGTV PQWRVDDMAVRIMAAYYKVG :					345
Tr3B :	MPGD---TAFNTGASYFG SNLTLAVLN GTVPEWRIDDMVMRIMAPFFKVG :					352
Nh3A :	MPGD---TLFNTGYSFWG GNLTLAVN GTVPDWRIDDMAMRIMAAFFKVG :					359
Gz3A :	MPGD---TEFNTGFSFWG GNLTLAVIN GTVPAWRIDDMATRIMAAFFKVG :					359
Fv3C :	MPGD---TAFDSGYSFWG GNLTLAVIN GTVPAWRVDDMALRIMS AFFKVG :					372
Fo3A :	MPGD---TAFDSGYSFWG GNLTLAVIN GTVPAWRVDDMALRIMS AFFKVG :					372
Pa3G :	MPGD---TEFNTGV SFWGTNLTVAVLN GTVPAYRIDDMAMRIMAAFFKVE :					354
Vd3A :	MPGD---TRFNTGVAFW GANLTNAILN GTVPEYRLDDMAMRIMAAFFKVG :					360

	*	420	*	440	*	
Tn3B :	-----VNAPSEFKNYRYSNK PDL-----EKHAKVAYE :					330
Fv3G :	QDQ-----DTEAPGHGLAAKL-WE PPHPVVDARNASSKPTIWD :					366
Fv3D :	QDK-DYPSVDPSSGDLNTFSPKSSW FREF-NLTGERSRDRV RGNHGD LIRK :					417
Tr3A :	QDQAGYPSFNISR-----NVQGN HKTNVRA :					356
Pa3D :	QNQ-GYPAINIRA-----NVQGN HKENVRA :					350
Te3A :	RDRYSVP-INFDSWTLDTYGPEHYAV GQG-QTKINEHVDVRGNHAEI IHE :					390
An3A :	RDRLWTP-PNFSSWTRDEYGF KYYYVSEG PYEKVNQFVNVQRNHSELIRR :					394
Tr3B :	KTVDSLIDT NFDSWTNGEYGYVQA AVNEN-WEKVNYGVDVRANHANHIRE :					401
Nh3A :	KTVEDLDPDINFSSWSRDTFGYVQAAA QEN-WEQINFGVDVRHDHSEHIRE :					408
Gz3A :	RSVEEEPDI NFSAWTRDEYGFVQTYAQ EN-REKVNFAVNVQHDHKRHIRE :					408
Fv3C :	KTIEDLDPDINFSSWTRDTFGFVHTFAQ EN-REQVNFGVNVQHDHKSHIRE :					421
Fo3A :	KTVEDLDPDINFSSWTRDTFGFVQTF AQEN-REQVNFGVNVQHDHKNHIRE :					421
Pa3G :	KSIELDP-INF SFWSLDTYGPIHWA AGEG-HQQIN YHVDVRADHANLIRE :					402
Vd3A :	KTLD DVPDINFSSWTKDTIGPLHWA AQDN-VQVINQHVDVRQDHGALIRT :					409

FIG. 43A-3

63 / 111

	460	*	480	*	500	
Tn3B :	AGAEGVLLRNEE-ALPLS-ENSKIALFG-----TGQ-----					: 360
Fv3G :	GAVEGHVLVKNTNNALPFKPNMKLVSLFGYSHKAPDKNIPDPAQGMFSAW					: 416
Fv3D :	HGAESTVLLKNEKNALPLK-KPKSIAVFG-----NDA--GDITEGFYNQN					: 459
Tr3A :	IARDGIVLLKNDANILPLK-KPASIAVVG-----SAAIIGNHARNSPSCN					: 400
Pa3D :	VARDGIVLLKNDG-ILPLS-KPRKIAVVG-----SHS--VNNPQGINACV					: 391
Te3A :	IGAASAVLLKNKG-GLPLTGTERFVGTVFG-----KDA--GSNPWGVNGCS					: 432
An3A :	IGADSTVLLKNDG-ALPLTGKERLVALIG-----EDA--GSNPYGANGCS					: 436
Tr3B :	VGAKGTVIFKNNG-ILPLK-KPKFLTIVIG-----EDA--GGNPAGPNGCG					: 442
Nh3A :	SAAKGTVLLKNSG-SLPLK-KPKFLAVVG-----EDA--GPNPAGPNGCN					: 449
Gz3A :	AGAKGSVVLKNTG-SLPLK-KPQFLAVIG-----EDA--GSNPAGPNGCA					: 449
Fv3C :	AAAKGSVVLKNTG-SLPLK-NPKFLAVIG-----EDA--GPNPAGPNGCG					: 462
Fo3A :	SAAKGSVILKNTG-SLPLN-NPKFLAVIG-----EDA--GPNPAGPNGCG					: 462
Pa3G :	IAAKGTVLLKNTG-SLPLN-KPKFVAVIG-----EDA--GPNPAGPNGSCA					: 443
Vd3A :	IAARGTVLLKNEG-SLPLN-KPKFVAVIG-----EDA--GPRPVGPNGCP					: 450

	*	520	*	540	*	
Tn3B :	-----		IETIKGGTGSGDTHPRYAISI			: 381
Fv3G :	SIGAQSANITELNLGFLGNLSLTYSIAIPNGTIIISGGGSGASAWTLFSSP					: 466
Fv3D :	D--YE-----		FGTLVAGGGSGTGRLTYLVSP			: 483
Tr3A :	DKGCD-----		DGALGMGWGSGAVNYPYFVAP			: 426
Pa3D :	DKGCN-----		VGTLGMGWGSGSVNYPYLVSP			: 417
Te3A :	DRGCD-----		NGTLAMGWGSGTANFPYLVTP			: 458
An3A :	DRGCD-----		NGTLAMGWGSGTANFPYLVTP			: 462
Tr3B :	DRGCD-----		DGTLAMEWGSGTTNFPYLVTP			: 468
Nh3A :	DRGCN-----		NGTLAMSWGSGTAQFPYLVTP			: 475
Gz3A :	DRGCD-----		NGTLAMAWGSGTSQFPYLVTP			: 475
Fv3C :	DRGCD-----		NGTLAMAWGSGTSQFPYLITP			: 488
Fo3A :	DRGCD-----		NGTLAMAWGSGTSQFPYLITP			: 488
Pa3G :	DRGCN-----		NGTLAMGWGSGTANFPYLITP			: 469
Vd3A :	DQGCN-----		NGTLAAGWGSGTASFYPYLITP			: 476

	560	*	580	*	600	
Tn3B :	LEGIKERGLNFDEELAKTYEDYIKKMRETEEYKPRRDSWGTTIKPKLPEN					: 431
Fv3G :	FDAFVSRAK-----		KEGTALF-----W			: 483
Fv3D :	LAAINARAK-----		QDGTLVQQWMNNT			: 505
Tr3A :	YDAINTRAS-----		SQGTQVT--LSNT			: 446
Pa3D :	YDALRTRAQ-----		ADGTQIS--LHNT			: 437
Te3A :	EQAIQREVL-----		SRNGTFTGITDNG			: 480
An3A :	EQAISNEVL-----		KNKNGVFTATDNW			: 484
Tr3B :	DAALQSQAL-----		QDGTRYESILSNY			: 490
Nh3A :	DSALQNQAV-----		LDGTRYESVLRNN			: 497
Gz3A :	DQGISLQAI-----		QDGTRYESILNNN			: 497
Fv3C :	DQGLSNRAT-----		QDGTRYESILTNN			: 510
Fo3A :	DQGLQNRAA-----		QDGTRYESILTNN			: 510
Pa3G :	DAALQAQAI-----		KDGSRYESILTNY			: 491
Vd3A :	DSALQFQAV-----		SDGSRYESILSNW			: 498

FIG. 43A-4

SUBSTITUTE SHEET (RULE 26)

64 / 111

	*	620	*	640	*	
Tn3B	:	FLSEKEIHK--LAKKNDVAVIVISRISGEGY----	DRKPVKGDFYLSDD	:	475	
Fv3G	:	DFESWDPY---VNPTSEACIVAGNAWASEGW-----	DRPATY--DAYT	:	521	
Fv3D	:	LIATTNVTDLWIPATPDVCLVFLKTWAE-----	AADREHLSVDWDG	:	547	
Tr3A	:	DNTSSGAS---AARGKDVAIVFITADSGEGYITVEGNAGDRNNLDPWHNG	:	493		
Pa3D	:	DSTNGVSN---VVSDADAVVVITADSGEGYITVEGHAGDRSHLDPWHNG	:	484		
Te3A	:	ALAEMAA----AASQADTCLVFANADSGEGYITVDGNEGDRKNLTLWQGA	:	526		
An3A	:	AIDQIEA----LAKTASVSLVFVNADSGEGYINVDGNLGDRRNLTWLWRNG	:	530		
Tr3B	:	AISQTQAL---VSQPDIAIAIVFANSDSGEGYINVDGNEGDRKNLTLWKNG	:	537		
Nh3A	:	QWEQTRSL---ISQPNVTAIVFANANSGEGYIDVDGNEGDRKNLTLWNEG	:	544		
Gz3A	:	QWPQTQAL---VSQPNVTAIVFANADSGEGYIEVDGNYGDRKNLTLWKQG	:	544		
Fv3C	:	EWASVQAL---VSQPNVTAIVFANADSGEGYIEVDGNFGDRKNLTLWQQG	:	557		
Fo3A	:	EWAQTQAL---VSQPNVTAIVFANADSGEGYIEVDGNFGDRKNLTLWQQG	:	557		
Pa3G	:	AASQTRAL---VSQDNVTAIVFVNADSGEGYINFEGNMGDRNNLTWLWRGG	:	538		
Vd3A	:	DYERTEAL---VSQADATALVFVNANSGEGYISVDGNEGDRKNLTLWNGG	:	545		
		660	*	680	*	700
Tn3B	:	TDLIKTVSREFHEQGKKVIVLLNIGSPVEVVS	WRDLVDGILLVWQA--GQ	:	523	
Fv3G	:	DELINNVA----	DKCANTIVVLHNAGTRLVDGFFGHPNVTAIIYAHLPGQ	:	567	
Fv3D	:	NDVVESVA----	KYCNNTVVVTHSSGINTLP--WADHPNVTAILAAHFPGQ	:	592	
Tr3A	:	NALVQAVA----	GANSNVIVVHVSVAIILEQILALPQVKAVVWAGLPSQ	:	539	
Pa3D	:	NQLVQAAA----	AANKNVIVVHVSVGQITLETILNTNGVRAIVWAGLPGQ	:	530	
Te3A	:	DQVIHNVS----	ANCNNTVVVLHTVGPVLIDDWDYDHPNVTAILWAGLPGQ	:	572	
An3A	:	DNVIKAAA----	SNCNNTIVIIHSVGPVLVNEWYDNPNVTAILWGGLPGQ	:	576	
Tr3B	:	DDLIKTVA----	AVNPKTIVVIHSTGPPVILKDYANHPNISAILWAGAPGQ	:	583	
Nh3A	:	DDLIKNVS----	SICPNTIVVLHTVGPVILTEWYDNPNTAIVWAGVPGQ	:	590	
Gz3A	:	DELIKNVS----	AICPNTIVVLHTVGPVLLTEWHNNPNNTAIVWAGVPGQ	:	590	
Fv3C	:	DELIKNVS----	SICPNTIVVLHTVGPVLLADYEKNPNNTAIVWAGLPGQ	:	603	
Fo3A	:	DELIKNVS----	SICPNTIVVLHTVGPVLLADYEKNPNNTAIVWAGLPGQ	:	603	
Pa3G	:	DDLKVNVS----	SWCSNTIVVIHSTGPPVLISEWYDSPNTAILWAGLPGQ	:	584	
Vd3A	:	DELIQ RVA----	AANNNTIVIIHSVGPVLVTDWYENPNNTAIIWAGLPGQ	:	591	
		*	720	*	740	*
Tn3B	:	ETGRIVADVLTGRINPSGKLPTTFPRDYSD-----	VPSWTFPG--EPKDN	:	566	
Fv3G	:	DSGDALVSLLYGDENPSGRLPYTVARNETDYGHLLKPDLTLAPN--QYQHF	:	616		
Fv3D	:	ESGNSLVDLLYGDVNPSGRLPYTIAFN GTDYN----	APPTTAVNTTGKED	:	638	
Tr3A	:	ESGNALVDVLWGDVSPSGKLVYTI AKSPNDYN----	TRIVS-----GGSD--	:	580	
Pa3D	:	ENGNALVDVLYGLVSPSGKLPYTIGKRES DYG-----	TAVV-----RGDD--	:	570	
Te3A	:	ESGNSLVDVLYGRVNP--GKTPFTWGRARDDYG-----	APLIVKPN--NGKGA	:	616	
An3A	:	ESGNSLADVLYGRVNPGAKSPFTWGKTREAYQ-----	DYLYTEPN--NGNGA	:	621	
Tr3B	:	ESGNSLVDILYGKQSP--GRTPFTWGPSLESYG-----	VSVMTTPN--NGNGA	:	627	
Nh3A	:	ESGNALVDILYGKTSP--GRSPFTWGRTRKSYG-----	TDVLYEPN--NGQGA	:	634	
Gz3A	:	ESGNAIADILYGKTSP--GRSPFTWGR TYDSYG-----	TKVLYKAN--NGEGA	:	634	
Fv3C	:	ESGNAIADLLYGKVSP--GRSPFTWGR TRESYG-----	TEVLYEAN--NGRGA	:	647	
Fo3A	:	ESGNAIADLLYGKVSP--GRSPFTWGR TRESYG-----	TEVLYEAN--NGRGA	:	647	
Pa3G	:	ESGNSITDVLYGKVNPSGKSPFTWGATREGYG-----	ADVLYTPN--NGEGA	:	629	
Vd3A	:	ESGNSIADILYGRVNPGGKTPFTWGPTVESYG-----	VDVLEPN--NGNGA	:	636	

FIG. 43A-5

65 / 111

	760	*	780	*	800	
Tn3B :	PQKVVEEDIYVG	YRY	YDT-----	FGVE	PAYEFGYGLSYT	: 601
Fv3G :	PQS-DFSEGI	FIDYRH	FDA-----	KNIT	PRFEFGFGLSYT	: 650
Fv3D :	WQS-WFDEK	LEIDYR	YFDA-----	HNIS	VRYEFGFGLSYS	: 672
Tr3A :	----SFSEGL	FIDYKH	FDD-----	ANIT	PRYEFgyGLSYT	: 611
Pa3D :	----NFREGL	FVDYRH	FDN-----	ARIE	PRYEFgyGLSYT	: 601
Te3A :	PQQ-DFTEGI	FIDYRR	FDK-----	YNIT	PIYEFgyGLSYT	: 650
An3A :	PQE-DFVEGV	FIDYRG	FDK-----	RNET	PIYEFgyGLSYT	: 655
Tr3B :	PQD-NFNEG	AFIDYR	YFDKVAPGKPRS-----	SDKAP	TYEFgyGLSWS	: 669
Nh3A :	PQD-DFTEGV	FIDYRH	FDDQVSPSTDGSKSN----	DESS	PIYEFghGLSWT	: 679
Gz3A :	PQE-DFVEGN	FIDYRH	FDRQSPSTNGKSATN----	DSSAP	LYEFgyGLSWT	: 680
Fv3C :	PQD-DFSEGV	FIDYRH	FDRRSPSTDGKSSPN----	NTAAP	LYEFghGLSWS	: 693
Fo3A :	PQD-DFSEGV	FIDYRH	FDRRSPSTDGKSAPN----	NTAAP	LYEFghGLSWT	: 693
Pa3G :	PQQ-DFSEGV	FIDYRY	FDK-----	ANTSV	IYEFghGLSYT	: 663
Vd3A :	PQS-DFDEGV	FIDYRW	FDRQSGVDNNASAPRNSSSSHAPIFEFGYGLSYT			: 685

	*	820	*	840	*	
Tn3B :	TFEYSD	LNVSF-----				: 612
Fv3G :	TFEYAS	LQISK-----				: 661
Fv3D :	TFEISD	ISAEP-----				: 683
Tr3A :	KFNYSR	LSVLSTAKS-----	G-----			: 627
Pa3D :	NFTFS	DIKITSNVKP-----	G-----			: 617
Te3A :	TFEFSQ	LNVPINAPPYTPASGFTKAAQSFG--	QPSNASDNL	YPSD-IER		: 697
An3A :	TFNYSN	LQVEVLSAPAYEPASGETEAAPTFG--	EVGNASDYL	YPDG-LQR		: 702
Tr3B :	TFKFSN	LHIQKNNVGPMSPNGKTIAAPSLG-SFSKNL	KDYGFPKN-VRR			: 717
Nh3A :	TFEYSEL	NIQAHNKIPFDPPIGETIAAPVLG-NYSTDL	LADYTFPDG-IRY			: 727
Gz3A :	TFEYSD	LKVESVSNASYS	SPSVGNTIPAPTYG-NFSKNL	DDYTFPSG-VRY		: 728
Fv3C :	TFEYSD	LNQKNVENPYSP	PAGQTI	PAPTFG-NFSKNL	NDYVFPKG-VRY	: 741
Fo3A :	TFEYSD	LNQKNVNSTYS	PAGQTI	PAPTFG-NFSKNL	NDYVFPKG-VRY	: 741
Pa3G :	TFEYSN	IQVTKKNAGPYKPTTGQTAPAPTFG-NFSTD	LSDYLFDEEFPY			: 712
Vd3A :	TFEFSN	LQIERHVDVHDYVPTTGQTS	PAPRFGANYSTNYDDYVFPEGEIRY			: 735

	860	*	880	*	900	
Tn3B :	-----				DGET-----	: 616
Fv3G :	-----				SQAQTPEYPAG	: 672
Fv3D :	-----				LASDITSQPED	: 694
Tr3A :	-----				PAT	: 630
Pa3D :	-----				PAT	: 620
Te3A :	VPLYI	YPWLNSTDL-KASAND--	PDYGLPTEKYVPPNATNGDPQPIDPAG			: 744
An3A :	ITKFI	YPWLNSTDL-EASSGD--	ASYGQDASDYLPEGATDGSAQPILPAG			: 749
Tr3B :	IKEFI	YPYLSTTTSGKEASGD--	AHYGQTAKEFLPAGALDGSPQPRSAAS			: 765
Nh3A :	IYQFI	YPWLNTSSSGREASGD--	PDYGKTAEEFLPPGALDGSAQPRPPSS			: 775
Gz3A :	LYKFI	YPYLNTSSSAEKASGDVKGRFGETGDEFLPPNALNGSSQPRLPSS				: 778
Fv3C :	IYKFI	YPFLNTSSSASEASND-GGQFGKTAEEFLPPNALNGSAQPRLPAS				: 790
Fo3A :	IYKFI	YPFLNTSSSASEASND-GGQFGKTAEEFLPPNALNGSAQPRLPSS				: 790
Pa3G :	VYQYI	YPYLNTTDP-RNASGD--	PHFGQTAEEFMPPHAIDDSPQPLLPSS			: 759
Vd3A :	IYQHI	YPYLNSSDP-KEALAD--	PKYGQTAEEFLPEGALDASPQPRLPAS			: 782

FIG. 43A-6

SUBSTITUTE SHEET (RULE 26)

66 / 111

	*	920	*	940	*
Tn3B	:	-----LRVQYRIENTGGRAGKEVSQVYIKAPKGKI--DKPF	:	650	
Fv3G	:	A-LTEGGRSDLWDVVATVTASVRNTGSVDGKEVAQLYV----GVP--GGPM	:	716	
Fv3D	:	LPVQPGGNPALWETVYNVTVSVSNTGKVDGATVPQLYVTFPDSAPAGTPP	:	744	
Tr3A	:	GAVVPGGPSDLFQNVATVTVDIANSQVGTGAEEVAQLYITYPSSAP--RTPP	:	679	
Pa3D	:	GQTIPGGPADLWEDVATVTATITNSGAVEGAEEVAQLYIGLPSSAP--ASPP	:	669	
Te3A	:	G---APGGNPSLYEPVARVTIIITNTGKVTGDEVPQLYVSL---GGP--DDAP	:	789	
An3A	:	G---GAGGNPRLYDELIRVSVTIKNTGKVAGDEVPQLYVSL---GGP--NEPK	:	794	
Tr3B	:	G---EPGGNRQLYDILYTVTATITNTGSVMDDAVPQLYLSSH---GGP--NEPP	:	810	
Nh3A	:	G---APGGNPHLWDVLYTVSAIIITNTGNATSDEIPQLYVSL---GGE--NEPV	:	820	
Gz3A	:	G---APGGNPQLWDIMYTVTATITNTGDATSDEVPQLYVSL---GGE--GEPV	:	823	
Fv3C	:	G---APGGNPQLWDILYTVTATITNTGNATSDEIPQLYVSL---GGE--NEPI	:	835	
Fo3A	:	G---APGGNPQLWDILYTVTATITNTGNATSDEIPQLYVSL---GGE--NEPV	:	835	
Pa3G	:	GKNSPGGNRALYDILYEVTADITNTGEIVGDEVVQLYVSL---GGP--DDPK	:	806	
Vd3A	:	G---GPGGNPMLWDVIFTVTATVTNTGKVAGDEVAQLYVSL---GGP--DDPI	:	827	
		960	*	980	*
				1000	
Tn3B	:	QELKAFHKTRLLNPGESEEVVLEIPVRDLASFN---GEEWVVEAGEYEVVRV	:	698	
Fv3G	:	RQLRGFTKP-AIKAGETATVTFELTRRDLVWDVNAQEWQLQQGNyaiyv	:	765	
Fv3D	:	KQLRGFDKV--FLEAGESKSVSFELMRRDLSYWDIIISQKWLIPGEFTIRV	:	793	
Tr3A	:	KQLRGFAKL-NLTPGQSGTATFNIRRRDLSYWDITASQKWVVPSSGSGISV	:	728	
Pa3D	:	KQLRGFSKL--KLAPGASGTATFNLRRRDLSYWDTRLQNWVVPSSGNFVSV	:	718	
Te3A	:	KVLRGFDRI--TLAPGQQYLWTTTLTRRDISNWDVPTQNWVVVTNYTKTIYV	:	838	
An3A	:	IVLRQFERI--TLQPSKETQWSTTLTRRDLANWNVETQDWEITSYPKMFVA	:	843	
Tr3B	:	KVLRGFDRIERIAPGQSVTFKADLTRRDLSNWDTKKQQWVITDYPKTVYV	:	860	
Nh3A	:	RVLRGFDRIENIAPGQSVRFTTDTITRRDLSNWDVVSQNWVITDYEKTVYV	:	870	
Gz3A	:	RVLRGFERLENIAPGESATFTAQLTRRDLSNWDVNVQNWVITDHAKKIWV	:	873	
Fv3C	:	RVLRGFDRIENIAPGQSAIFNAQLTRRDLSNWDVNAQNWVITDHPKTVWV	:	885	
Fo3A	:	RVLRGFDRIENIAPGQSAIFNAQLTRRDLSNWDVDAQNWVITDHPKTVWV	:	885	
Pa3G	:	VVLRDFGKL--RIEPGQTAKFRGLLTRRDLSNWDVVSQDWVISEHTKTVFV	:	855	
Vd3A	:	RVLRGFDRI--HIAPGASQTFRAELTRRDLSNWDVVTQNWFISQYEKTVFV	:	876	
	*	1020			
Tn3B	:	GASSRNIKLKGTFSVGEERRFKP	:	721	
Fv3G	:	GRSSRDLPLQSTLSI-----	:	780	
Fv3D	:	GFSSRDLKEETKVTVVEA-----	:	811	
Tr3A	:	GASSRDIRLTSTLSVA-----	:	744	
Pa3D	:	GASSRDIRLTGTITA-----	:	733	
Te3A	:	GNSSRNLPPLQAPLKPYPGI----	:	857	
An3A	:	GSSSRKLPLRASLPTVH-----	:	860	
Tr3B	:	GSSSRDLPLSARLP-----	:	874	
Nh3A	:	GSSSRNLPLKATLK-----	:	884	
Gz3A	:	GSSSRNLPLSADL-----	:	886	
Fv3C	:	GSSSRKLPLSAKLE-----	:	899	
Fo3A	:	GSSSRKLPLSAKLE-----	:	899	
Pa3G	:	GKSSRDLGLSAVLE-----	:	869	
Vd3A	:	GSSSRNLPLSTRLE-----	:	890	

FIG. 43A-7

67 / 111

		*	20	*	40	*	
Te3A	-----	MRNGLLKVAALAAA-----	SAVNGENLAY	:	24		
Tr3B	-----	MKTLSVFCAAALLAAVAEANPYPP-----	PHSNQAY	:	30		
Fv3C		MKLNWVAAALSIGAAGTDSAVALASAVPDTLAGVKKADAQKVVTRDTLAY	:	50			
Fv3C/Tr3B		MKLNWVAAALSIGAAGTDSAVALASAVPDTLAGVKKADAQKVVTRDTLAY	:	50			
Fv3C/Te3A/Tr3B		MKLNWVAAALSIGAAGTDSAVALASAVPDTLAGVKKADAQKVVTRDTLAY	:	50			
		60	*	80	*	100	
Te3A		SPPFYPSPWANGQG--DWAEAYQKAVQFVSQTLAEKVNLTGTGTGWEQDRC	:	73			
Tr3B		SPPFYPSPWMDPSAPGWEQAYAQAKEFVSGLTLLEKVNLTGTGVGWMGEKC	:	80			
Fv3C		SPPHYPSPWMDPNAVGWEEAYAKAKSFVSQTLMEKVNLTGTGVGWOGERC	:	100			
Fv3C/Tr3B		SPPHYPSPWMDPNAVGWEEAYAKAKSFVSQTLMEKVNLTGTGVGWOGERC	:	100			
Fv3C/Te3A/Tr3B		SPPHYPSPWMDPNAVGWEEAYAKAKSFVSQTLMEKVNLTGTGVGWOGERC	:	100			
		*	120	*	140	*	
Te3A		VGQVGSIPRLGFPGLCMQDSPLGVRDTDYNSAFFPAGVNVAATWDRNLAYR	:	123			
Tr3B		VGNVGTVPRLGMRSLCMQDGPLGLRFNTYNSAFSVGLTAAASWSRHLWVD	:	130			
Fv3C		VGNVGSIPRLGMRGLCLQDGPLGIRLSDYNSAFFPAGTTAGASWSKSLWYE	:	150			
Fv3C/Tr3B		VGNVGSIPRLGMRGLCLQDGPLGIRLSDYNSAFFPAGTTAGASWSKSLWYE	:	150			
Fv3C/Te3A/Tr3B		VGNVGSIPRLGMRGLCLQDGPLGIRLSDYNSAFFPAGTTAGASWSKSLWYE	:	150			
		160	*	180	*	200	
Te3A		RGVAMGEEHRGKGVDVQLGFPVAGPLGRSPDAGRNWEGFAPDPVLTGNMMA	:	173			
Tr3B		RGTALGSEAKGKGVDVLLGFPVAGPLGRNPNGGRNVEGFGSDPYLAGLALA	:	180			
Fv3C		RGLLMGTEFKEKIDIALGPATGPLGRTAAGGRNWEGFTVPDYPMAGHAMA	:	200			
Fv3C/Tr3B		RGLLMGTEFKEKIDIALGPATGPLGRTAAGGRNWEGFTVPDYPMAGHAMA	:	200			
Fv3C/Te3A/Tr3B		RGLLMGTEFKEKIDIALGPATGPLGRTAAGGRNWEGFTVPDYPMAGHAMA	:	200			
		*	220	*	240	*	
Te3A		STIQGIQDAGVIACAKHFILYEQEHFRQGAQ---DGYDISDSISANADDDK	:	220			
Tr3B		DTVTGIQNAGTIACAKHFLLNEQEHFRQVGEANGYGYPITEALSSNVDDK	:	230			
Fv3C		EAVKGIQDAGVIACAKHYIANEQEHFRQSSEVQSRKYNISESLSSNLDDK	:	250			
Fv3C/Tr3B		EAVKGIQDAGVIACAKHYIANEQEHFRQSSEVQSRKYNISESLSSNLDDK	:	250			
Fv3C/Te3A/Tr3B		EAVKGIQDAGVIACAKHYIANEQEHFRQSSEVQSRKYNISESLSSNLDDK	:	250			
		260	*	280	*	300	
Te3A		TMHELYLWPFADAVRAGVGSVMCSYNQVNNNSYACSNSTMTNKLKSELGF	:	270			
Tr3B		TIHEVYGWPFQDAVKAGVGSFMCSSYNQVNNNSYACQNSKLLINGLLKEEYGF	:	280			
Fv3C		TMHELYAWPFADAVRAGVGSVMCSYNQINNSYGCQNSKLLNGILKDEMGE	:	300			
Fv3C/Tr3B		TMHELYAWPFADAVRAGVGSVMCSYNQINNSYGCQNSKLLNGILKDEMGE	:	300			
Fv3C/Te3A/Tr3B		TMHELYAWPFADAVRAGVGSVMCSYNQINNSYGCQNSKLLNGILKDEMGE	:	300			
		*	320	*	340	*	
Te3A		QGFVMTDWGGHHSVGVSALAGLDMSMPGDTAFDSGTSFWGNTLVAVLNG	:	320			
Tr3B		QGFVMSDWQAQHTGVASAVAGLDMTMPGDTAFNTGASYFGSNLTLAVLNG	:	330			
Fv3C		QGFVMSDWAAQHTGAASAVAGLDMSMPGDTAFDSGYSFWGGNLTAVING	:	350			
Fv3C/Tr3B		QGFVMSDWAAQHTGAASAVAGLDMSMPGDTAFDSGYSFWGGNLTAVING	:	350			
Fv3C/Te3A/Tr3B		QGFVMSDWAAQHTGAASAVAGLDMSMPGDTAFDSGYSFWGGNLTAVING	:	350			

FIG. 43B-1

68 / 111

	360	*	380	*	400	
Te3A	SIPEWRVDDMAVRIMSAYYKVGRDRYSVP- INFDSWTLDTYGPEHYAVGQ	:	369			
Tr3B	TVPEWRIDDMVMRIMAPFFKVGKTVDLSLIDTNFDSWTNGEYGYVQAAVNE	:	380			
Fv3C	TVPAWRVDDMALRIMS AFFKV GKTIEDLPDINFSSWTRDTFGFVHTFAQE	:	400			
Fv3C/Tr3B	TVPAWRVDDMALRIMS AFFKV GKTIEDLPDINFSSWTRDTFGFVHTFAQE	:	400			
Fv3C/Te3A/Tr3B	TVPAWRVDDMALRIMS AFFKV GKTIEDLPDINFSSWTRDTFGFVHTFAQE	:	400			
	*	420	*	440	*	
Te3A	GQTKINEHVDVRGNHAEIIHEIGAASAVLLKNKGGLPLTGTERFVGVF GK	:	419			
Tr3B	NWEKVNYGVDVRANHANHIREVGAKGT VIFKNNGILPLK-KPKFLT VIGE	:	429			
Fv3C	NREQVNFGVNVQHDHKSHIREAAAAGSVVLKNTGSLPLK-NPKFLAVIGE	:	449			
Fv3C/Tr3B	NREQVNFGVNVQHDHKSHIREAAAAGSVVLKNTGSLPLK-NPKFLAVIGE	:	449			
Fv3C/Te3A/Tr3B	NREQVNFGVNVQHDHKSHIREAAAAGSVVLKNTGSLPLK-NPKFLAVIGE	:	449			
	460	*	480	*	500	
Te3A	DAGSNPWGVNGCSDRGCDNGTLAMGWGSGTANFPYLVTPEQAIQREVLSR	:	469			
Tr3B	DAGGNPAGPNGCGDRGCDGTLAMEWGSGTTNFPYLVT PDAALQS QALQD	:	479			
Fv3C	DAGPNPAGPNGCGDRGCDNGTLAMAWGSGTSQFPYLITPDQGLSNRATQD	:	499			
Fv3C/Tr3B	DAGPNPAGPNGCGDRGCDNGTLAMAWGSGTSQFPYLITPDQGLSNRATQD	:	499			
Fv3C/Te3A/Tr3B	DAGPNPAGPNGCGDRGCDNGTLAMAWGSGTSQFPYLITPDQGLSNRATQD	:	499			
	*	520	*	540	*	
Te3A	NGTFTGITDNGALAEMAAAASQAD-TCLVFANADSGEGYITVDGNEGDRK	:	518			
Tr3B	GTRYESILSNY AISQTQALVSQPD AIAIVFANS DSGEGYINVDGNEGDRK	:	529			
Fv3C	GTRYESILTNN EWASVQALVSQPNVTAIVFANADSGEGYIEVDGNF GDRK	:	549			
Fv3C/Tr3B	GTRYESILTNN EWASVQALVSQPNVTAIVFANADSGEGYIEVDGNF GDRK	:	549			
Fv3C/Te3A/Tr3B	GTRYESILTNN EWASVQALVSQPNVTAIVFANADSGEGYIEVDGNF GDRK	:	549			
	560	*	580	*	600	
Te3A	NLTLWQGADQVIHNVSANCNNTVVVLHTVGPVLIDDWYDHPNVTAI LWAG	:	568			
Tr3B	NLTLWKNGDDLIKTVAAVNPKTIVVIHSTGPVILKDYANHPNISAILWAG	:	579			
Fv3C	NLTLWQQGDELIK NVSSICPNTIVVLHTVGPVLLADYEKNPNITAI VWAG	:	599			
Fv3C/Tr3B	NLTLWQQGDELIK NVSSICPNTIVVLHTVGPVLLADYEKNPNITAI VWAG	:	599			
Fv3C/Te3A/Tr3B	NLTLWQQGDELIK NVSSICPNTIVVLHTVGPVLLADYEKNPNITAI VWAG	:	599			
	*	620	*	640	*	
Te3A	LPGQESGNSLVDVLYGRVNP GKTPFTWGRARDDYGAPLIVKPNNGKGAPQ	:	618			
Tr3B	APGQESGNSLVDILY GKQSPGRTPFTWGPSLESYGVSVM TTPNNGNGAPQ	:	629			
Fv3C	LPGQESGNAIADLLYGKVSPGRSPFTWGRTRRESYGTEVLYEANNRGRAPQ	:	649			
Fv3C/Tr3B	LPGQESGNAIADLLYGKVSPGRSPFTWGRTRRESYGTEVLYEANNRGRAPQ	:	649			
Fv3C/Te3A/Tr3B	LPGQESGNAIADLLYGKVSPGRSPFTWGRTRRESYGTEVLYEANNRGRAPQ	:	649			
	660	*	680	*	700	
Te3A	QDFTEGIFIDYRRFDKYNIT-----PIYEF GFGLSYTTFEFSQ	:	656			
Tr3B	DNFNEGAFIDYRYFDK VAPG----KPRSSDKAPT YEF GFGLSWSTFKFSN	:	675			
Fv3C	DDFSEGVFIDYRHFDRRSPSTDGKSSPNNTAAPLYEFGHGLSWSTFEYSD	:	699			
Fv3C/Tr3B	DDFSEGVFIDYRHFDRRSPSTDGKSSPNNTAAPLYEFGHGLSWSTFKFSN	:	699			
Fv3C/Te3A/Tr3B	DDFSEGVFIDYRHFDKYNIT-----PIYEF GFGLSWSTFKFSN	:	687			

FIG. 43B-2

69 / 111

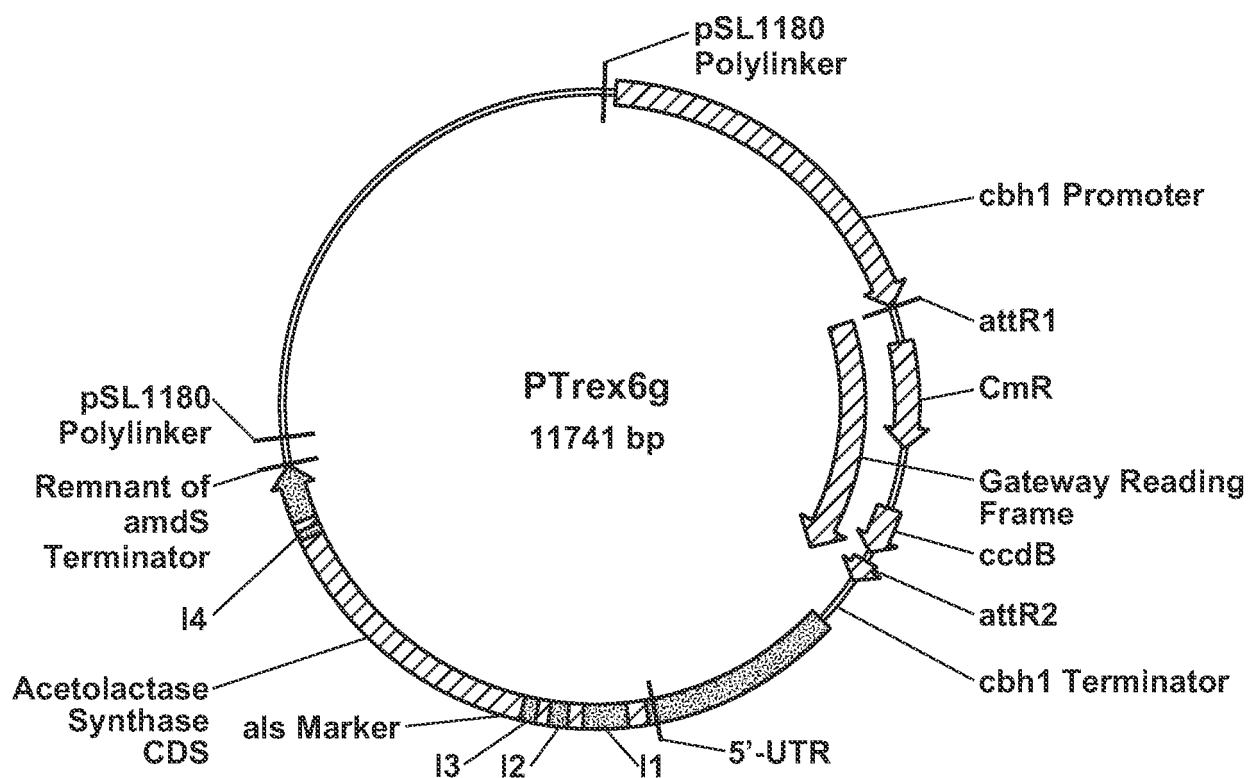
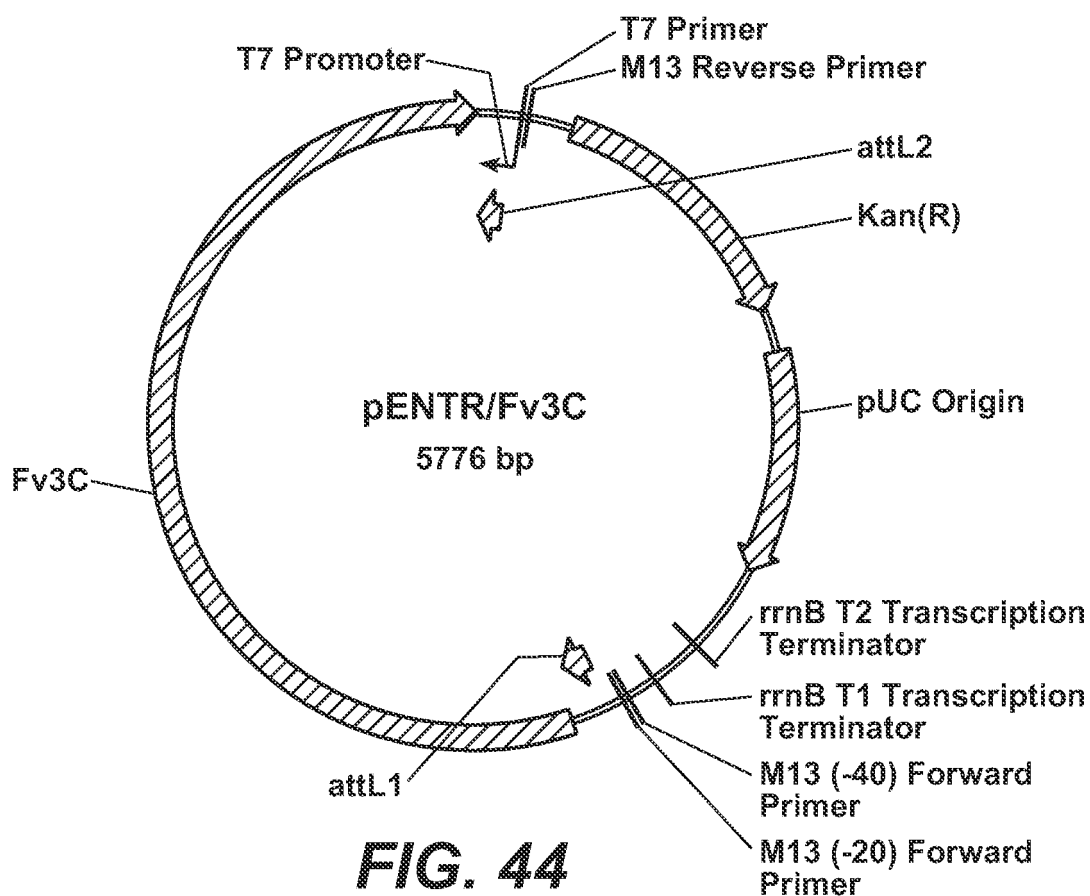
		*	720	*	740	*		
Te3A	LN	VQ	PINAPPYTPASGFTKAAQSF	GQ-PSNASD	NLYPSDI	ERVPLYIYPW	: 705	
Tr3B	LHI	QKNNVG	FMSPPNGKTIAAPSLG	SFSK	NLKDYGF	PKNVRR	IKEFIYPY : 725	
Fv3C	LNI	QKNVEN	PYSPPAGQTIPAP	TFGN	FSK	NLDYVF	PKGVRIYKFIYPF : 749	
Fv3C/Tr3B	LHI	QKNNVG	FMSPPNGKTIAAPSLG	SFSK	NLKDYGF	PKNVRR	IKEFIYPY : 749	
Fv3C/Te3A/Tr3B	LHI	QKNNVG	FMSPPNGKTIAAPSLG	NFSK	NLKDYGF	PKNVRR	IKEFIYPY : 737	
			760	*	780	*	800	
Te3A	LN	STD	L-KASAND-PDYGLP	TEKYVPP	NATNGDP	QPIDPAGG	APGGNPSL : 753	
Tr3B	LST	TTSGKE	ASGD-AHYGQ	TAKEFL	PAGALDG	SPQPRSA	ASGEPGGNRQL : 774	
Fv3C	LNT	SSSASE	ASNDGGQ	FGKTAEE	FLPPNAL	NGSAQ	PRLPASGAPGGNPQL : 799	
Fv3C/Tr3B	LST	TTSGKE	ASGD-AHYGQ	TAKEFL	PAGALDG	SPQPRSA	ASGEPGGNRQL : 798	
Fv3C/Te3A/Tr3B	LNT	TTSGKE	ASGD-AHYGQ	TAKEFL	PAGALDG	SPQPRSA	ASGEPGGNRQL : 786	
		*	820	*	840	*		
Te3A	YEP	VARVT	TIITNTGK	VTGDEVP	QLYVSL	GPGDDAP	KVLRGFDRI-TLAP : 802	
Tr3B	YDI	LYTV	TATITNTG	SVMDDAV	PQLYLS	HGGPNE	PPKVLRGFDRIERIAP : 824	
Fv3C	WDI	LYTV	TATITNTG	NATSD	EIPQLY	VSLGGE	NEPIRVLRGFDRIENIAP : 849	
Fv3C/Tr3B	YDI	LYTV	TATITNTG	SVMDDAV	PQLYLS	HGGPNE	PPKVLRGFDRIERIAP : 848	
Fv3C/Te3A/Tr3B	YDI	LYTV	TATITNTG	SVMDDAV	PQLYLS	HGGPNE	PPKVLRGFDRIERIAP : 836	
			860	*	880	*	900	
Te3A	GQ	QYLW	TTTLTRR	DISNWD	PVTQN	WVVTNY	TKTIYVGNSSRNLP	LQAPLK : 852
Tr3B	GQ	SVTF	KADLTRR	DLSNWD	TKKQ	QWVITD	YPKTVYVGSSSRDL	PLSARLP : 874
Fv3C	GQ	SAIF	NAQLTRR	DLSNWD	TNAQ	NWVITD	HPKTVWVGSSSRKL	PLSAKLE : 899
Fv3C/Tr3B	GQ	SVTF	KADLTRR	DLSNWD	TKKQ	QWVITD	YPKTVYVGSSSRDL	PLSARLP : 898
Fv3C/Te3A/Tr3B	GQ	SVTF	KADLTRR	DLSNWD	TKKQ	QWVITD	YPKTVYVGSSSRDL	PLSARLP : 886

Te3A PYPGI : 857
Tr3B ----- : -
Fv3C ----- : -
Fv3C/Tr3B ----- : -
Fv3C/Te3A/Tr3B ----- : -

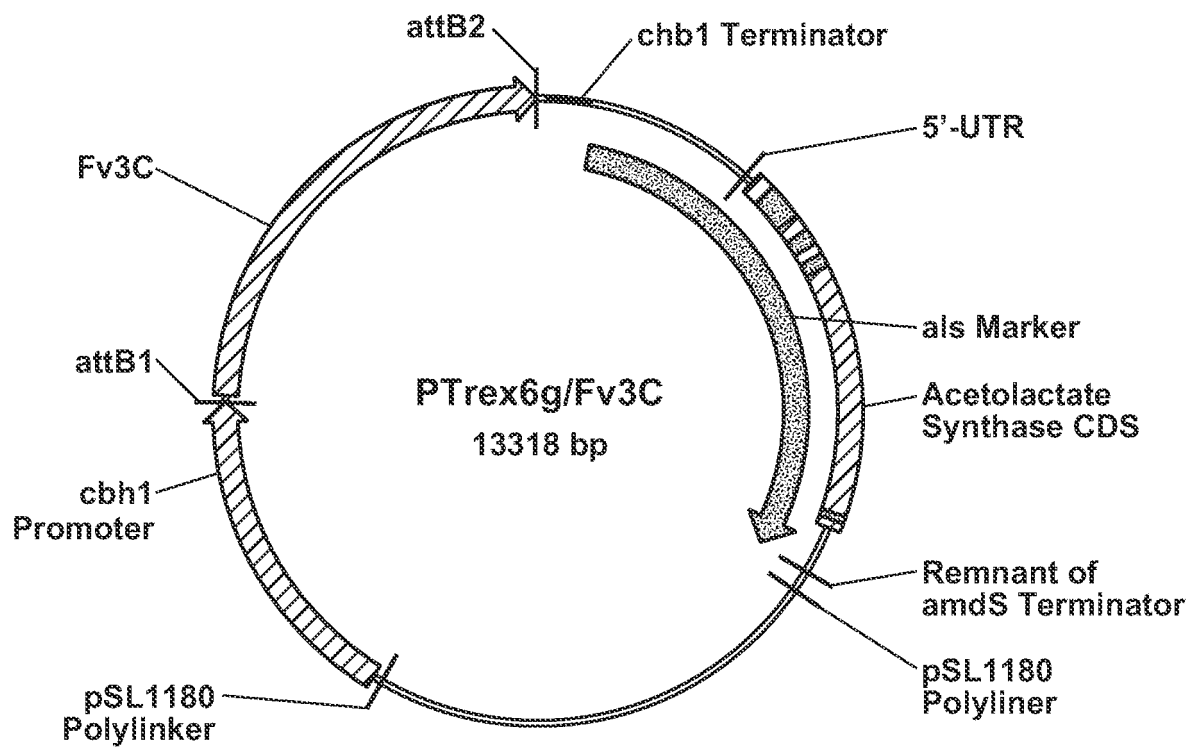
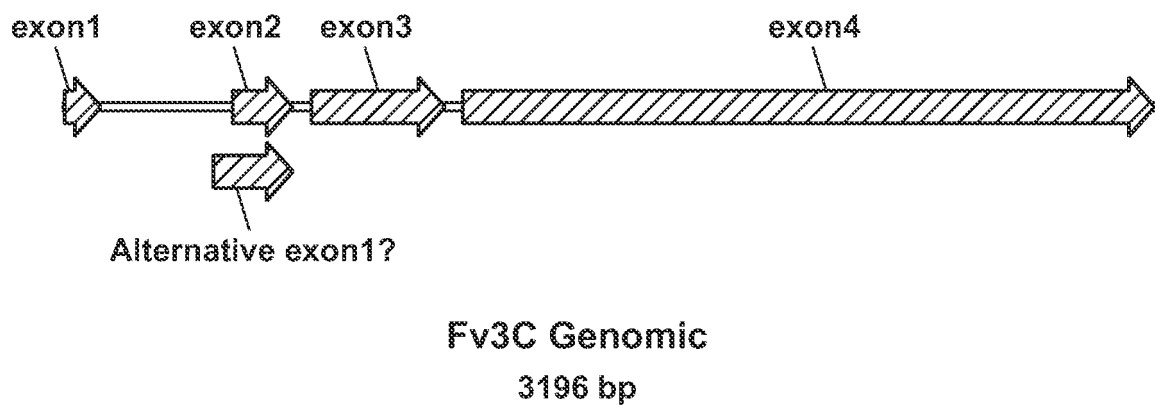
Te3A: always produced intact
Tr3B: always produced intact
Fv3C: clipped around position 760 in alignment
Fv3C/Tr3B: clipped around position 680 in alignment
Fv3C/Te3A/Tr3B: always produced intact

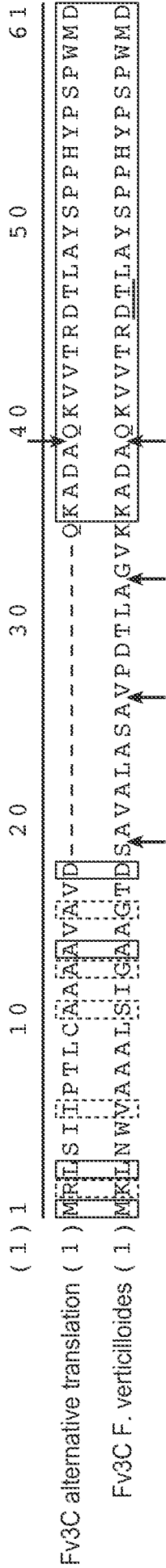
FIG. 43B-3

70 / 111

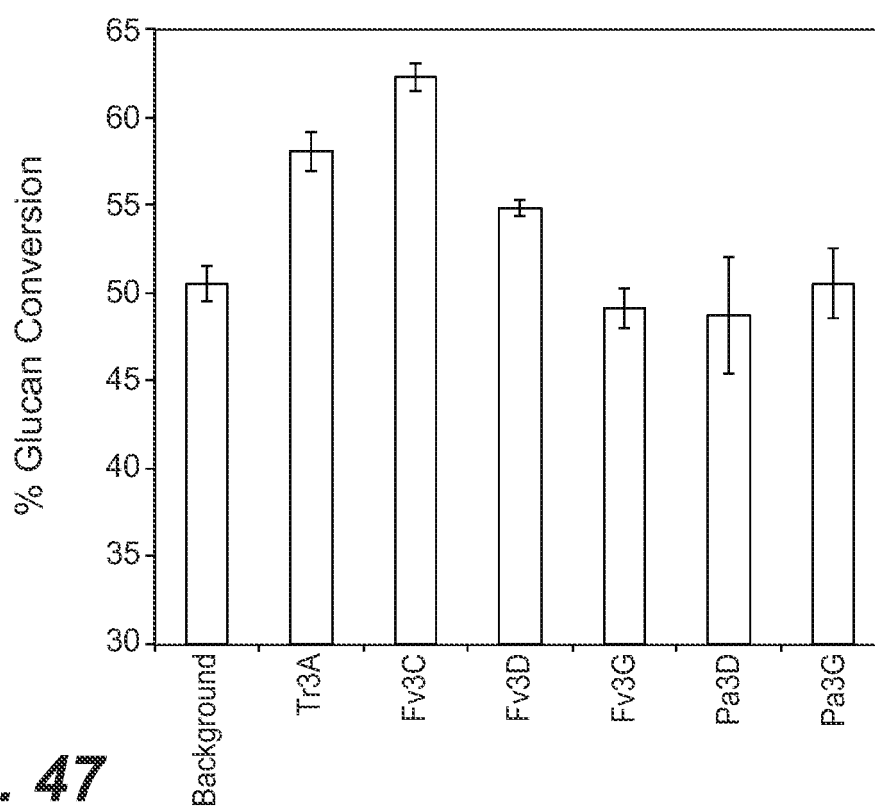
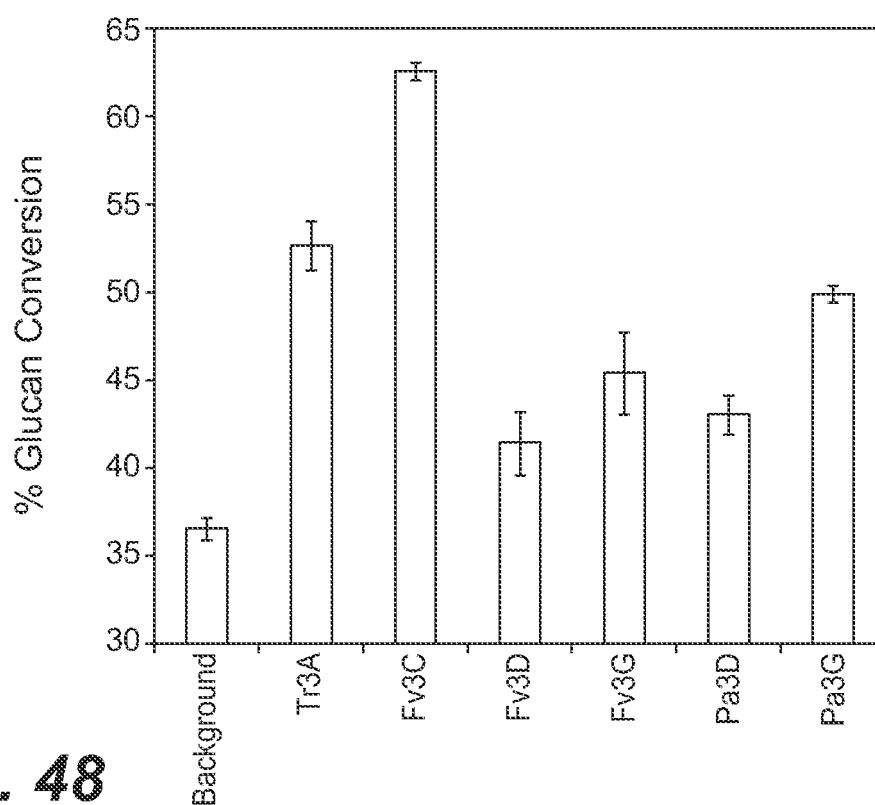


71 / 111

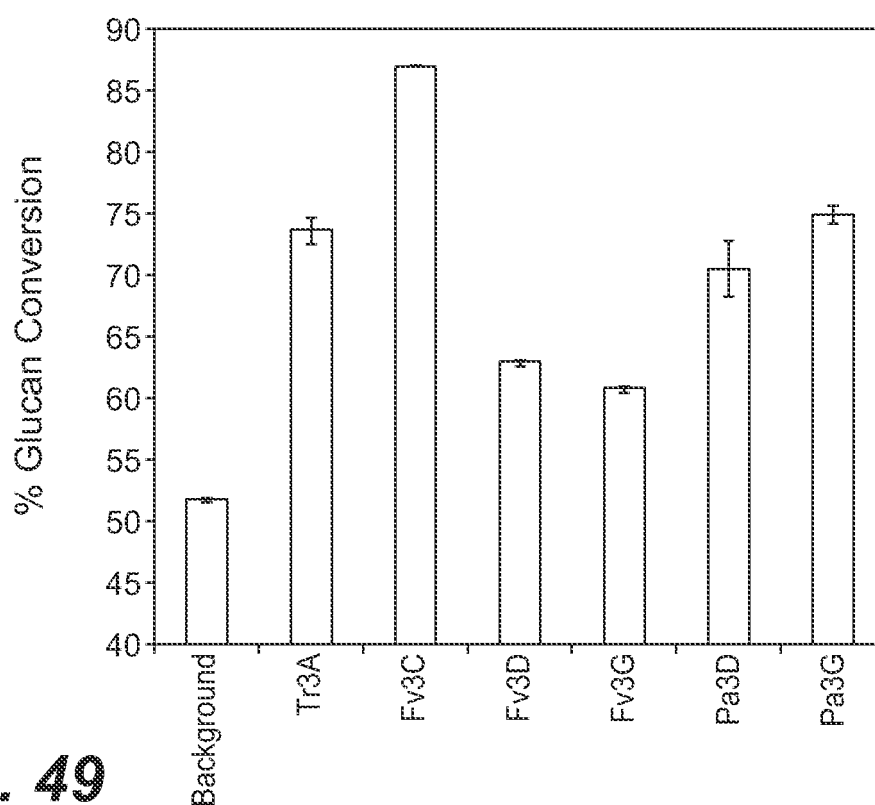
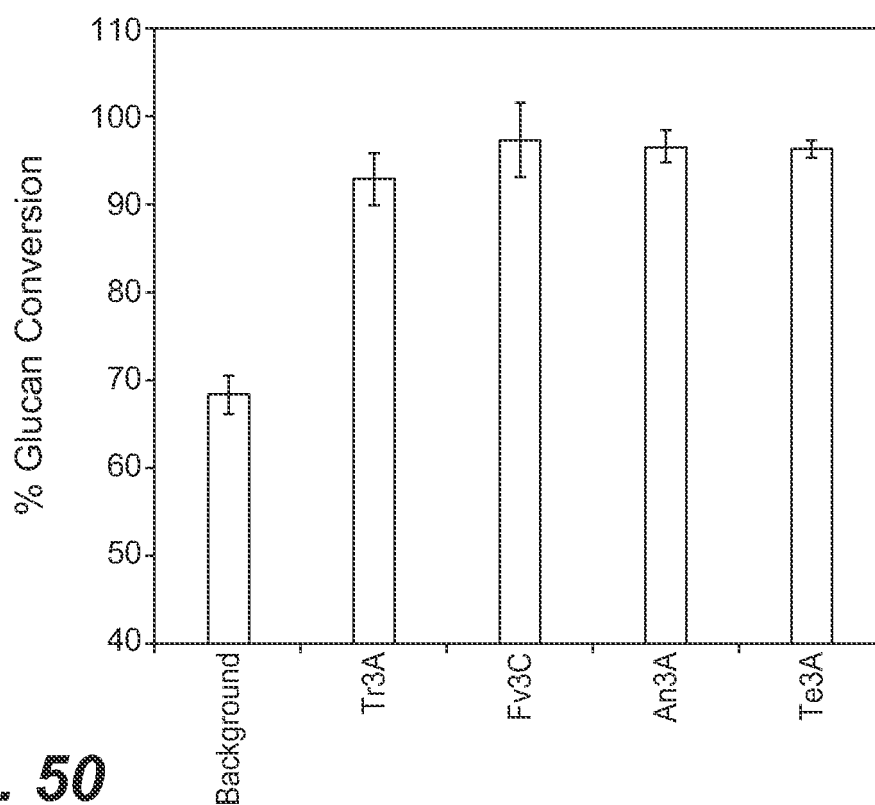
**FIG. 45B****FIG. 46A**



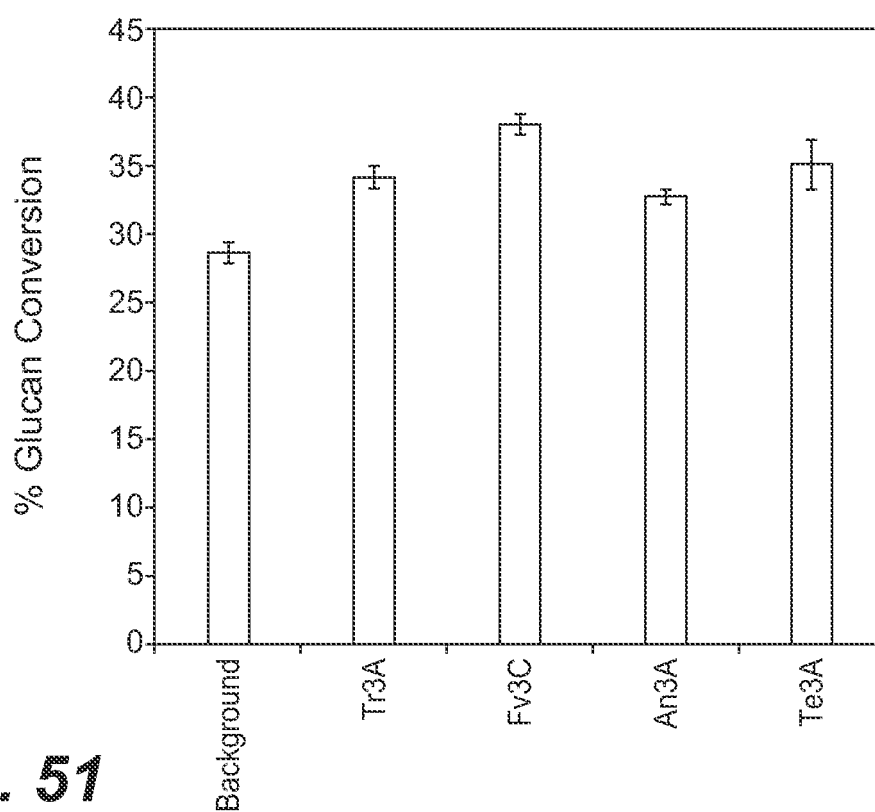
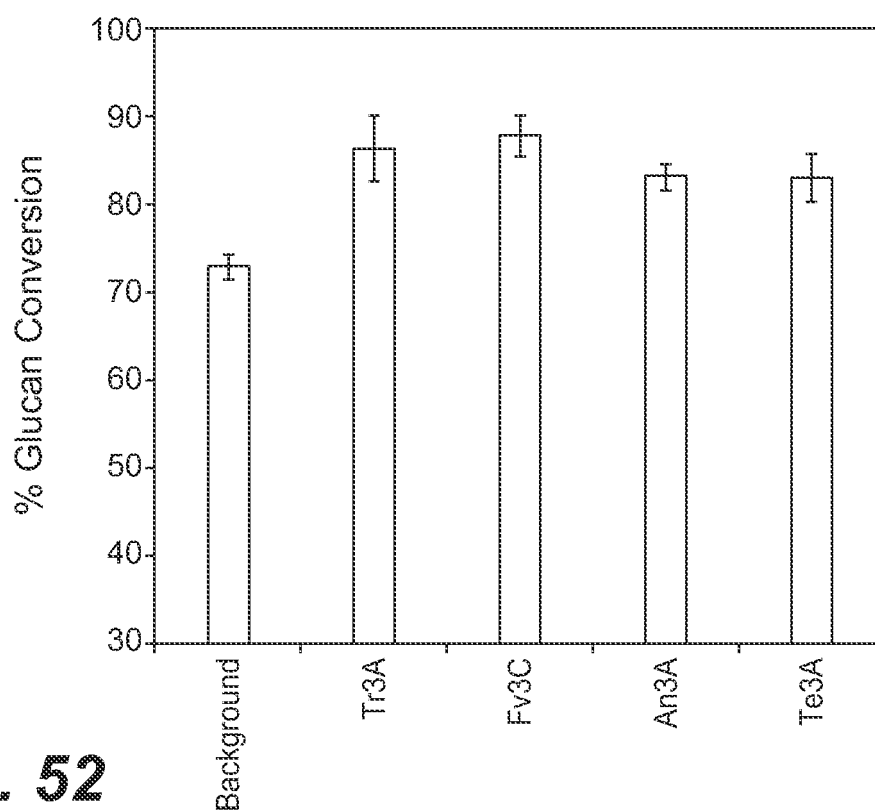
73 / 111

**FIG. 47****FIG. 48**

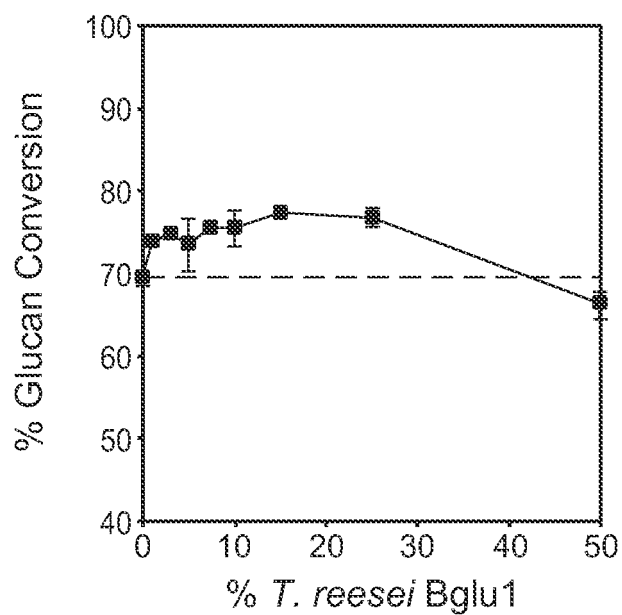
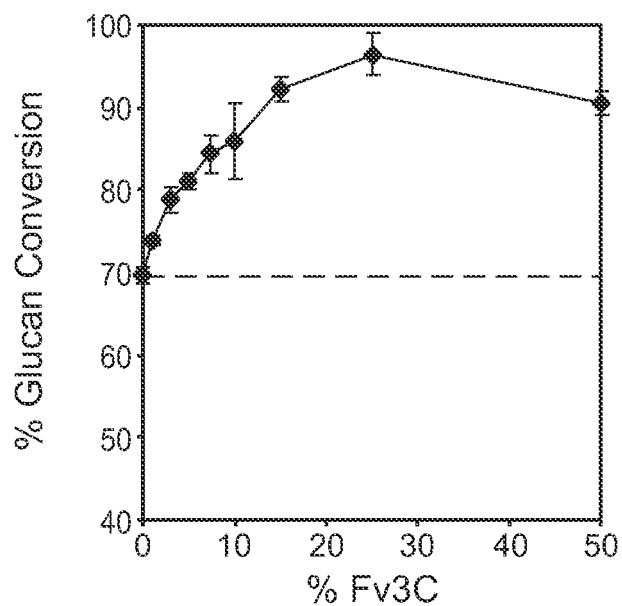
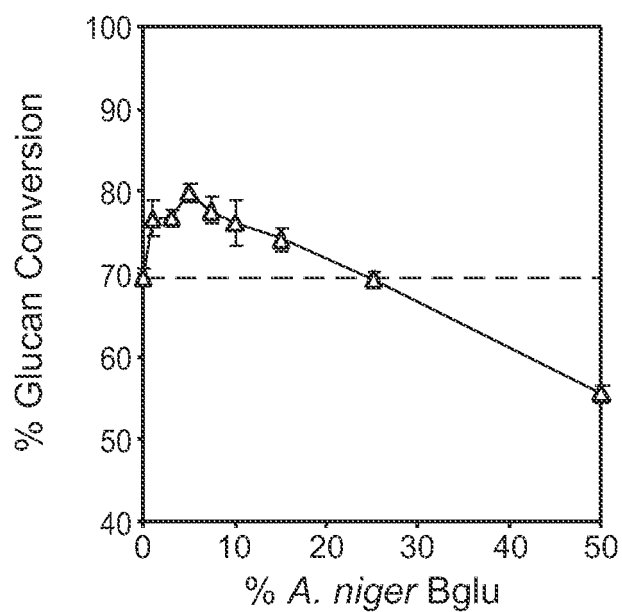
74 / 111

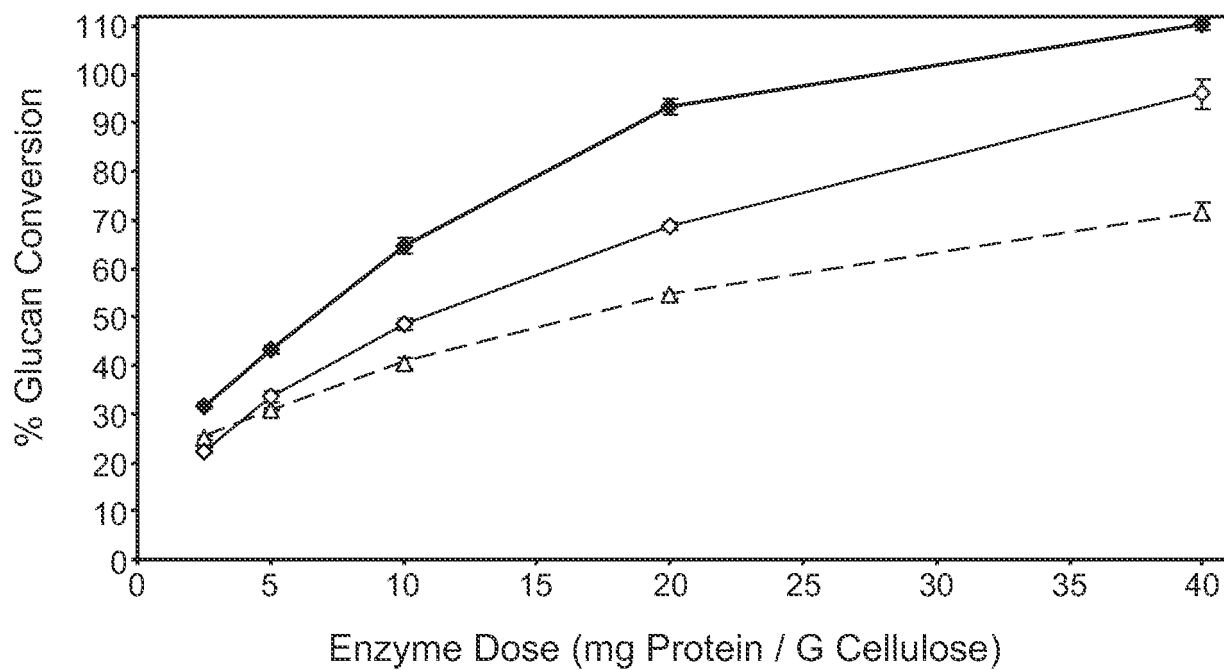
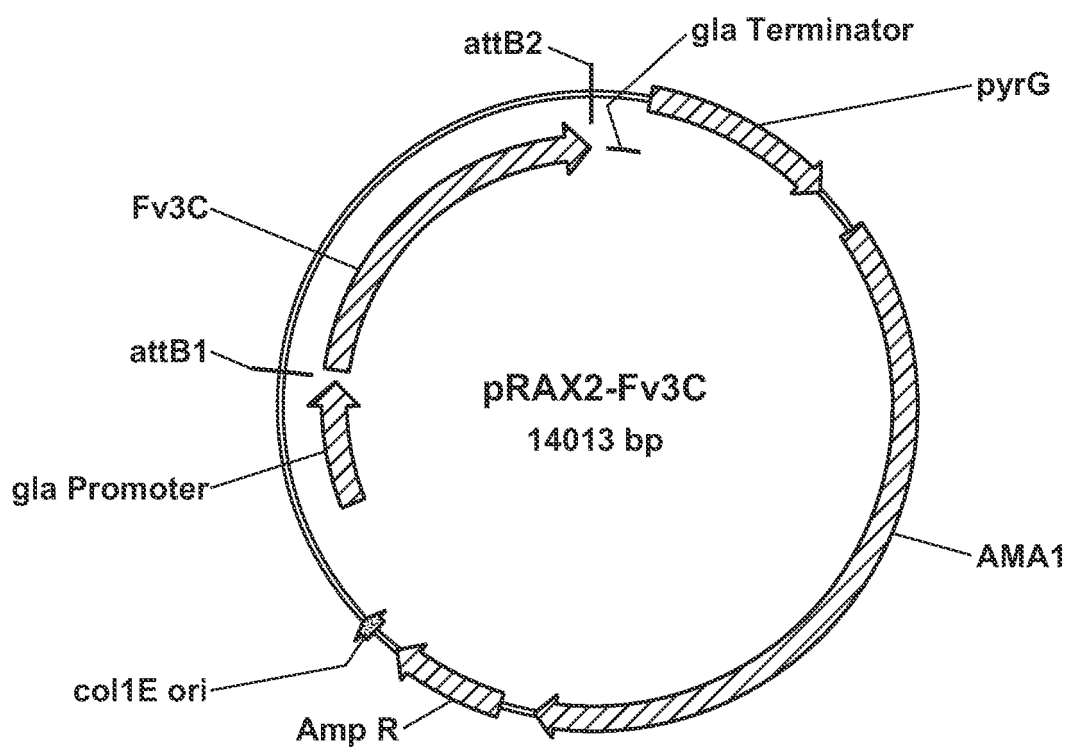
**FIG. 49****FIG. 50**

75 / 111

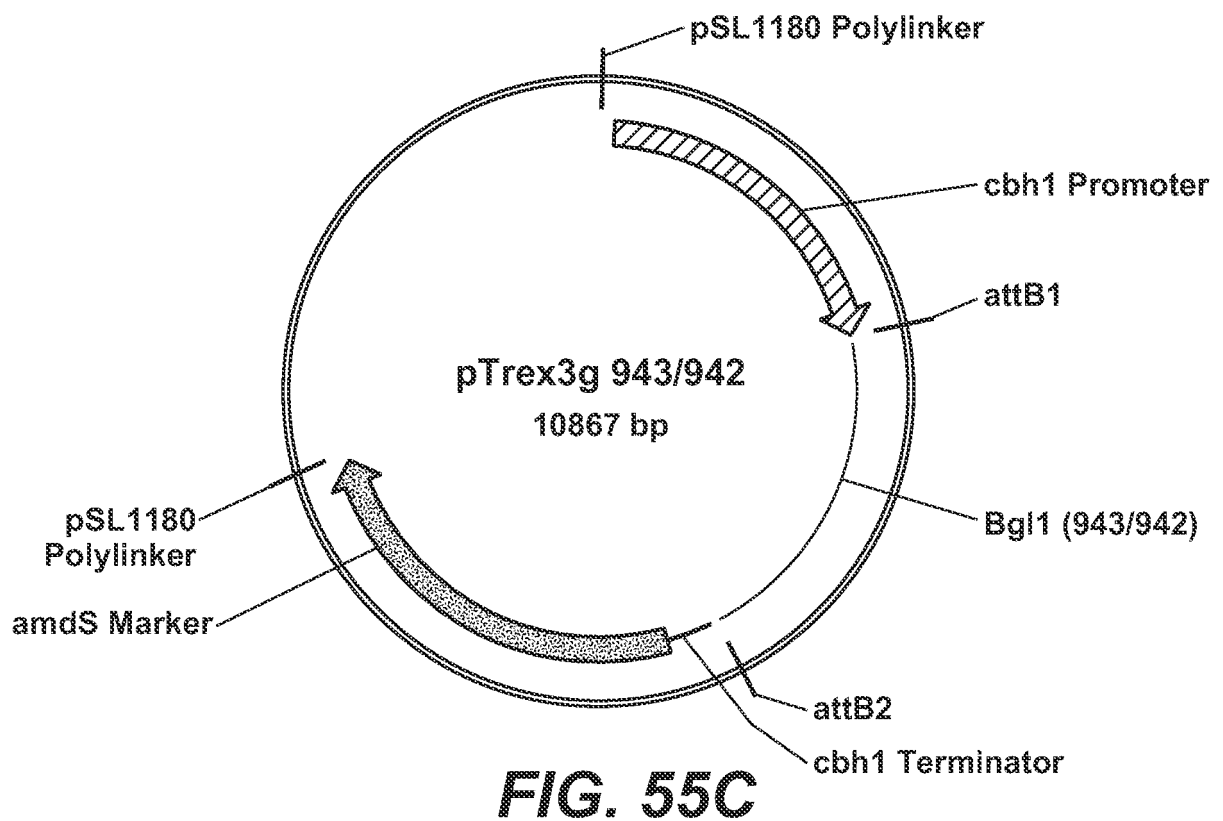
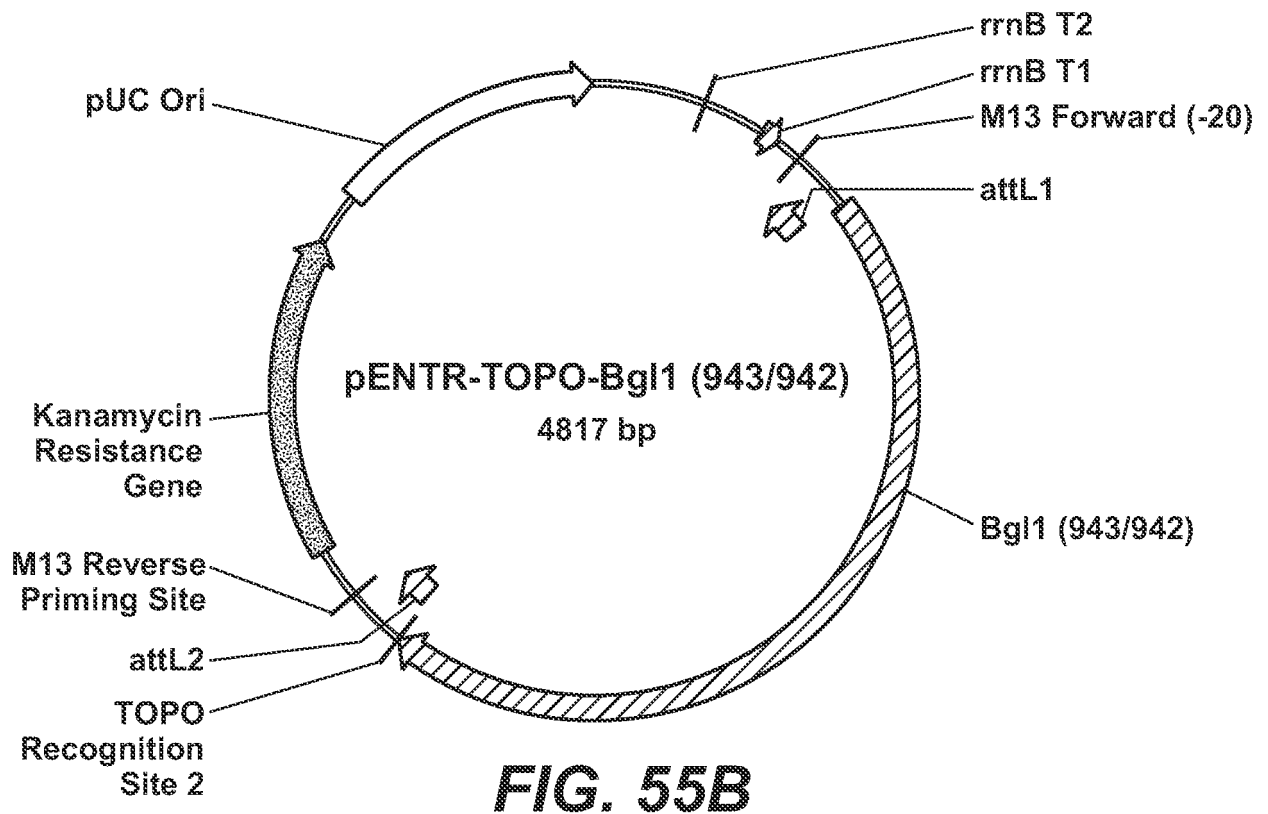
**FIG. 51****FIG. 52**

76 / 111

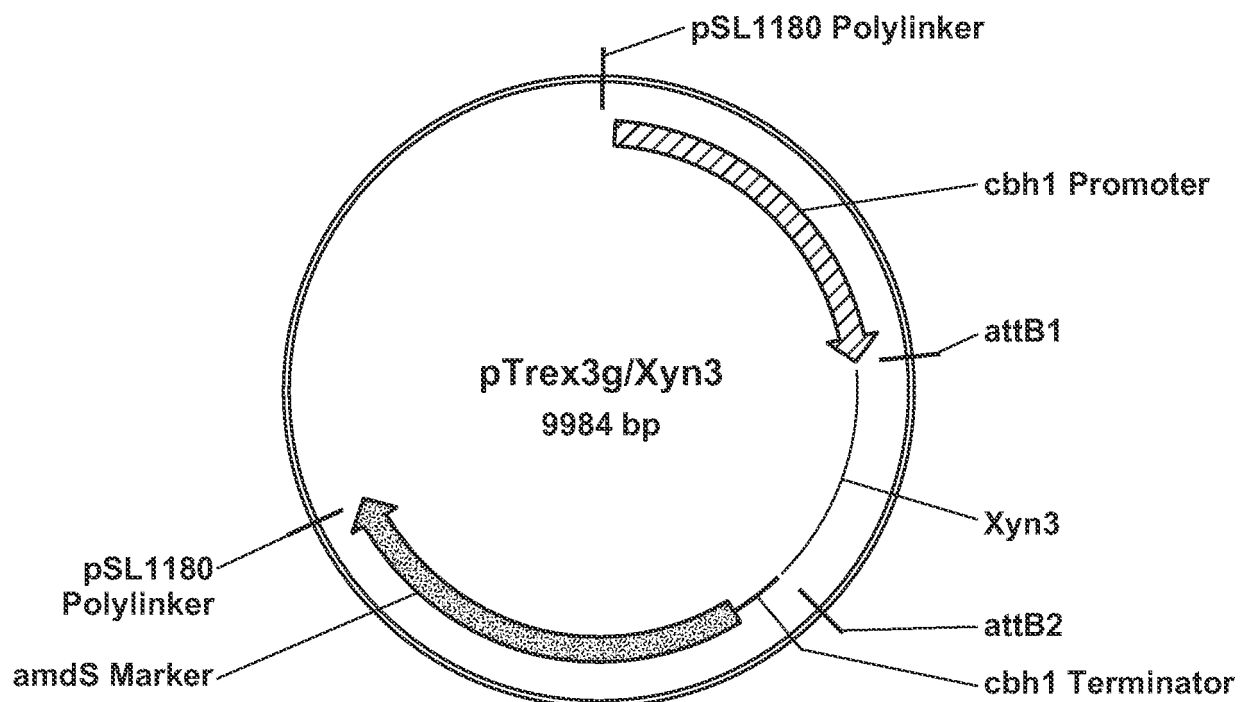
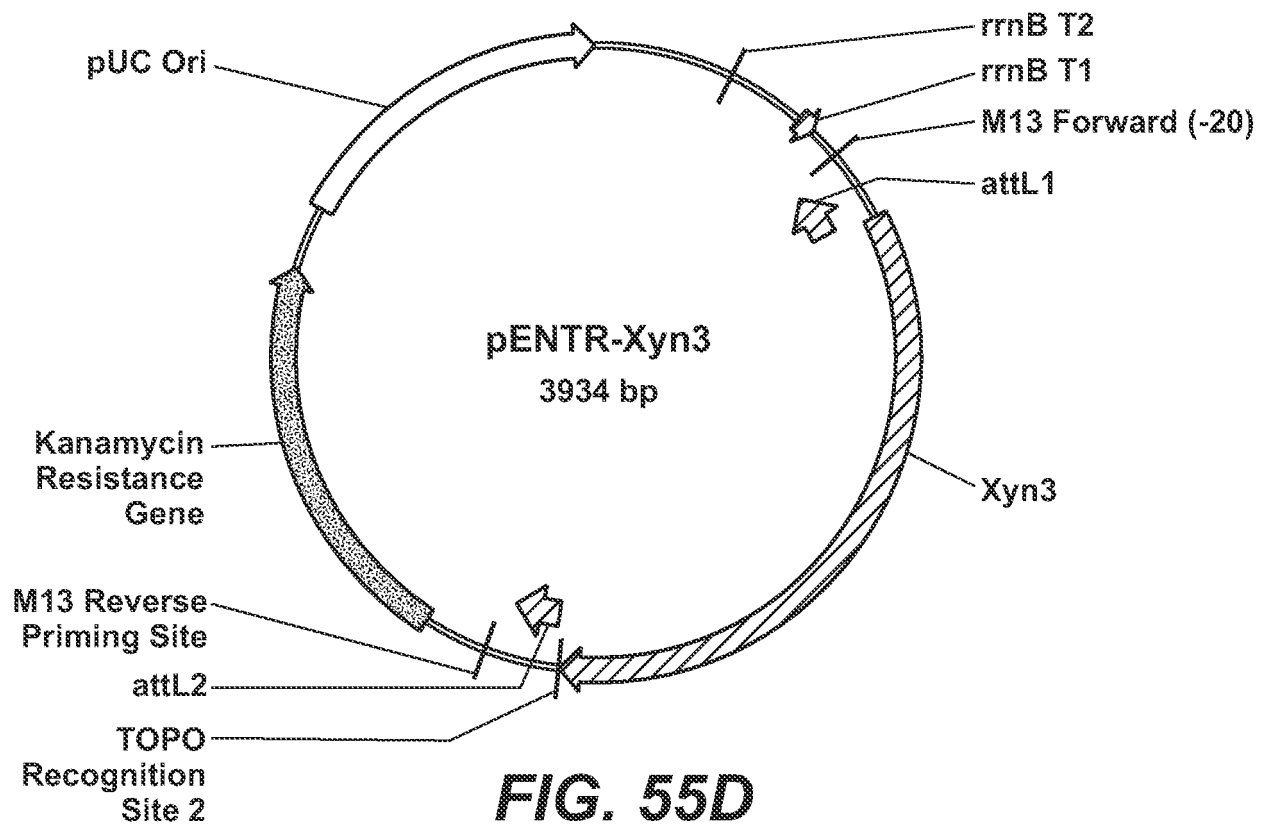
FIG. 53A**FIG. 53B****FIG. 53C**

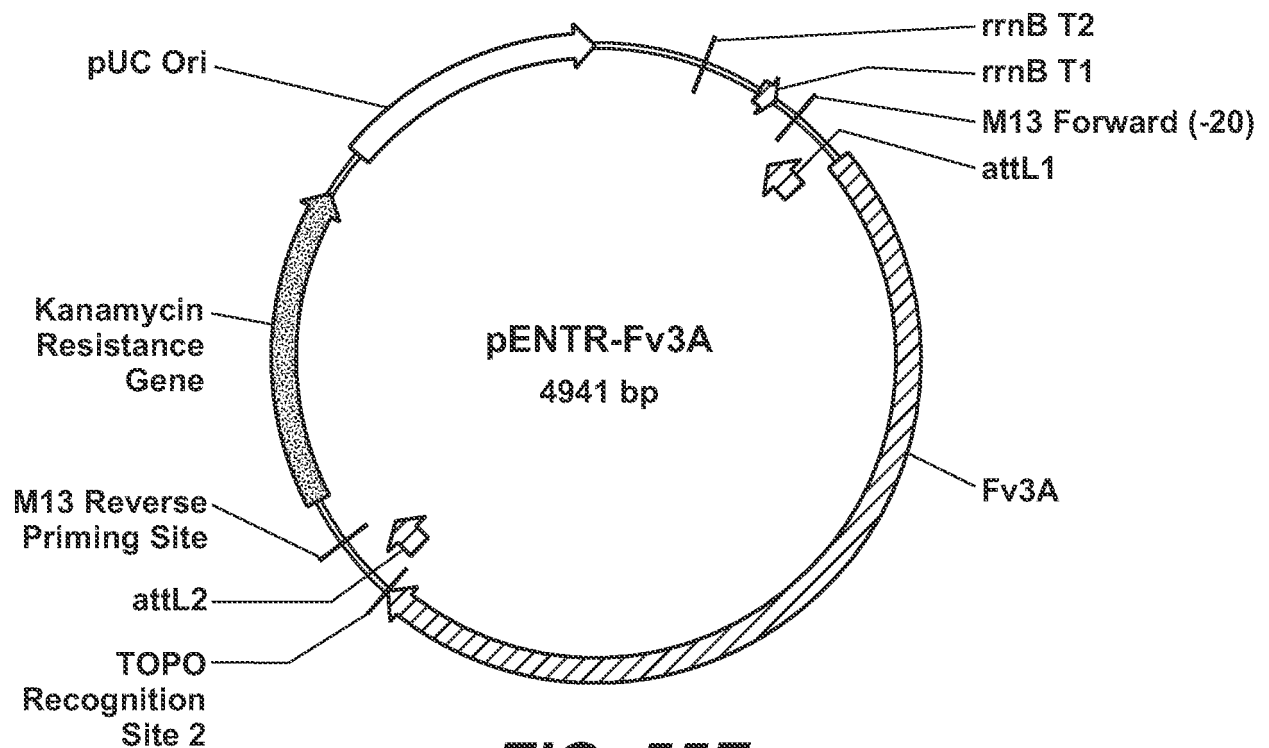
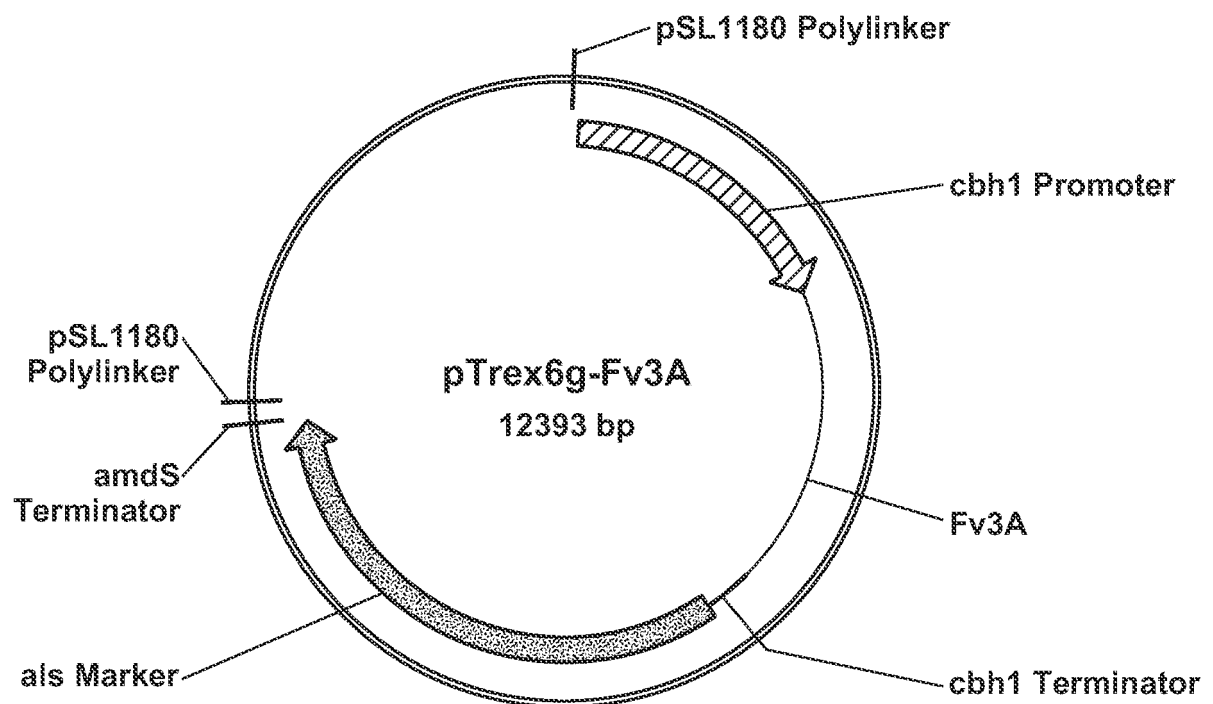
**FIG. 54****FIG. 55A**

78 / 111

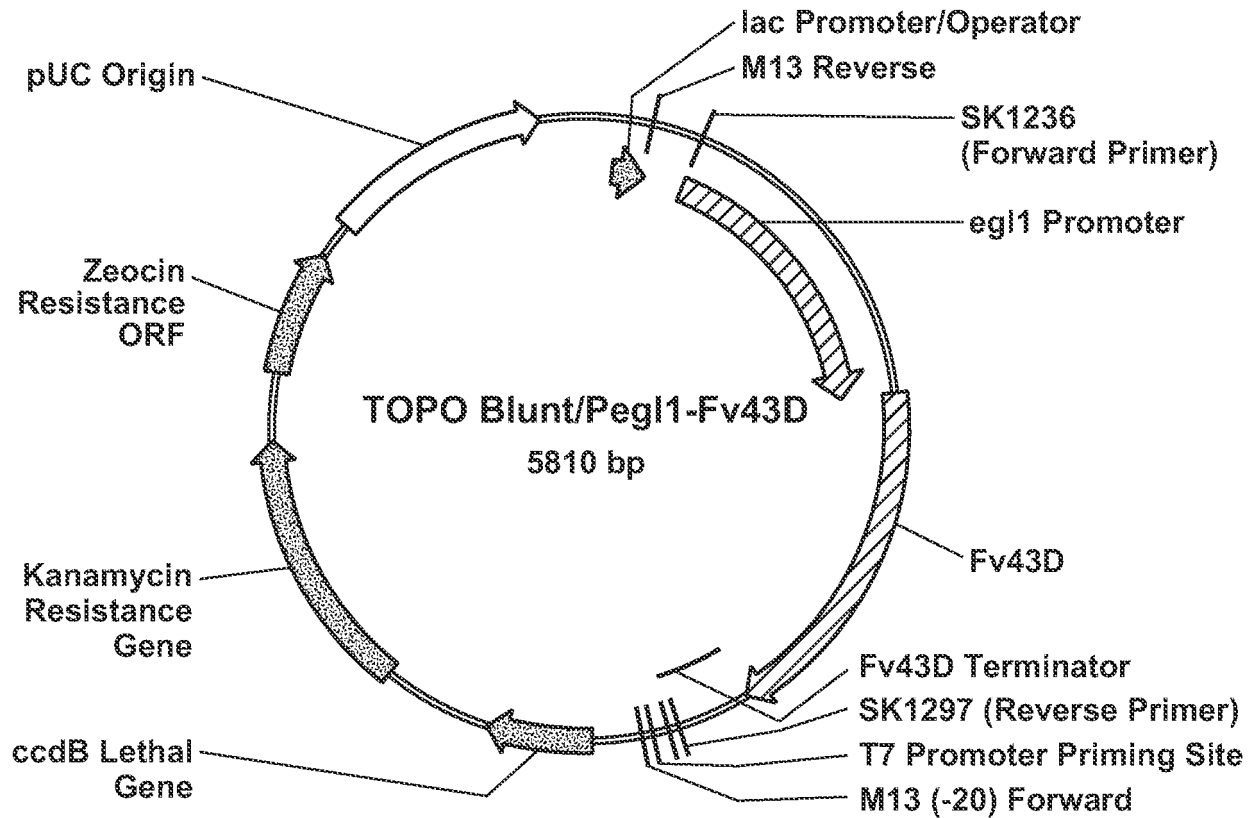
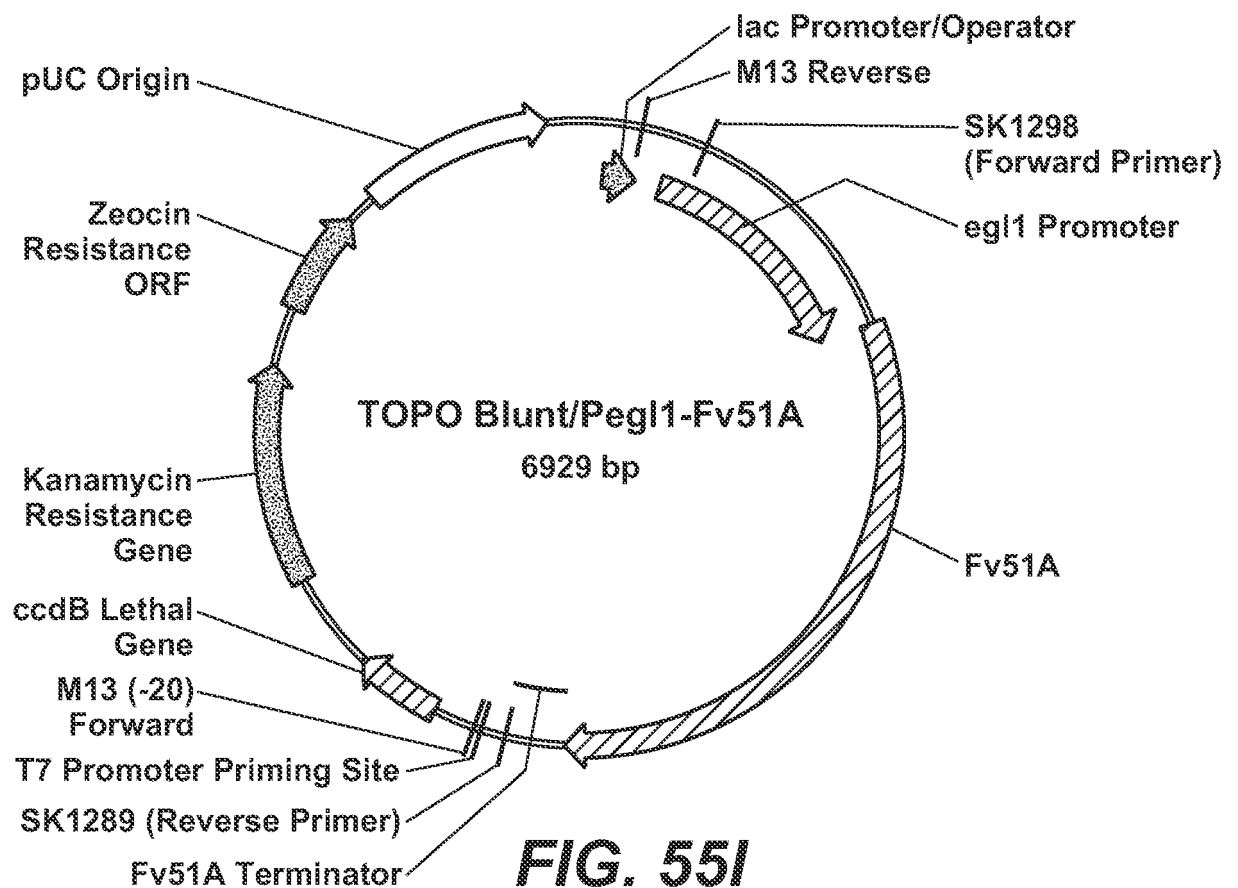


79 / 111



**FIG. 55F****FIG. 55G**

81 / 111

**FIG. 55H****FIG. 55I**

82 / 111

```

gi|reesei|Bx11 -MVNNAALLAALSALLPTALAQNNTYANYSAQQQPDLYPETLATLTLSFPDCEHGPKLN
gi|fvert| Fv3A MLLNLQVAASALSLSLLGGLAEAAATPYT-----LPDCTKGPLSK
      :* . :*** * .** :* :*** :***.:
gi|reesei| NLVCDSSAGYVERAQUALISLFTLEELILNTQNSGPGVPRGLPNYQVWNEALHGLDRAN-
gi|fvert| NGICDTSLSPAKRAAALVAALTPEEKVGNLVSNTATGAPRIGLPRYNWWNEALHGLAGSPG
      * :***: * . :** ***: :* ** : * ....*.**:***.*: ***** :
gi|reesei| ---FATKGGQFEWATSFPMPIITTAALNRTLIHQIADIISTQARAFNSNGRYGLDVYAPNV
gi|fvert| GRFADTP-PYDAATSFPMPLLMAAAFDDDLIHDIGNVVGTEARAFTNGGWRGVDFWTPNV
      ** . : : *****:* :***: ***.*:.....*:*****:* * :*.:***
gi|reesei| NGFRSPLWGRGQETPGEDAFFLSSAYTYEYITGIQGGVDPEHLKVAATVKHFAGYDLENW
gi|fvert| NPFKDPRWGRGSETPGEDALHVS-RYARYIVRGLEG--DKEQRRIVATCKHYAGNDFEDW
      * *:. * ****.*****.:* * : :*:* * * : :.* **:* * :*:*
gi|reesei| NNQSRLGFDALITQQDLSEYYTPQFLAAARYAKSRSLMCAYNSVNGVPSCANSFFLQTL
gi|fvert| GGFTRHDFDAKITPQDLAEYYVRPFQECTRDAKVGSIMCAYNAVNGIPACANSYLQETIL
      .. :* .*** ** ***:***. * .:* ** * :*****:***:*:*****.: :*:*
gi|reesei| RESWGFP-EWGYVSSDCDAVYNVFNPHDYASNQSSAAASSLRAGTDIDCGQTPWHLNES
gi|fvert| RGHWNWTRDNNWITSDCGAMQDIWQNHKYVKTNAEGAQVAFENGMDSSCEYTTTSDVSDS
      * *:. : :***:***: :***: *.*****.* :.. * * . * . :..*
gi|reesei| FVAGEVSRGEIERSVTRLYANLVR LGYFD-KKNQYRSLGWKDVVKTDAWNISYEAAVEGI
gi|fvert| YKQGLLTEKLMDRSLKRLFEGLVHTGFFDGAQAQWNSLSFADVNTKEAQLALRSVEGA
      : * :.. :***:***: .**:*:* * * :.*.: ** ..* :.. :.****
gi|reesei| VLLKNDGTLPLSKKVR-SIALIGPWANATTQM QGNYYGPAPYLISPLEAAKKAGYHVNF
gi|fvert| VLLKNDGTLPLKLLKKKDSVAMIGFWANDTSKLQGGYSGRAPFLHSPLYAAEKLGLDTNVA
      *****.* : *:*:* * * * :***.* * *:* * * * :* * * ..*
gi|reesei| LGTEIAGNSTTG--FAKAIAAAKSDAIYLGIDNTIEQEGADRTDIAWPGNQDLIKQ
gi|fvert| WGPTLQNSSSHDNWTTNAVAAAKSDYILYFGGLDASAAGEDRDRENLDWPESQLTLLQK
      *. : ..* : . :***:***** *:*:*:* : * . ** : : ** .** * : :
gi|reesei| LSEVGKPLVVLQMGQQVDSSSLKSNKKVNSLVWGGYPGQSGGVALFDILSGKRAPAGRL
gi|fvert| LSSLGKPLVVIQLG-DQVDDTALLKNKKINSILWVNYPGQDGGTAVMDLLTGRKSPAGRL
      **.:*****:*:* .***.:* .***:***:* .****.*.*.*:***:***:*****
gi|reesei| VTTQYPAEYVHQFPQNDMNLRPDGKSNPGQTYIWTGKPVYEFSGSLFYTTFKETLASHP
gi|fvert| PVTQYPSKYTEQIGMTDMDLRPT-KSLPGRTYRWYS--TPVLPYGFGLHYTKFQAKFKSN-
      .****.:*..* : .**:* * * *:* * * : ** :* **.*.*. : : * :
gi|reesei| KSLKFNNTSSILSAPHPGYTYSEQIPVFTFEANIKNSGKTESPYTAMLFVRTSNAGPAPYP
gi|fvert| -KLTFDIQKLLKG--CSAQYSDTCALPPIQVSVKNTGRITSDFVSLVFIKS-EVGPKPYP
      .*. : :.*.. . ** : : : :***:* : * : : : : : : .** ***
gi|reesei| NKWLVGFDRLADIKPGHSSKLSIPIVVSALARVDSHG NRIVYPGYELALNTDES VKLEF
gi|fvert| LKTLAAYGRLHDVAPSSTKDISLEWTLDN IARRGENGDLVVYPGTYTLLLDEPTQAKIQV
      * *...** * : * . :***: .. :** ..* : :*****.* * * : ..*:.
gi|reesei| ELVGEEVTIENWPLEEQQIKDATPDA
gi|fvert| TLTGKKAILDKWPQDPKSA-----

```

FIG. 56

83 / 111

Fv43D ---MQLKFLSSALLLSLTGNCAAQDNDIPPLITDLWSADPSAHVFEGKLWVYPSHDIEA
Fo43A ---MQLKFLSSALLFSLTSKCAAQDNDIPPLITDLWSADPSAHVFEGKLWVYPSHDIEA
Gz43A ---MKSLLLFP--LLSFVG--QSLATNDDCPLITSRWTADDPSAHVFNDTLWLYP SHDIDA
Pf43A ---MLQRFAYILPLALLSVG--VKADN-----PFVQSIYTADPAPMVYNDRVYVFMHDHNTG
Fv43A -MWLTSPLLFASTLLGLTGVALADN-----PIVQDIYTADPAPMVYNGRVYLFTGHDNDG
Fv43B --MRFSWLLCPLLAMGSALPETKTDVSTYTNPVLPGWHSDPSC-IQKDGLFLCVTSTFI
Af43A -----MAAPSLSYPTGIQSYTNPLFPGWHSDPSCAYVAEQDTFFCVTSTFI
Pf43B ----MSRSILPYASVFALLGGAIAEP----FLVLNSDFPDPSLIETSSGYAFGTGNGV
Fv43E MKVYWLVAWATSLTPALAGLIGHRRATTFNNPIIYSDFPDNDVFLGPDNYYYSASNFHF

Fv43D NVVNGTGGAQYAMRDYHTYSMKTIYGKDPVIDHGVALSVDDVPWAKQQMWAPDAAYK--N
Fo43A NVVNGTGGAQYAMRDYHTYSMKSIYGKDPVVDHGVALSVDDVPWAKQQMWAPDAAHK--N
Gz43A GFENDPDGGQYAMRDYHVYSIDKIYGLP-VDHGTALSVEDVPWASRQMWAPDAAHK--N
Pf43A -----ATYYNMTDWHLFSSADMANWQD----HGIPMSLANFTWANANAWAPQVI PR--N
Fv43A -----STDFNMTDWRLFSSADMVNWQH----HGVPMSLKTFSWANSRAWAGQVVAR--N
Fv43B FP----GLPVYASRDLVNWRLISHVWNRE---KQLPGISWKTAGQQQGMYP TIRYH--K
Af43A AFP----GLPLYASRDLQNWKLASNI FNRP---SQIPDLR-VTDGQSGIYAPT LRYH--E
Pf43B N-----AQVASSPDFNTWTLLSGT-----DALGPFPSWVASSPQIWAPDVLVKA-D
Fv43E SP----GAPVLKSKDLLNWDLIGHSI PRLNFGDGYDLPPGSRYRG-GTWASSLRYRKS N

Fv43D GKYYLYFPAK-DK-DEIFRIGVAVSNKPSGPFK----ADK-SWIPGTYSIDPASYVDTNGE
Fo43A GKYYLYFPAK-DK-DEIFRIGVAVSNKPSGPFK----ADK-SWIPGTYSIDPASYVDTDNE
Gz43A GKYYLYFPAK-DK-DDIFRIGVAVSPTPGPFV---PDK-SWIPHTFSIDPASFVDDDDR
Pf43A GQFYFYAPVR-HN-DGSMAIGVGVSTITGPYH---DAIGKPLVENNEIDPTVFIDDDGQ
Fv43A GKIFYFYPVRNAK-TGGMAIGVGVSTNILGPYT---DALGKPLVENNEIDPTVYIDTDGQ
Fv43B GTYYVICEYLGVG-DIIGVIFKTTNPWDESSWS---DPV---TFKPNHIDPDLFWDDDGK
Af43A GQFYLVSYLGP--QTKGLLFTSSDPYDDA AWS---DPL---EFAVHGIDPDIFWDHGT
Pf43B GTYVMYFSASAASDSGKHCVGAATATSPEGPYTPVDSAVACPLDQGAIDANGFIDTDGT
Fv43E GQYWIGCIN-----FWQTWVYTASSPEGPWY-----NKGNF GDNNCYYDNGILIDDDDT

Fv43D AYLIWGGI-WGGQLQAWQDHKTFNESWLGDKAAPNGTNALS PQIAKLSKDMHKITETPRD
Fo43A AYLIWGGI-WGGQLQAWQDKKNFNESWIGDKAAPNGTNALS PQIAKLSKDMHKITETPRD
Gz43A AYLAWGGI-MGGQLQRWQDKNKYNES--GTEPG-NGTAALS PQIAKLSKDMHTLAEKPRD
Pf43A AYLYWG-----NPD LWYVKLNQDMISYSGSPTQ
Fv43A AYLYWG-----NPGLYYVKLNQDMLS YSGSINK
Fv43B VYCATHG-----ITLQEI DLETGELSPELNIWNGTGGVWPEGPHIYKRDGYY LMI AEGGT
Af43A VYVTS AED-QMIKQYTLDLKTGAIGPVDYLWNGTGGVWPEGPHIYKRDGYY LMI AEGGT
Pf43B IYVVYKID-----GNSLDGDGTTHPTPI MLQQMEADGT
Fv43E MYVVYGS GEVKVSQLSQDGFSQVKSQVVFKNTDIGVQDLEG NRM YKING-----LYYI

Fv43D LVILAPETGKPLQAEDNKRRFFEGP-----WVHKRGKLYYLMYSTG-----
Fo43A LVILAPETGKPLQAEDNKRRFFEGP-----WIHKRGKLYYLMYSTG-----
Gz43A MLILDPKTGKPLLS EDEDRRFFEGP-----WIHKRNKIYYLTYSTG-----
Pf43A IPLTTAGFGTRTGNAQRPTTFEEAP-----WVYKRNGIYYIAYAAD-----
Fv43A VSLTTAGFGSRPNNAQRPTTFEEGP-----WLYKRG NLYYMIY AAN-----
Fv43B -----AEDHAIT IARARKITGPYEAYNNNPILTNRG TSEYFQTVGHGDLFQDTKGNWWGLC
Af43A -----ELGHSETMARSRTRTGPWEPYPHNP LLSNKG TSEYFQTVGHADLFQDGNGNWWAVA
Pf43B --TPTGSP IQLIDRS DLDGPLIEAP-----SLLLSNGIYYLSFSSN-----
Fv43E LNDSPSGSQTWIWKSKSPWGPYESKVLADKVTPPI SGGNSPHQGS LIKTPNGGWY-----

Fv43D -DTHFLVYATSKN---IYGPYT-----YQGKILDPVDG-----WTHG
Fo43A -DTHFLVYATSKN---IYGPYT-----YRGKILDPVDG-----WTHG
Gz43A -TTHYL VYATSKT---PYGPYT-----YQGRILEPVDG-----WTHS
Pf43A CCSEDI RYSTGTS---ATGPWT-----YRGVIMPTQGS S-----FTNHE

FIG. 57A

SUBSTITUTE SHEET (RULE 26)

84 / 111

Fv43A CCSEDIRYSTGPS---ATGPWT-----YRGVVMNKAGRS-----FTNH
Fv43B LATRITAQGVSPMGREAVLFNGTWNKGWPKLQPVGRMPGNLLPKPTRN-----VPGD
Af43A LSTRSGPAWKNYPMGRETVLAPAAWEKGEWPVIQPVRGQMGG-PFPPPNKR----VPRGE
Pf43B YYNTNYYDTSYAYASSITGPWT-----KQSAPYAPLLVTGT-----ETSND
Fv43E FMSFTWAYPAGRLPV LAPITWG-----SDGFPI LVK GANGGWSSSYPTLPGT

Fv43D SIVEYKGQWWLFFAD-AHTSGKDYLRQVKARKIWDKDG-----KILLTRPKI-----
Fo43A SIVEYKGQWWLFFAD-AHTSGKDYLRQVKARKIWDKNG-----KILLHRP-----
Gz43A SIVKYQGQWWLFYHD-AKTSGKDYLRQVKAKKIWDYDSKG-----KILTCKP-----
Pf43A GIIDFQNNSYFFYHNGALPGGGGYQRSVCVEQFKYNADG-----TIPTIEMTTAG-----
Fv43A GIIDFENNSYFFYHNGALDGGSGYTRSVAVESFKYGS DG-----LIPEIKMTTQG-----
Fv43B GPFNADPDNYNLKKTCKI PPHFVHHRVPRDGAFSLSSKG-----LHIVPSRNNVTG SVLP
Af43A GGWIKQPDKVDFRPGSKI PAHFQYWRYPKTEDFTVSPRGHPNTLR LTPSFYNLTG-----
Pf43B GALSAPGGADFSVDG TKMLFHANLNGQDISGGRALFAAS-----ITEASDVVT LQ-----
Fv43E DGVTKNWTRTDTFRGTS LAPSW EWNHNP DVNSFTVNNGLT LR TASITKDIYQARN-----

Fv43D -----
Fo43A -----
Gz43A -----
Pf43A -----PAQIGTLN PYVRQEAE TAAWSSGITTEVCSEGGIDVGF INNG
Fv43A -----PAQLKSLN PYVKQEAE TIAWSEGIETEVCSEGG LNVAFIDNG
Fv43B DEIELSGQRGLAFI GR RQTH TLPKYSVDIDFKPKSDDQEAGITVFRTQFDHIDL GIVRLP
Af43A -TADFKPDDGLSLVMRKQTD TLF TYTVDV SFDPKVADEEAGVTVFLTQQQHIDL GIVLLQ
Pf43B -----
Fv43E -----T LSHRTHGDHPTGIVKIDFSPMKDGD RAGLSAFRDQSAYIGIHRDNGK

Fv43D -----
Fo43A -----
Gz43A -----
Pf43A DYIK-----VKGVAFGS-GAHSFSARVASANS GG TIAIHLGSTTGTLVGTCTV
Fv43A DYIK-----VKGVDFGSTGAKTFSARVASNS SGGKIELRLGSKTGKLVGTCTV
Fv43B TNQGSNKKSKLAFRFRATGAQNVPAPK----VVPVPGWEKGVISLHIEAANATHYNLGAS
Af43A TTEG-----LSLSFRFRVEGRGN YEGPLPEATVPVPKEWCGQTIRLEIQAVSDTEYVF AAA
Pf43B -----
Fv43E FTIAT----KHGMNMDEWNGTTTDLGQIKATANVPSGR TKIWLRLQLDTNPAGTGNTIFS

Fv43D -----
Fo43A -----
Gz43A -----
Pf43A PSTGGWQTWTTVTCSVSGASGTQ-----DVYFVFGSGGTGYLFN-----FDYWQFA
Fv43A TTTGNWQTYKTVDCPVSGATGTS-----DLFFVFTGSGSGSLFN-----FNWWQFS
Fv43B --SHRGKTLDIATASASLVSGGTG SFVGSLLGPYATCNGKSGSVECPKGGDVYVTQW TYK
Af43A PARHPAQRQIISRANSLIVSGDTGRFTGSLVGVYATSNG-GAGSTP-----AYISRWR YE
Pf43B -----
Fv43E YSWDGVKYETLGPNEFKLYNG-----WAFFIAYRFGIFNFAETALGGSIKVESFT

Fv43D -----
Fo43A -----
Gz43A -----
Pf43A -----
Fv43A -----
Fv43B PVAQEIDHGVFVKSEL
Af43A GRGQMIDFGRVVP SY-
Pf43B -----
Fv43E AA-----

FIG. 57B

85 / 111

Pa51A MIHLKPALAALLALSTQCVAIDL FVKSSGGNKT TDIMYGLMHEDINNSGDGGIYAELISN
Fv51A MVR FESSILAAAACF-VAVESVNIKVDSKGGNATSGHQYGFLHEDINNSGDGGIYAELIRN
Pf51A MGKMWHSILVVLGLLSVGHAITINVSQSGGNKTSPLQYGLMFEDINHGGDGGLYAELVRN

Pa51A RAFQGSEKFPSNLDNWSPVGGATLTLQKLAKPLSSALPYSVNVANPKEGKGKGKDKTKGKK
Fv51A RAFQYSKKYPVSLSGWRPINDAKLSLNRLDTPLSDALPVSMNVK----PGKGK-----AKE
Pf51A RAFQGSTVYPANLDGYDSVNGAILALQNLTNPLSPMPSSLNVA-----KGS-----NNGS

Pa51A VGLANAGFWGMDVVRQKYTG SFHVTGEYKGD FEVSLRSAITGETFGKKVVKGGSKKKGKWT
Fv51A IGFLNEGYWGMDVKKQKYTG SFWVKGAYKGHFTASLRSNLTD DVFSGVKVSKANKKQWV
Pf51A IGFANEGWWGIEVKPQRYAGSFYVQGDYQGD FDISLQSKLTQEVFATAKVRSSGKHEDWV

Pa51A EKEFELVPFKDAPNSNNTFV VQWDAEGAKDGS LLDNLISLFPPTFKGRKNGLRIDLAQTM
Fv51A EHEFVLTPNKNAFNSNNTFAITYDPKGA-DGALDFNLISLFPPTYKGRKNGLRVDLAEAL
Pf51A QYKYELVPKKAASNTNNTLTITFDSKGLKDGSLNFNLISLFPPTYNNRPNGLRIDLVEAM

Pa51A VELKPTFLRFPGGNMLEGNLTLDTWK WYETIGPLKDRPGMAGVWEYQQT LGLGLVEYMEW
Fv51A EGLHPSLLRFPGGNMLEGN TNKTWWDWKDTLGPLRNRPGFEGVWNYQQT HGLGILEY LQW
Pf51A AELEGKFLRFPGGSDVEGVQAPYWKWNETVGDLKDRYSRPSAWTYEESNGIGLIEY MNW

Pa51A ADDMNLEPIVGVFAGLALDGSFVPESEMGWVIQQALDEIEFLTGD AKTTKWGA VRAKLGH
Fv51A AEDMNLEIIVGVYAGLSLDG SVTPK DQLQPLID DALDEIEFIRG-PVTSKWGKKRAELGH
Pf51A CDDMGLEPILAVWDGHYLSNEVIS ENDLQPYIDDTLNQLEFLMG-APDTPYGSWRASLGY

Pa51A PKPWKVKWVEIGNEDWLAGRPAGFESYIN YRFPMMMKAFNEKYPDIKIIASPSIFD----
Fv51A PKPFRLSYVEVGNE DWLAGYPTGWN SYKEYRFP MFLEAIKKAHPDLTVISSGASIDPVGK
Pf51A PKPWTINYVEIGNEDNLYG---GLETYIAYRFQAYYDAITAKYPHMTVMESLTEMPG---

Pa51A ---NMTIPAGAAGDHHPYLTPDEFV ERFAKFDNL SKDNVT LIGEAASTHPNG---GIAWE
Fv51A KDAGFDIPAPGIGDYHPYREPDVLVEEFNLFDNNKYG--HIIGEVASTHPNG---GTGWS
Pf51A -----PAAAASDYHQYSTPDGFVSQFNYFDQMPVTNR TLNGEIATVYPNNPSNSVAWG

Pa51A GDLMPLPWWGGSVAEAI FLISTERN GDKII GATYAPGLRSLDRWQWSMTWVQHAADPALT
Fv51A GNLMPYPWWISGVGEAVALCGY ERNADRI PGTFYAPILKNENRWQWAITMIQFAADSAMT
Pf51A SPFPLYPWWIGSVAEAVFLIGEERN SPKII GASYPMFRNINN WQWSPTLIAFDADSSRT

Pa51A TRSTSWYVWRILAHHIIRETLPVDAPAGKPNFDPLFYVAGKSES-GTGIFKAAVYNSTES
Fv51A TRSTSWYVWSLFAGHPMTHTLPTTA-----DFDPLYVAGKNE DKGT LIWKGAAYNTTKG
Pf51A SRSTSWHVIKLLSTNKITQNLPTTWSGG--DIGPLYWVAGRNDNTGSNIFKAAVYNSTSD

Pa51A ---IPVSLKFDGLNEGAVANLTVLTGPE-DPYGYNDPFTGINVVKEKTTFIKAGKGGKFTF
Fv51A ADVPVSLSFKGVKPGAQAE LTLTNKEKDPFAFN DPHKGNNVVDTKKTVLKADGKGAFNF
Pf51A ---VPVTVQFAGCN-AKSANLTI LSSDD--PNASNYPG-GPEVVKTEIQSVTANAHGAFEF

Pa51A TLPGLSVAVLETADAVKGGKGKGKGGKGN
Fv51A KLPNLSVAVLET LK-----KGKPYSS
Pf51A SLPNLSVAVLKTE-----

FIG. 58

86 / 111

		*	20	*	40	*	
xyn3	:	-MKANVILC--LLAPLVAALPTETIHLDP	ELAALRANLTERTADLWDRQA	:	47		
P56588	:	-----	QA	:	2		
P23360	:	MVRPTILLTSLLLAPFAAASPI-----	LEERQA	:	28		
		60	*	80	*	100	
xyn3	:	SQSIDQLIKRKGLYFGTATDRGLLQRE-KNA	AIQADLGQVTPENSMKW	:	96		
P56588	:	SVSIDAKFKAHGKKYLGITIGDQYTLTKNT	KNPAIIKADFGQLTPENSMKW	:	52		
P23360	:	AQSVDQLIKARGKVYFGVATDQNRLLTG-K	NAAIIQADFGQVTPENSMKW	:	77		
		*	120	*	140	*	
xyn3	:	QSLENNQGQLNWDADYLVNFAQQNGKSIR	GHTLIWHSQLPAWVNNINNA	:	146		
P56588	:	DATEPNRGQFTFSGSDYLVNFAQSNGKLIR	GHTLVWHSQLPGWVSSITDK	:	102		
P23360	:	DATEPSQGNFNFAGADYLVNWAQQNGKLIR	GHTLVWHSQLPSWVSSITDK	:	127		
		160	*	180	*	200	
xyn3	:	DTLRQVIRTHVSTVVGRYKGIKIRAWDVV	NEIFNEDGTLRSSVFSRLLGEE	:	196		
P56588	:	NTLISVLKNHITTMTRYKGIYAWDLVNEI	FNEDGSLRNSVFYNVIGED	:	152		
P23360	:	NTLTNVMKNHITTLMTRYKGIKIRAWDVV	NEAFNEDGSLRQTVFLNVIGED	:	177		
		*	220	*	240	*	
xyn3	:	FVSI AFRAARDADPSARLYINDYNLDRAN	YGKVNGLKTYVSKWISQGVPI	:	246		
P56588	:	YVRI AFETARSVDPNAKLYINDYNLDSAG	YSKVNGMVSHVKKWLAAGIPI	:	202		
P23360	:	YIPI AFQTARAADPNAKLYINDYNLDSAS	YPKTQAIVNRVKQWRAAGVPI	:	227		
		260	*	280	N	*	300
xyn3	:	DGIGSQSHLSGGGGSGTLGALQQLATVPV	TELAIT EL DIQGAPTTDYTQV	:	296		
P56588	:	DGIGSQTHLGAGAGSAVAGALNALASAGT	KEIAIT EL DIAGASSTDYVNV	:	252		
P23360	:	DGIGSQTHLSAGQGAGVLQALPLLASAGT	PEVAIT EL DVAGASPTDYVNV	:	277		
		*	320	*	340	*	
xyn3	:	VQACLSVSKCVGITVWGISDKDSWRASTN	PLLEFDANFNPKPAYNSIVGIL	:	346		
P56588	:	VNACLNQAKCVGITVWGVADPDSWRSSSS	PLLEFDGNYNPKAAYNAIANAL	:	302		
P23360	:	VNACLVQSCVGITVWGVADPDSWRASTT	PLLEFDGNFNPKPAYNAIVQDL	:	327		
xyn3	:	Q-	:	347			
P56588	:	--	:	-			
P23360	:	QQ	:	329			

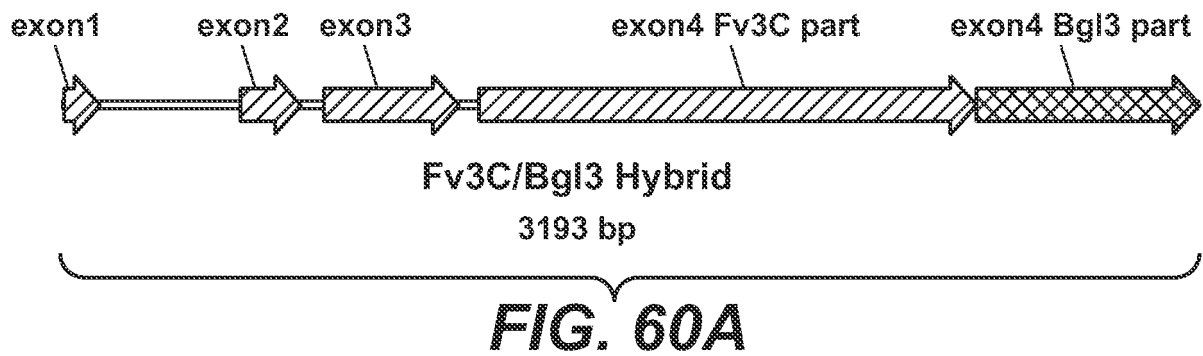
FIG. 59A

87 / 111

1	M	V	S	F	S	Y	L	L	L	A	C	S	A	I	G	-	A	L	A	A	P	V	E	P	E	T	T	S	F	N	AfuXyn2		
1	M	I	S	I	S	S	L	L	L	A	G	L	A	A	I	A	G	A	A	L	P	S	D	-	K	S	V	S	L	A	AfuXyn5		
1	M	V	S	F	T	S	L	L	A	S	P	P	S	R	A	S	C	R	P	A	A	E	V	E	S	V	A	V	E	Xyn2			
30	E	T	A	L	H	E	F	A	E	R	A	G	T	P	S	S	T	G	W	N	N	G	Y	Y	S	F	W	T	D	AfuXyn2			
30	E	R	-	-	-	-	-	-	Q	T	I	T	I	T	S	Q	T	G	T	N	N	G	Y	Y	S	F	W	T	N	AfuXyn5			
31	K	R	-	-	-	-	-	-	Q	T	I	Q	P	G	-	T	G	Y	N	N	G	Y	F	Y	S	Y	W	N	D	Xyn2			
60	G	G	D	V	T	Y	T	N	G	A	G	G	S	Y	S	V	N	W	R	N	-	-	V	G	N	F	V	G	G	AfuXyn2			
53	G	A	G	S	V	Q	Y	T	N	G	A	G	G	E	Y	S	V	T	W	A	N	Q	N	G	D	F	T	C	G	AfuXyn5			
53	G	H	G	G	V	T	Y	T	N	G	P	G	G	Q	F	S	V	N	W	S	N	-	S	G	N	F	V	G	G	Xyn2			
88	K	G	W	N	P	G	S	A	-	R	T	I	N	Y	G	G	S	F	N	P	S	G	N	G	Y	L	A	V	Y	G	AfuXyn2		
83	K	G	W	N	P	G	S	D	-	H	D	I	T	F	S	G	S	F	N	P	S	G	N	A	Y	L	S	V	Y	G	AfuXyn5		
81	K	G	W	Q	P	G	T	K	N	K	V	I	N	F	S	G	S	Y	N	P	N	G	N	S	Y	L	S	V	Y	G	Xyn2		
117	W	T	N	P	L	I	E	Y	Y	Y	V	V	E	N	Y	G	T	Y	N	P	G	S	G	T	F	R	G	T	V	AfuXyn2			
112	W	T	N	P	L	V	E	Y	Y	Y	I	L	E	N	Y	G	S	Y	N	P	G	S	G	M	T	H	K	G	T	V	AfuXyn5		
111	W	S	R	N	P	L	I	E	Y	Y	I	V	I	E	N	F	G	T	Y	N	P	S	T	G	A	T	K	L	G	E	V	Xyn2	
147	N	T	D	G	G	T	Y	N	I	Y	T	A	V	R	Y	N	A	P	S	I	E	G	T	K	T	F	T	Q	Y	W	AfuXyn2		
142	T	S	D	G	S	T	Y	D	I	Y	I	Y	E	R	Q	Q	V	N	Q	P	S	I	V	G	T	A	T	F	N	Q	Y	W	AfuXyn5
141	T	S	D	G	S	V	Y	D	I	Y	I	Y	E	R	T	Q	V	N	Q	P	S	I	I	G	T	A	T	F	Y	Q	Y	W	Xyn2
177	S	V	R	T	S	K	R	T	G	G	T	V	T	M	A	N	H	F	N	A	W	S	R	L	G	M	N	L	G	T	AfuXyn2		
172	S	I	R	Q	N	K	R	S	S	G	T	V	T	T	A	N	H	F	K	A	W	A	S	L	G	M	N	L	G	T	AfuXyn5		
171	S	V	R	R	N	H	R	S	S	G	S	V	N	T	A	N	H	F	N	A	W	A	Q	Q	G	L	T	L	G	T	Xyn2		
207	H	N	Y	Q	I	V	A	T	E	G	Y	Q	S	S	G	S	A	S	I	T	V	Y	S	G	S	S	S	G	G	AfuXyn2			
202	H	N	Y	Q	I	V	S	T	E	G	Y	E	F	S	S	G	T	S	T	I	T	V	S	S	G	S	S	G	G	AfuXyn5			
201	M	D	Y	Q	I	V	A	V	E	G	Y	E	F	S	S	G	S	A	S	I	T	V	S	S	S	S	S	S	G	Xyn2			
228	S	G	G	S	S	T	T	S	S	G	S	S	P	T	G	G	S	G	S	C	S	A	L	W	G	Q	C	G	G	AfuXyn2			
232	S	G	G	S	S	T	T	S	S	G	S	S	S	P	T	G	G	S	G	S	C	S	A	L	W	G	Q	C	G	AfuXyn5			
222	S	G	G	S	S	T	T	S	S	G	S	S	S	P	T	G	G	S	G	S	C	S	A	L	W	G	Q	C	G	Xyn2			
228	I	G	-	W	S	G	P	T	C	C	S	S	G	T	C	Q	V	S	N	S	Y	Y	S	Q	C	L				AfuXyn2			
262	I	G	-	W	S	G	P	T	C	C	S	S	G	T	C	Q	V	S	N	S	Y	Y	S	Q	C	L				AfuXyn5			
222	I	G	-	W	S	G	P	T	C	C	S	S	G	T	C	Q	V	S	N	S	Y	Y	S	Q	C	L				Xyn2			

FIG. 59B

88 / 111

**SEQ ID NO: 82****The nucleotide sequence encoding Fv3C/Bgl3**

atgaagctgaattgggtcgccgcagccctgtctataggtgctgctggcactgacagcgca
 gttgctcttgccttctgcagttccagacactttggctgggtgttaaaggctcagtttttttca
 ccatttctcgtctaatctcagccttgttgccatatcgcccttggttcgctcggaagccac
 gcaccagatcgcatcatttctcccttgccagccttgggttctcttaacgatcttccctcc
 gcaattatcagcgcccttagtctacacaaaaacccccgagacagtctttcattgagtttg
 tcgacatcaagttgcttctcaactgtgcatttgcggtggctgtctacttctgcctctagac
 aaccaaactctgggcgcaattgacgcgtcaaaccttgttcaaataaccttttttattcgag
 acgcacatttataaatatgcgcctttcaataataccgactttatgcgcggcggtgtgtgt
 ggcggttgatcagaaagctgacgctcaaaagggttgacagagagatacactcgcatactc
 gccgctcattatccttcaccatggatggaccctaattgctgttggctgggaggaagetta
 cgccaaagccaagagctttgtgtcccaactcactctcatggaaaagggtcaacttgaccac
 tgggtgttgggtgaagcagctccttgcaaacagggtatctcaatccctcagctaacaactt
 ctccagatggcaaggcgaacgctgtgttaggaaacgtgggatcaattcctcgtctcggtatg
 cgaggtctctgtctccaggatgggtcctcttggaattcgtctgtccgactacaacagcgct
 tttcccgctggcaccacagctgggtgcttcttgagcaagtctctctgggtatgagagaggt
 ctctgatgggcactgagttcaaggagaagggtatcgatatcgctcttggtcctgctact
 ggacctcttggtcgcactgctgctgggtggacgaaactgggaagggttcaccggtgatcct
 tatatggctggccacgccatggccgagggcggtcaagggtattcaagacgcaggtgtcatt
 gcttgtgctaagcattacatcgcaaacgagcagggttaagccaacttggaacgatttgaggaa
 ttgacagagaactgacctcttgtagagcacttccgacagagtggcgaggtccagtcgccg
 caagtacaacatctccgagtcctctctcctccaacctggatgacaagaactatgcacgagct
 ctacgcctggcccttcgctgacgcgcgtccgcgcggcgctcggttcggtcatgtgctcgta
 caaccagatcaacaactcgtagcggttgccagaactccaagctcctcaacgggtatcctcaa
 ggacgagatgggcttccagggtttcgctcatgagcgattgggcgggccagcataccggtgc
 cgcttctgccgtcgtggtctcgatatgagcatgcctgggtgacactgccttcgacagcgg
 atacagcttctggggcggaacttgactctggctgtcatcaacggaactgttcccgcctg
 gcgagttgatgacatggctctgcgaatcatgtctgccttcttcaagggttggaagacgat
 agaggatcttcccgacatcaacttctcctcctggaccgcgacaccttcggcttctgtgca
 tacatttgctcaagagaaccgcgagcagggtcaactttggagtcacacgtccagcacgacca
 caagagccacatccgtgaggccgctgccaaagggaagcgtcgtgctcaagaacaccgggtc
 ccttccctcaagaacccaaagtctcctcgtgtcattgggtgaggacgcgggtcccaaccc
 tgctggaccaaatgggtgtggtgaccgtgggttgcgataatggtaaccttggttatggcttg

FIG. 60B-1

89 / 111

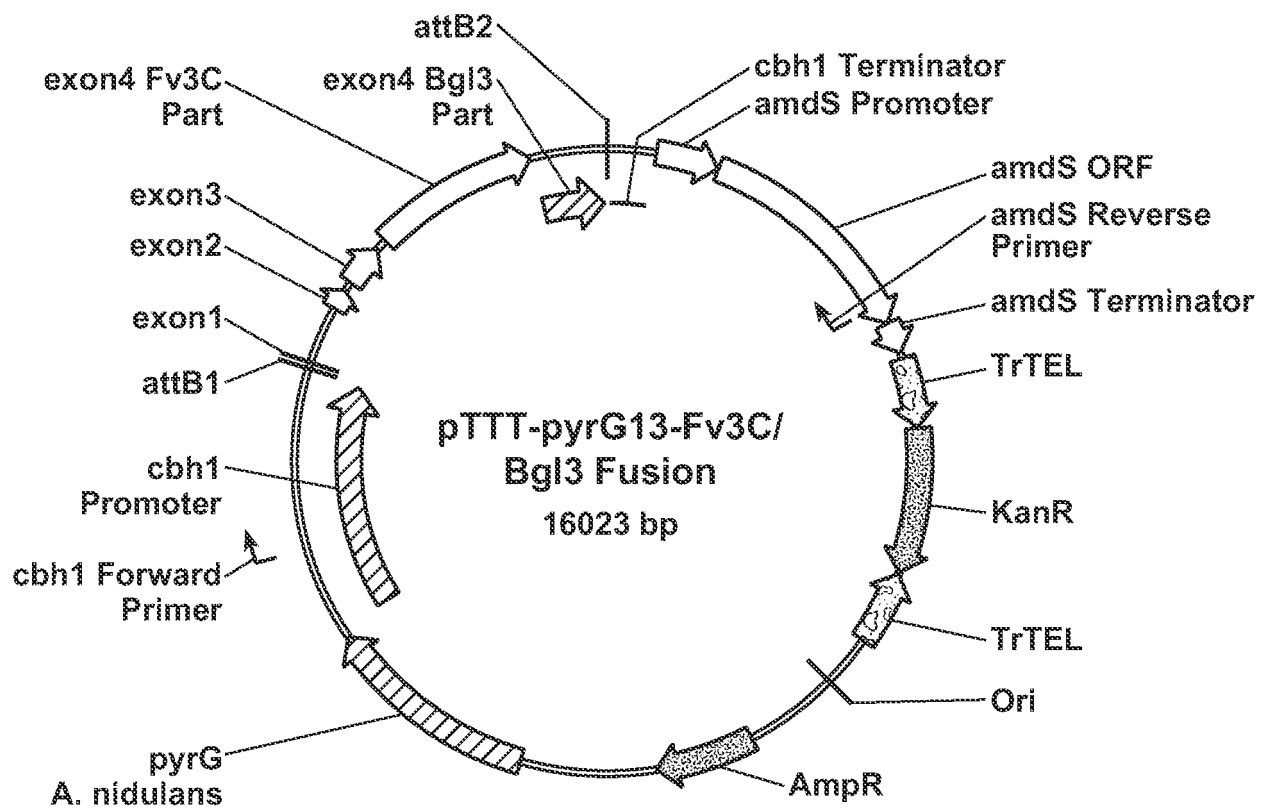
gggctcgggaacttcccaattcccttacttgatcacccccgatcaagggctctctaactcg
 agctactcaagacgggaactcgatatgagagcatcttgaccaacaacgaatgggcttcagt
 acaagctcttgtcagccagcctaactgacgcgtatcggttttcgccaatgccgactctgg
 tgagggatacattgaagtcgacggaaacttttggtgatcgcaagaacctcaccctctggca
 gcagggagacgagctcatcaagaacgtgtcgtccatatgccccaacaccattgtagttct
 gcacaccgtcgggcccctgtcctactcgcgcgactacgagaagaacccccaacatcactgccat
 cgtctgggctggtcttcccggccaagagtcaggcaatgccatcgctgatctcctctacgg
 caaggtcagccctggccgatctcccttcaacttggggccgcacccgcgagagctacggtac
 tgaggttctttatgaggcgaacaacggccgtggcgctcctcaggatgacttctctgaggg
 tgtcttcacgcactaccgtcacttcgaccgacgatctccaagcaccgatggaaagagctc
 tcccaacaacaccgctgctcctctctacgagttcgggtcacggtctatcttgggtcgacggt
 caagttctccaacctccacatccagaagaacaatgtcggccccatgagcccgcccaacgg
 caagacgattgcggctccctctctgggcagcttcagcaagaaccttaaggactatggctt
 cccaagaacggttcgcccgcacatcaaggagtttatctaccttacctgagcaccactacctc
 tggcaaggaggcgctcgggtgacgctcactacggccagactgcgaaggagttcctccccgc
 cgggtgccctggacggcagccctcagcctcgcctctgcggcctctggcgaacccggcgga
 ccgccagctgtacgacattctctacaccgtgacggccaccattaccaacacgggctcgggt
 catggacgacgcgcttccccagctgtacctgagccacggcggtcccaacgagccgccccaa
 ggtgctgctggttctgacccgcacgcgacattgctcccgccagagcgctcacgttcaa
 ggcagacctgacgcgcgctgacctgtccaactgggacacgaagaagcagcagtggggtcat
 taccgactaccccaagactgtgtacgtgggcagctcctcgcgcgacctgccgctgagcgc
 ccgctgccatga

FIG. 60B-2**SEQ ID NO:159**

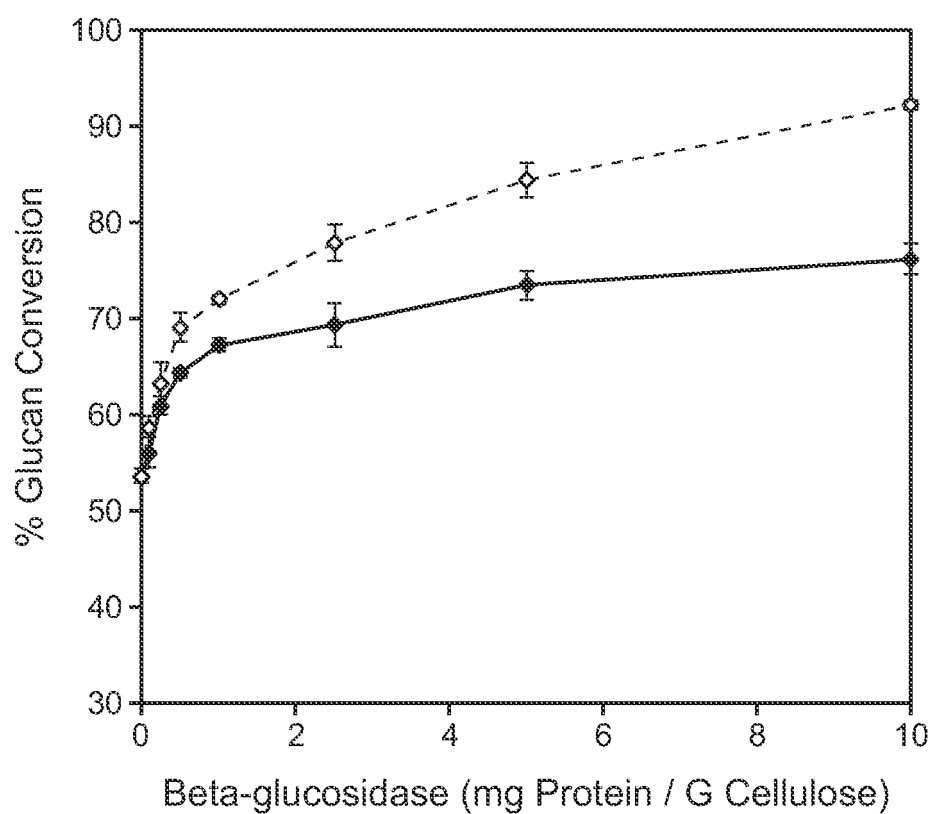
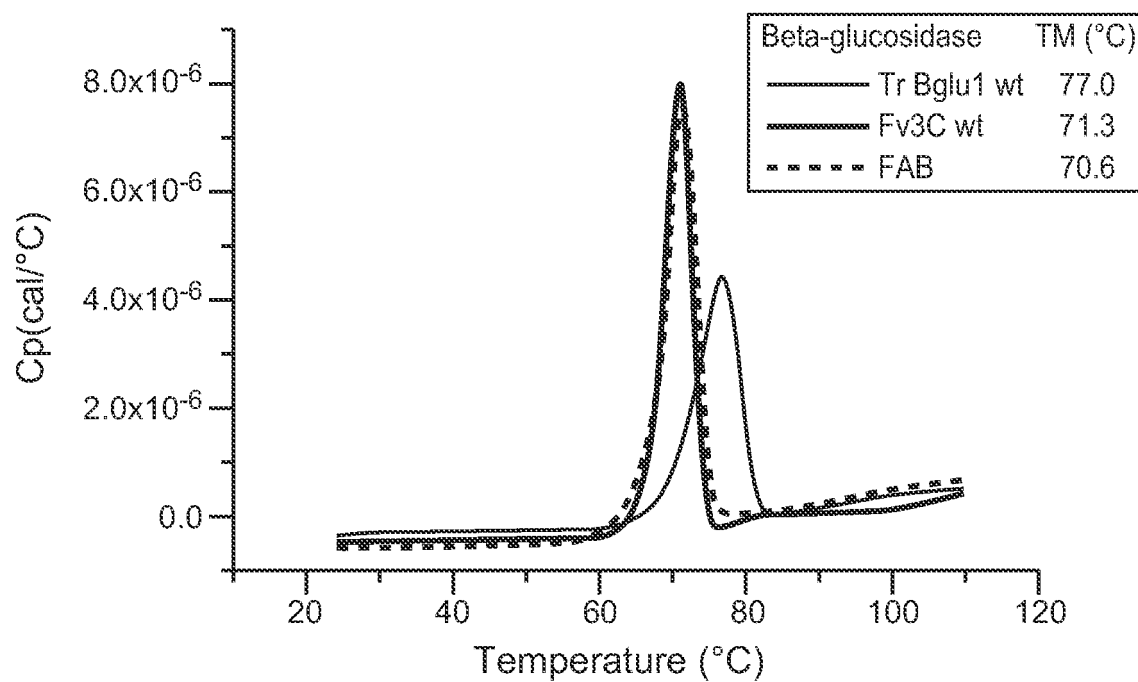
The Fv3C/Bgl3 chimeric polypeptide sequence (the Bgl3 chimeric part is in bold and upper case)

mklmwaaalsigaagtdsavalasavpdtlagvkkadaqkvvtrdtlayspphyppspwmdpna
 vgweeayakaksfvsqtlmekvnlttgvgwqgercvgnvgsiprlgmrglclqdgplgirlsd
 ynsafpagttagaswskslwyergllmgtefkekgidialgpatgplgrtaaggrnwegftvdp
 ymaghamaeavkgiqdagviacakhyaneeqehfrqsgevqsrkyniseslssnlddktmhely
 awpfadavragvgsvmsynqinnsygcqnsklngilkdemgfggfvmssdwaaghtgaasava
 gldmsmpgdtafdsgysfwggnltlavingtvpawrvddmalrimsaffkvgtiedlpdinfs
 swtrdtfgfvhtfaqenreqvnfgvnnvqhdkshireaaakgsvvlkntgslplknkpkflavig
 edagpnpagpncgdrgcdngtlamawgsqtsqfpylitpdqglsnratqdgtryesiltnew
 asvqalvsgpvnvtaivfanadsgegyiev dgnfgdrknltlwqggdeliknvssicpntivlh
 tvgvpvlladyeknpnitaivwaglpqgesgnaiadllygkvspgrspftwgrtresygtevlye
 anngrgapqddfsegvfidyrrhfdrrspstdgksspnntaaplyefghgls**WSTFKFSNLHIQK**
NNVGPMSPNGKTIAAPSLGFSKLNLDYGFKNVRIKEFIYPYLSTTTSGKEASGDAHYGQT
AKEFLPAGALDGSPQPRSAASGEPGGNRQLYDILYTVTATITNTGSVMDDAVPQLYLSHGGPNE
PPKVLRGFDRIERIAPGQSVTFKADLTRDLNWDTKKQQWVITDYPKTVYVGSSSRDLPLSARLP

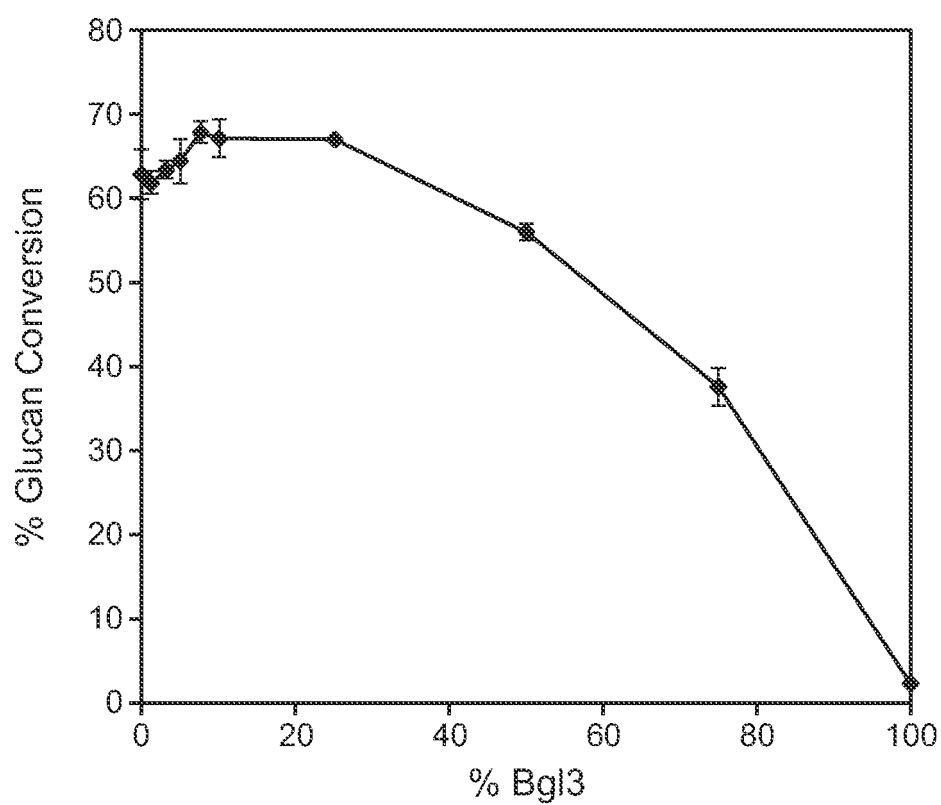
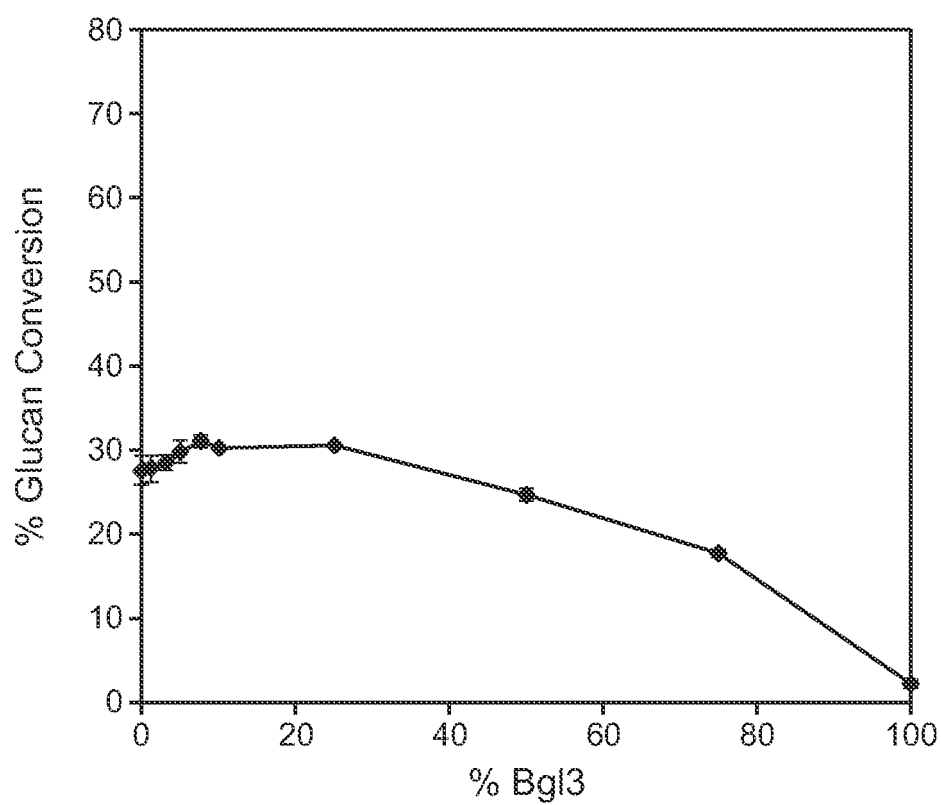
FIG. 60C

**FIG. 61**

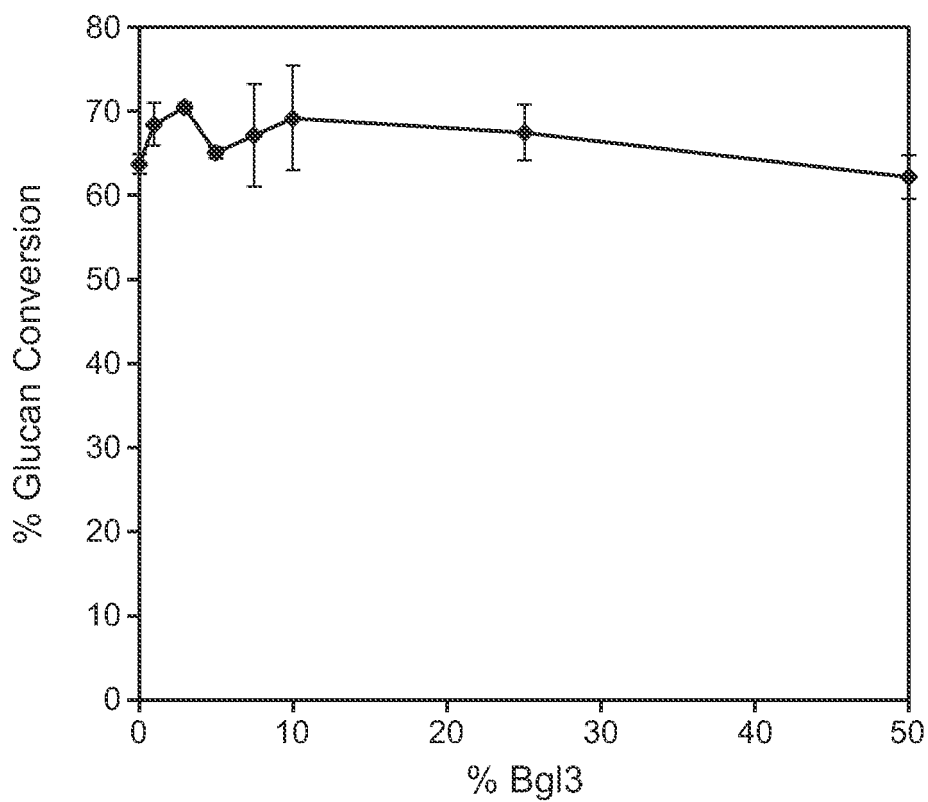
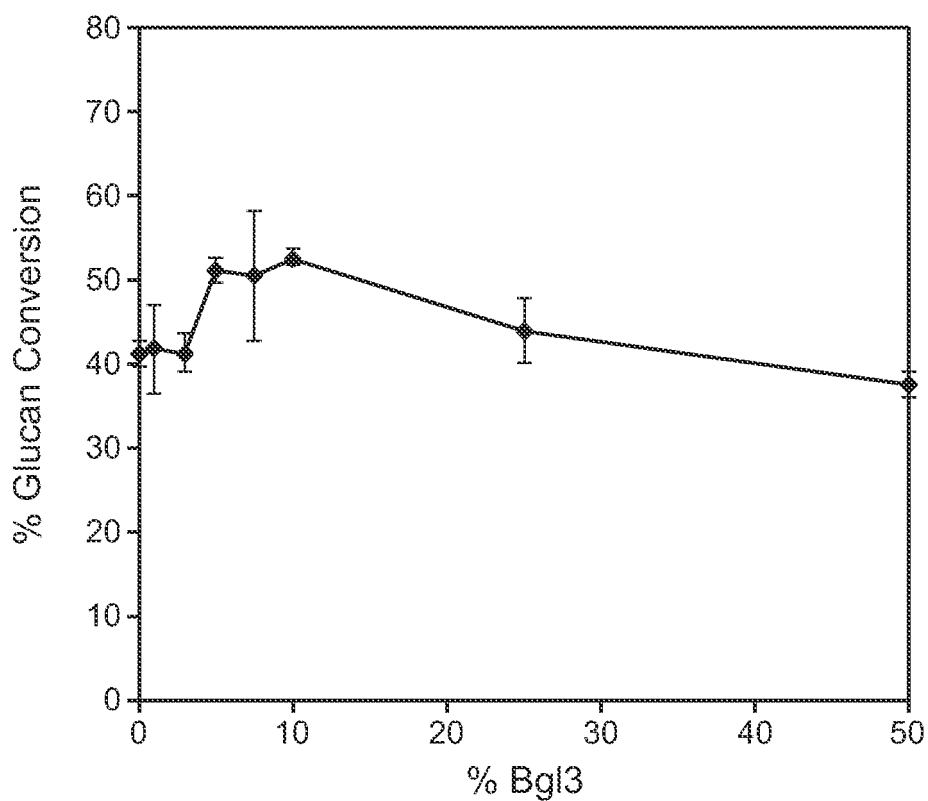
91 / 111

**FIG. 62****FIG. 63**

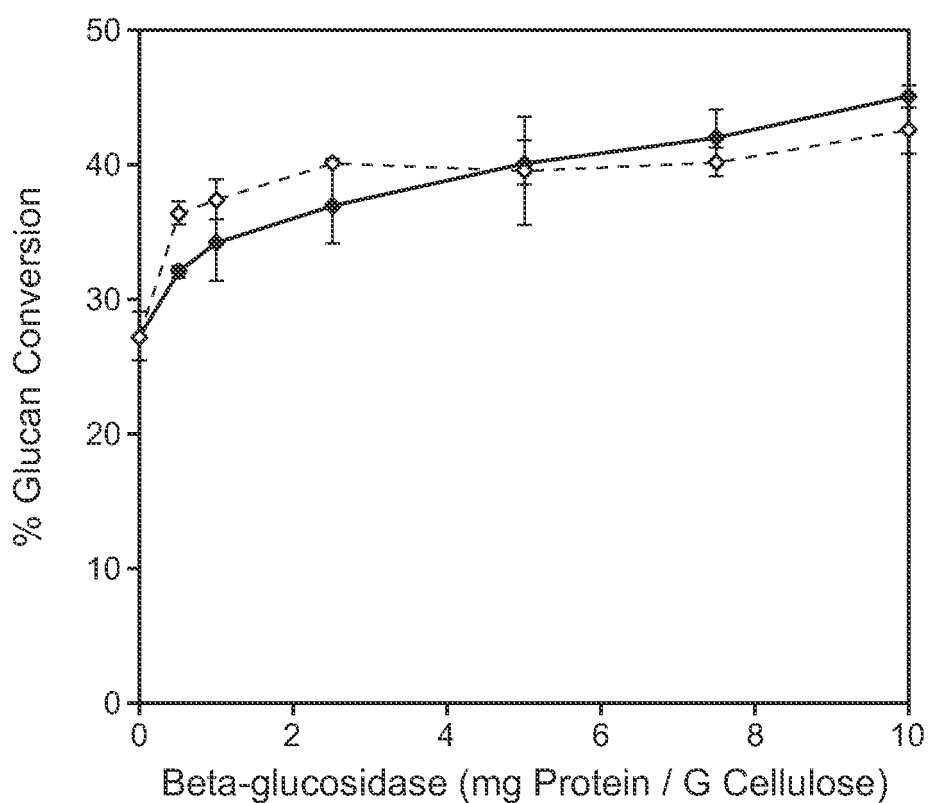
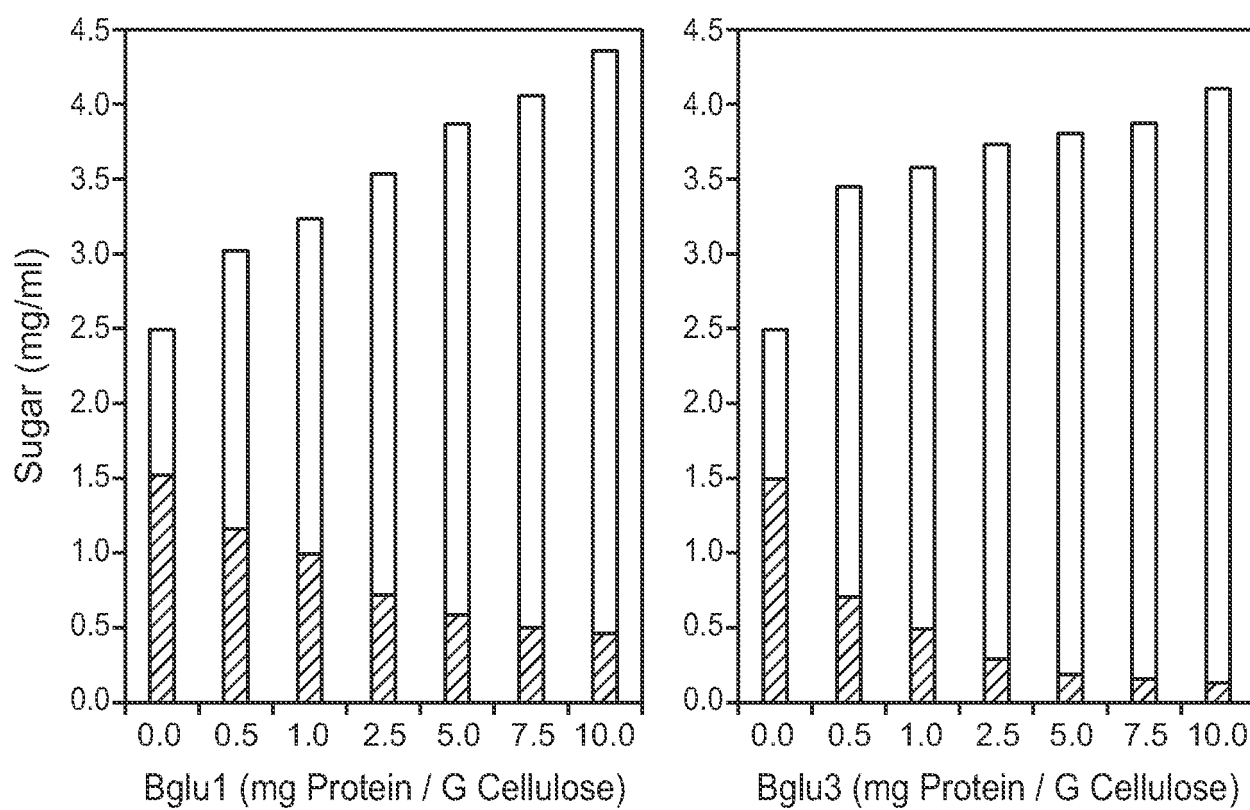
92 / 111

**FIG. 64A****FIG. 64B**

93 / 111

**FIG. 64C****FIG. 64D**

94 / 111

**FIG. 65A****FIG. 65B**

SEQ ID NO:	PRIMER	SEQUENCE
92	Forward SK943	5'-CACCATGAGATATAGAACAGCTGCCGCT-3'
93	Reverse SK941	5'-CGACGGCCCTGCGGAGTCTTGCCAGTGGTCCCGGACAG-3'
94	Forward (SK940)	5'-CTGTCCGGGACCACTGGGCAAGACTCCGCAAGGCGGTGG-3'
95	Reverse (SK942)	5'-CCTACGCTACCGACAGAGTG-3'
96	Forward SK771	5'-GTCTAGACTGGAAACGCAAC-3'
97	Reverse SK745	5'-GAGTTGTGAAGTCGGTAATCC-3'
98	Forward xyn3F-2	5'-CACCATGAAAGCAAAACGTCATCTTGTGCTCCTCTGG-3'
99	Reverse (xyn3R-2)	5'-CTATTGTAAGATGCCAACAATGCTGTTATATGCCGGCTTGGG-3'
100	Forward SK745	5'-GAGTTGTGAAGTCGGTAATCC-3'
101	Reverse SK822	5'-CACGAAGAGCGCGGATTTC-3'
102	Forward MH124	5'-CAC CCA TGC TGC TCA ATC TTC AG-3'
103	Reverse MH125	5'-TTA CGC AGA CTT GGG GTC TTG AG-3'
104	Forward SK1334	5'-GCTTGAGTGTATCGTGTAAAG-3'
105	Forward Primer SK1335	5'-GCAACGGCAAGCCCCACTTC-3'
106	Reverse SK1299	5'-GTAGCGCGCCCTCATCTCATCTCATCCATCC-3'
107	Forward SK1322	5'-CACCATGCAGCTCAAGTTCTGTC-3'
108	Reverse SK1297	5'-GGTTACTAGTCAACTGCCCGTTCTGTAGCGAG-3'
109	Forward SK1236	5'-CATGCGATCGCGACGTTTGGTCAGGTGG-3'
110	Reverse SK1321	5'-GACAGAAACTTGAGCTGCATGGTGTGGGACAAACAAGAGG-3'
111	Forward SK1159	5'-CACCATGGTTCGCTTCAGTTCAATCCTAG-3'
112	Reverse SK1289	5'-GTGGCTAGAAGATATCCAACAC-3'
113	Forward SK1236	5'-CATGCGATCGCGACGTTTGGTCAGGTGG-3'
114	Reverse SK1262	5'-GAACTGAAGCGGAACCATGGTGTGGGACAAACAAGGAC-3'
115	Forward SK1298	5'-GTAGTTATGCGCATGCTAGAC-3'
116	Forward MH234	5'-CACCATGAAGCTGAATTGGTGGC-3'
117	Reverse MH235	5'-TTACTCCAACTTGGCGCTG-3'

FIG. 66A

SEQ ID NO:	PRIMER	SEQUENCE
118	MH255	5'-AAGCCAAAGAGCTTTGTGTCC-3'
119	MH256	5'-TATGCACGAGCTCTACGCCT-3'
120	MH257	5'-ATGGTACCCCTGGCTATGGCT-3'
121	MH258	5'-CGGTCACGGTCTATCTTTGGT-3'
122	pDonor Forward	5'- GCTAGCATGGATGTTTCCAGTCACGACGTTGTAAACGACGGC- 3'
123	Fv3C/Bgl3 reverse	5'-GGAGGTTGGAGAACTTGAACGTCGACCAAGATAGACCGTGACCCGAAC TCGTAG-3'
124	pDonor Reverse	5'-TGCCAGGAAACAGCTATGACCATGTAATACGACTCACTATAGG-3'
125	Fv3C/Bgl3 forward	5'- CTACGAGTTCGGTCACGGTCTATCTTTGGTCGACGTTCAAGTTCTCCA ACCTCC-3'
126	Att L1 forward	5'-TAAGCTCGGGCCCCAAATAATGATTTTATTTTGGACTGATAGT-3'
127	AttL2 reverse	5'-GGGATATCAGCTGGATGGCAAATAATGATTTTATTTGACTGATA-3'
128	Cbh1 forward	5'-GAGTTGTGAAGTCGGTAATCCCGCTG-3'
129	AmdS reverse	5'-CCTGCACGAGGGCATCAAGCTCACTAACCCG-3'
130	Pr Cbhl forward	5'-CGGAATGAGCTAGTAGGCAAAAGTCAGC-3'
131	725/751 reverse	5'-CTCCTTGATGCGGCGAACGTTCTTTGGGGAAGCCATAGTCCTTAAGGTTCTT GCTGAAGTTGCCCAGAGAG-3'
132	725/751 forward	5'-GGCTTCCCCAAGAAGCTTCGCCGCATCAAGGAGTTTATCTACCCCTACC TGAACACCACTACCTC-3'
133	Ter Cbhl reverse	5'-GATACACGAAGAGCGCGGATTCTACGG-3'
134	Forward MH234	5'-CACCATGAAGCTGAATTGGGTCGC-3'
160	Te3A reverse	5'-GATAGACCGTGACCCGAACCTCGTAGATAGGCGTGATGTT GTACTTGTCGAAG TGACGGTAGTCGATGAAGAC-3'
161	Te3A2 forward	5'-GTCTTCATCGACTACCGTCACCTTCGACAAGTACAACATCAC GCCTATCTACG AGTTCGGTCACGGTCTATC-3'

FIG. 66B

SEQ ID NO:135

Amino acid sequence of the Fv3C/Te3A/*T. reesei* Bgl3 (FAB) chimera

mklnwvaaalsigaagtdsavalasavpdtlagvkkadaqkvvtrdtlayssp phyppspwmdpna
vgweeayakaksfvsqltlmekvnlttgvgwggercvgnvgsiprlgmrglclqdgplgirlsd
ynsafpagttagaswskslwyergllmgtefkekgidialgpatgplgrtaaggrnwegftvdp
ymaghamaeavkgiqdagviacakhyaneghefrqsgevsrkyniseslssnlddktmhely
awpfadavragvgsvmcsynqinnsygcqnsklngilkdemgfqgfvm sdwaaghtgaasava
gldmsmpgdtafdsgysfwggnltlavingtvpawrvddmalrimsaffkvgktiedlpdinf s
swtrdtfgfvhtfaqenreqvnfgvvnvqhdkshireaaaakgsvvlkntgslplknpkflavig
edagpnpagpngcgdrgcdngt lamawgsqtsqfpyl itpdqglsnratqdgtryesiltnnew
asvqalvsgp nvtaivfanadsgegyievdgnfgdrknltlwqqgdeliknvssicpntivvlh
tvgpvlladyeknpnitaivwaglp ggesgnaiadllygkvspgrspftwgrtresygtevlye
annrggapqddfsegvfidy rhfd **KYNITPI** yefghgls WSTFKFSNLHIQKNNVGPMSPPNGK
TIAAPSLGNFSKNLKDYGFPKNVRRIKEFIYPYLNTTSGKEASGDAHYGOTAKEFLPAGALDG
SQOPRSAASGEPGGNROLYDILYTVTATITNTGSVMDDAVPOLYLSHGGPNEPPKVLRGFDRIE
RIAPGQSVTFKADLTRDLSNWDTKKQOWVITDYPKTVYVGSSSRDLPLSARLP

FIG. 67A

SEQ ID NO :83**Nucleic acid sequence encoding the Fv3C/Te3A/T. reesei Bgl3 (FAB) chimera:**

atgaagctgaattgggtcgccgcagccctgtctataggtgctgctggcaactgacagcgcagttg
ctcttgcttctgcagttccagacactttgggtggtgtaaagggtcagttttttttcaccatttcc
tcgtctaattctcagccctgttgccatatcgcccttggttcgctcggacgccacgcaccagatcgc
gatcatttctcctccttgagcccttggttccctcttacgatcttccctccgcaattatcagcgcgc
ttagtctacacaaaaacccccgagacagttcttcaattgagtttgctgacatcaagttgcttctc
aactgtgcatttgctggtgctgtctacttctgcctctagacaaccaaatctgggcgcaattgacc
gctcaaaccttggttcaataaccttttttattcgcagacgcacatttataaatatgcgcctttca
ataataccgactttatgctgcggcggtgctgtggtggtgatcagaaagctgacgctcaaaagg
ttgtcacgagagatacactcgcatactcgcgcctcattatccttcaccatggatggaccctaa
tgctgttggtggtgaggaagcttacgccaaagccaagagctttgtgtcccaactcactctcatg
gaaaagggtcaacttgaccaactggtgttggtgaagcagctccttgcaaacagggtatctcaatcc
cctcagctaacaacttctcagatggcaaggcgcaacgctgtgttaggaaacgtgggatcaattcct
cgtctcgggtatgcgaggtctctgtctccaggatgggtcctccttggaattcgtctgtccgactaca
acagcgccttttccgctggcaccacagctggtgcttcttgagcaagtctctctggtatgagag
aggtctcctgatgggcactgagttcaaggagaagggtatcgatatcgctccttggtcctgctact
ggacctccttggtcgcactgctgctggtggacgaaactgggaaggcttcaccggtgatccttata
tggttggtcgcacgccatggccgagggcgtaagggtattcaagacgcaggtgtcattgcttgtgc
taagcattacatcgcaaacgagcagggtaagccacttggaagatttgaggaattgacagagaac
tgacctcttctgtagagcacttccgacagagtggtgaggtccagtcgccgaagtacaacatctcc
gagtcctctcctccaacctggatgacaagactatgcacgagctctacgcctggcccttcgctg
acgcgctccgcgcggcgctcggttccgtcatgtgctcgtacaaccagatcaacaactcgtacgg
ttgccagaactccaagctcctcaacgggtatcctcaaggacgagatgggcttccagggtttcgtc
atgagcgaattgggcggcccagcataccgggtgcgccttctgcccgtcgtggtctcgatatgagca
tgcttggtgacactgccttcgacagcggatacagcttctggggcggaacttgactctggctgt
catcaacggaactgttcccgcctggcgagttgatgacatggctctgccaatcatgtctgccttc
ttcaagggttggaagacgatagaggatcttcccgacatcaacttctcctcctggaccgcgcaca
ccttcggcttcgtgcatacatattgtctcaagagaaccgcgcagcaggtcaactttggagtcacag
ccagcacgaccacaagagccacatccgtgaggccgctgccaaagggaagcgtcgtgctcaagaac
accgggtcccttcccctcaagaacccaaagtctcctcgtctgcatgttggtgaggacgcgggtccca
acctgctggaccacaatggttggtgacccgtggttgcgataatggtaccctggctatggcttg
gggtcgggaacttcccaattcccttacttgatcacccccgatcaagggtctctaatcgagct
actcaagacggaactcgatatgagagcatcttgaccaacaacgaatgggttccagtacaagctc
ttgtcagccagcctaactgacgcctatcggttttcgccaatgccgactctggtgaggagatacat
tgaagtcgacggaaactttggtgatcgcaagaacctcacctctggcagcaggagagacgagctc
atcaagaacgtgtcgtccatatgccccaacaccattgtagttctgcacaccgtcggccctgtcc
tactcggcgaactacgagaagaaccccaacatcactgccatcgtctgggtggtcttcccggcca
agagtcaggcaatgccatcgtgatctcctctacggcaagggtcagccctggccgatctcccttc
acttggggccgcacccgcgagagctacgggtactgaggttctttatgaggcgaacaacggccgtg
gcgtcctcaggatgacttctctgaggggtgtcttcatcgactaccgtcacttcgacaagtacaa
catcacgcctatctacgagttcgggtcacggtctatcttggtcgacgttcaagttctccaacctc
cacatccagaagaacaatgtcggccccatgagcccgcccaacggcaagacgattgctgggtccct
ctctgggcaacttcagcaagaaccttaaggactatggcttccccaaagaacgttcggccgatcaa
ggagtttatctacctctacotgaacaccactacctctggcaaggaggcgtcgggtgacgctcac
tacggccagactgcgaaggagttcctccccgcgggtgccttggaaggcagccctcagcctcgtc
ctgcccgtctgtggcgaacccggcggaacccgcagctgtacgacattctctacaccgtgacggc
caccattaccaaacggggtcggtcatggacgacgcgcgttccccagctgtacctgagccacggc
ggtcccaacgagccgccaaagggtgctgctggtggttcgacccgatcgagcgcattgtcccgcc
agagcgtcacgttcaaggcagacctgacgcgcgtgacctgtccaactgggacacgaagaagca
gcagtggtgctattaccgactaccccaagaactgtgtacgtgggcagctcctcgcgcgaacctgcgc
ctgagcgcgccgcctgccatga

FIG. 67B

SEQ ID NO:	TERMINAL	SEQUENCE MOTIFS
136	N	A-x-S-P-P-x-Y-P-S-P-W-M-D-P-x-A-x-G-W-E-x-A-Y
137	N	A-K-x-F-V-S-x-x-T-L-x-E-K-V-N-L-T-T-G-V-G-W-x-G-E-x-C-V-G-N-V-G
138	N	P-R-x-G-M-R-x-L-C-x-Q-D-G-P-L-G-x-R
139	N	Y-N-S-A-F-x-x-G-x-T-A-x-A-S-W-S
140	N	G-x-I-A-C-A-K-H-x-x-x-N-E-Q-E-H-x-R-Q
141	N	L-S-S-N-x-D-D-K-T-x-H-E-x-Y-x-W-P-F-x-D-A-V-x-A-G-V-G
142	N	M-C-S-Y-x-Q-x-N-N-S-Y-x-C-Q-N-S-K-L-x-N-G
143	N	G-F-Q-G-F-V-M-S-D-W-x-A-Q-H-x-G-x-A-x-A-V-A-G-L-D-M-x-M-P-G-D-T
144	N	N-L-T-L-A-V-x-N-G-T-V-P-x-W-R-x-D-D-M
145	N	P-x-F-L-x-V-x-G-E-D-A-G-x-N-P-A-G-P-N-G-C-x-D-R-G-C
146	N	G-T-L-A-M-x-W-G-S-G-T-x-F-P-Y-L
147	N	A-I-V-F-A-N-x-x-S-G-E-G-Y-I-x-V-D-G-N-x-G-D-R-K-N-L-T-L-W
148	N	D-x-L-Y-G-K-x-S-P-G-R-x-P-F-T-W-G
149	C	P-x-Y-E-F-G-x-G-L-S-W-x-T-F-x-x-S-x-L
150	C	L-x-D-Y-x-F-P
151	C	E-F-L-P-x-x-A-L-x-G-S-x-Q-P-R
152	C	S-G-x-P-G-G-N-x-x-L-x-D
153	C	Y-T-V-x-A-x-I-T-N-T-G
154	C	V-L-R-G-F-x-R-x-E-x-I-A-P-G-x-S
155	C	T-R-R-D-L-S-N-W-D-x-x-Q-x-W-V-I-T-D
156	C	V-G-S-S-S-R-x-L-P-L-x-A-x-L

FIG. 68A

FIG. 68B Amino acid sequence motifs used to design a suitable β -glucosidase polypeptide hybrid/chimera of the invention

SEQ ID NO:	TERMINAL	SEQUENCE MOTIFS
164	N	Y-P-S-P-W-M-D-P
165	N	E-K-V-N-L-T-T-G-V-G-W
166	N	K-G-(I/V)-D-(V/I)
167	N	C-Q-N-S-K-L-x-N-G
168	N	N-L-T-L-A-V-(L/I/V)-N-G-(S/T)-(V/I)-P-x-W
169	N	S-W-(T/S)-x-D-T-(Y/F)-G
170	C	E-F-L-P-x-x-A-L-x-G-S-x-Q-P-R

GH61 endoglucanase motifs of the disclosure:

Motif 1 of GH61 Family Endoglucanases:
 SEQ ID NO:84: (I/L/M/V)-P-a-a-a-G-a-Y-(I/L/M/V)-a-R-a-(E/Q)-a-a-a-(H/N/Q)

Motif 2 of GH61 Family Endoglucanases:
 SEQ ID NO:85: (I/L/M/V)-p-a-a-a-a-G-a-Y-(I/L/M/V)-a-R-a-(E/Q)-a-a-a-(H/N/Q)

Motif 3 of GH61 Family Endoglucanases:
 SEQ ID NO:86: (I/L/M/V)-p-a-a-a-G-a-Y-(I/L/M/V)-a-R-a-(E/Q)-a-a-A-(H/N/Q)

Motif 4 of GH61 Family Endoglucanases:
 SEQ ID NO:87: (I/L/M/V)-p-a-a-a-G-a-Y-(I/L/M/V)-a-R-a-(E/Q)-a-a-a-(H/N/Q)

Motif 5 of GH61 Family Endoglucanases:
 SEQ ID NO:88: (F/W)-(T/F)-K-(A/I/V)

Motif 6 of GH61 Family Endoglucanases:
 SEQ ID NO:89: H-a-a-G-P-a-a-(Y/W)-(A/I/L/M/V)

Motif 7 of GH61 Family Endoglucanases:
 SEQ ID NO:90: H-a-G-P-a-a-(Y/W)-(A/I/L/M/V)

Motif 8 of GH61 Family Endoglucanases:
 SEQ ID NO:91: (E/Q)-a-Y-a-C-a-(E/H/Q/N)-(F/I/L/V)-a-(I/L/V)

FIG. 68C

SEQ NO. ID : 81***P. anserina* Pa3C nucleotide sequence**

atggcataccgctcatttagtcttggggcgcttgcgctccacctctcttgcggccagcgctcgtgacgcct
cgagatcctgttccgcttgattcgtcgctgccccatactatccagcgctcatggaggatgggtcgct
tcgtgggaagaggcttacagcaaggcogaagccttggctcgcagatgaccttggctgaaaagaccaac
atcacctcaggcattggcatctttatgggtgagttattaaccagacatggcttatataaaagcacaaga
gactgactgacatgtgaatagggtcagtgccaccacctaatgagacggttttctgattttgactaaca
catgatacgcctagtcctatgcgtaggaaatactggaagcgcagaaagattgggggttcccgcgcatgtgtc
ttcaggactctgcgttgggtgtgtcgtcggtgacaacgctcactgcgtttcctgctggcatcaccactg
gtgcaacggttgacaagaagctgatctatgctcgtgggtgttgcctattgggtgaagagcatcgcggaagg
gcacaaatgtctatctgggtccttcgtaggcctcttgggcggaagccttgggtggccgcaactggg
agggctttggatctgacccagttcttcaagccaaggctgctgccctgacgatcaagggcggttcaggaac
aaggcatcattgctactatcaagcatctgatcggaacgagcaggagatgtatagaatgtacaacccct
tccagcctggatatagcgccaatattgggtgagtggaactcttgcctctttgacggactaaaaggctgactc
cccacagatgatcggaactctgcacgagctctacctgtggccctttgcgaatccgtccatgccgggtgtt
gggtcggcaatgacagcttacaatgctgtaaacgggtctgcttgcctcagcacagctatctcatcaac
ggatatttgaaggatgagcttggattccagggttcgtcatgtctgactggctgtcccatctccgga
gtcgactccgcttggcagggtctcgacatgaacatgccagggtgacaccaacattccctatttgggttc
agcaactggcactatgagctcagcagatcggttctcaacgggtctgtgcctcttgacagactgaacgac
atggtcaccagaatcgctcgacatggtacaagttcggtcaggatagggaccaccaaggcctaacttc
tcgtcaaacaccgctgacggtgacgggtctgctttatcctgcagctctcttctccccaagggtcagggtg
aactgggttctcaatgttcaggctgatcattatttgatcgccagagagggtcgccaggatgccatcacc
cttctcaagaacaatgggagcttccctccctgaagacttcgcagctctctccatgtcttcgggtactgct
gcccagggtcaaccccgatgggcccacgcttgcatgaacgcgcctgcaacaaaggaacacttggcatg
ggctgggggttctgggtgttgcgattatccttaacttggatgaccgatctcggtatcaggaagcgggtt
cccgacgtcaagttcttcaacacgcagcgttcccttgggtccaccctacacgctcgccgatgacgtt
gccatcggttcatcaccctcgatgctggagagaactcggttcaactgttgagggaacaacagggtgatcg
aacagtgccaagctgggtgcgtggcataacgggtgacgagctggtcaggaagactgcgagagaagtacaac
aacgttattgtggtagctcaaaccgtcgccctctcgatctcgaatcctggatcgacaacccctcgcgct
aagggcgctcctgtttcagcaccttcccggtcaagaagcgggcgagtcggttgcccaacattctcttggc
gatgtctccctagcgggtcacttccctactccatcaccaagcgcgccaacgacttcccgacagcatc
gccaacctccgtggcttttgcctttgggtcagggtccaggacacgtacagcgagggcctgtacattgactac
cgctggctcaacaaggagaagatcaggccccgcttggcttttggccacgggtctcagctacaccaacttc
tcgtttgatgccaccatcgagctctgtcactccactgtctctgggttccctcctgcccgtgcccccaagggc
tcaacgcgggtgtactcgaccgaaatcccccccgctcagaggcgtaactggccggaagggttcaacagg
atctggcgggtacctctactcctgggtcaacaagaacgacgcggataacgcctacgctgttgggtatcgcc
gggggtgaagaagtataactatcccgctgggtacagcaccgcccagaagcccggtcccgccagccgggtggc
ggggaggggggtaactcctgcgcttgggatattgctttccgtgtccaggttacgggtcaagaacactggg
gatacgttctcggaacgggttcgggtgcaggcttatgttcagtatcctgaggggatcccgatgatac
cctgttgtgcagctgagggactttgagaagacgaggggttttggctccgggggaggaggagacgggtgacg
gttgagctgaccaggaaggacttgagcgtgtgggacacggagctgcagaactgggttgtgcccgggggtt
ggggggaagaggtatacgggttggattggggaggcgagcgatagggttgggttacgggttgttatacggat
acgggggttctgtgaggggggagggtgcgcctgttttaa

FIG. 69A

SEQ NO. ID : 80***P. anserina* Pa3C protein sequence**

MAYRSLVLGAFASSTLAASVVTPRDPVPPGFVAAPYYPAPHGGWVASWEEAYSKAEALVSQMTLAEKTN
ITSGIGIFMGNTGSAERLGFPRMCLQDSALGVSSADNVTAFFAGITTGATFDKKLIYARGVAIGEEHRG
KGTNVYLGPSVGPLGRKPLGGRNWEFGSDPVLQAKAAALTIKGVQEQGIIATIKHLIGNEQEMYRMYN
PFQPGYSANIDDRTLHELYLWPF AESVHAGVGSAMTAYNAVNGSACSQHSYLINGILKDELGFQGFVMS
DWLSHISGVDSALAGLDMNMPGDTNIPLEFGFSNWHYELSRSVLNGSVPLDRLNDMVTRIVATWYKFGQD
RDHPRPNFSSNTRDRDGLLYPAALFSPKGQVNWVFNQADHYLIAREVAQDAITLLKNNGSFLPLTTSQ
SLHVEGTAAQVNPDPGNACMNRACNKGTLGMGWGSGVADYPYLDDPISAIRKRVDPVKFFNTDGF PWFH
PTPSPDDVAIVFITS DAGENSFTVEGNNGDRNSAKLAAWHNGDELVRKTAEKYNNVIVVAQT VGPLDLE
SWIDNPRVKGVLFQHLPGQEAGESLANILFGDVSPSGHLPYSITKRANDFPDSIANLRGF AFGQVQD TY
SEGLYIDYRWLNKEKIRPRFAFGHGLSYTNFSFDATIESVTPLSLVPPARAPKGSTPVYSTEIPPASEA
YWPEGFNRIWRYLYSWLNKNDADNAYAVGIAGVKKYNYPAGYSTAQKPGPAAGGGEGGNPALWDIAFRV
PVTVKNTGDTFSGRASVQAYVQYPEGIPYDTPVVQLRDFEKTRVLAPGEEETVTVELTRKDLSVWDTEL
QNWVVPGVGGKRYTVWIGEASDRLFTACYTDTGVCEGGRVPPV*

FIG. 69B

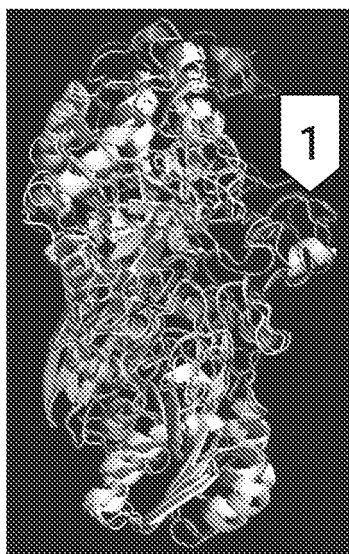


FIG. 70A

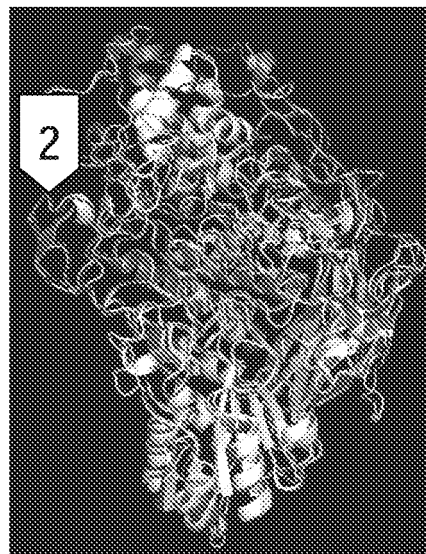


FIG. 70B

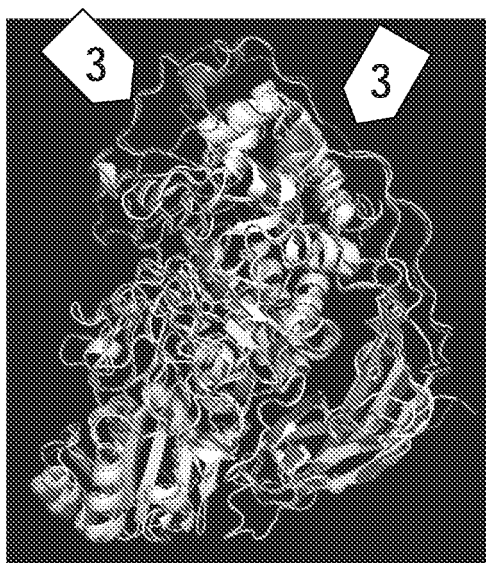


FIG. 70C

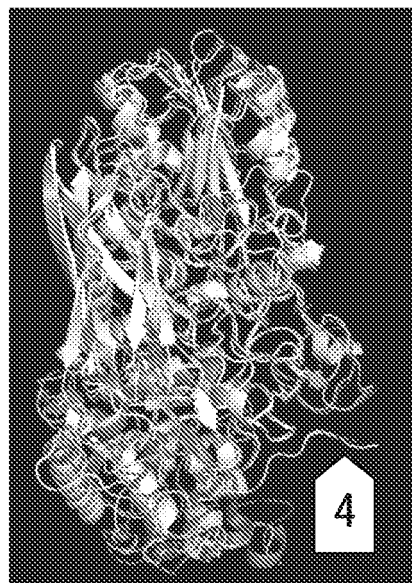


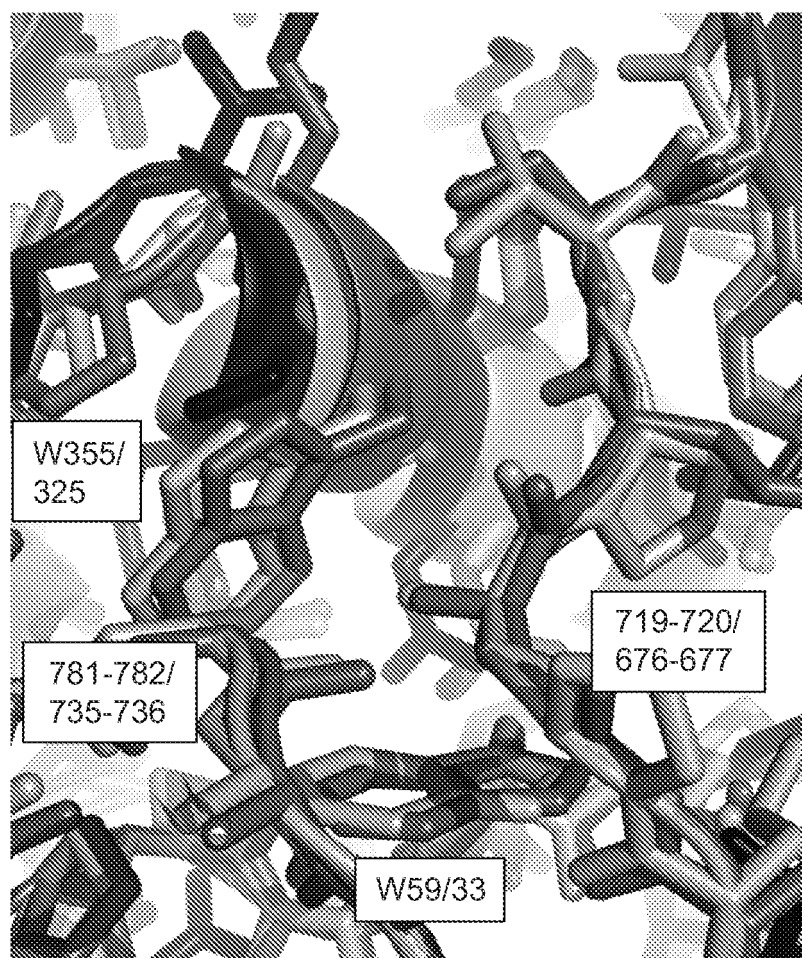
FIG. 70D

[illegible]

FIG. 70E-1

Alignment of <i>T. reesei</i> BGL1, Te3A, and Fv3C. Mature <i>T. reesei</i> BGL1 sequence is shown, mature start of Fv3C and ABG2 indicated by 'Mat'									
	500	*	520	*	540	*	560		
Q12715 TRI :	APYDAINTRASSQGTQVT--LSNTDNTSSGASAAARGKDVAIVFITADSGEGYITVEGNAGDRNNLDPWHN	:	461						
ABG2_T_eme :	TPEQAIQREVLSRNGFTTG--ITDNGALAEMAAASQADTCLVFANADSGEGYITVDGNEGDRKNLTILWQG	:	525						
Fv3C :	TPDQGLSNRATQDGTRYESILTNNEWASVQALVSQPNVTAIVFANADSGEGYIEVDGNEGDRKNLTILWQQ	:	556						
	*	580	*	600	*	620	*		
Q12715 TRI :	GNALVQAVAGANSNVIIVVHVSVAIILEQILALPQKAVVMAGLPQESGNALVDVLWGDVSPSGKLVT	:	531						
ABG2_T_eme :	ADQVIHNVSANCNTTVVLHTVGPVLIDDWYDHPNVTAILWAGLPQESGNLSVDVLYGRVNP-GKTPFT	:	594						
Fv3C :	GDELIKNVSSICPNTIVVLHTVGPVLLADYEKNPNITAIWAGLPQESGNALVDVLYGKVSP-GRSPFT	:	625						
	640	*	660	*	680	*	700		
Q12715 TRI :	IAKSPNDYNTRIVSGGSDS-----FSEGLFIDYKHFDDAN-----ITPRYEFYGLSYTKF	:	582						
ABG2_T_eme :	WGRARDDYGAPLIVKPNNGKGAPOQDFTGIFIDYRRFDKYN-----ITPIYEFYGLSYTTF	:	652						
Fv3C :	WGRTRSYGTEVLYEANNRGAPQDDFSEGVFIDYRHFDRRSPSTDGKSSPNNTAAPLYEFYGHGLSWSTF	:	695						
	*	720	*	740	*	760	*		
Q12715 TRI :	NYSRLSV-----	:	598						
ABG2_T_eme :	EFSQLNVQPINAPPYTPASGFTKAAQSEFQ-PSNASDNLVPSDIERVPLYIYEWLN--STDLKASANDPD	:	719						
Fv3C :	EYSDLNIQKNVENPYPSPAGQTIPTAPTEGNSKNLNDYVFPKGVRIYIKFIYFPFLNTSSSASEASNDGGQ	:	765						
	Insertion 3								
	780	*	800	*	820	*	840		
Q12715 TRI :	TGAVV-----PGGPSDLFQNVATVTVDIANSQGVGTGAQVLYITYPSSAPRT	:	646						
ABG2_T_eme :	YGLPTEKYVPPNATNGDPQIDPAGGAPGPNPSLYEPVARVTTIITNTGKVTGDEVFQLYVSL--GGPDD	:	787						
Fv3C :	FGKTAEEFLPPNALNGSAQPRLPASGAPGPNPQLWDILYTVTATITNTGNATSDIIPQLYVSL--GGENE	:	833						
	Loop 3								
	*	860	*	880	*	900	*		
Q12715 TRI :	PPKQLRGFAKL-NLTPGQSGTATFNIRRRDLSYWDTSQKWWVPVSGSFGISVGASSRDIRLTSTLSVA--	:	713						
ABG2_T_eme :	APKVLRGFDRI-TLAPGQQYLWTTTLTRRDISNWDPTQNWVVTNYTKTIYVGNSSRNPLQAPLKPYPG	:	856						
Fv3C :	PIRVLRGFDRIENIAPGQSAIFNAQLTRRDLNWDNNAQNWVITDHPKTVWVGSSSRKPLPSAKLE----	:	899						
Q12715 TRI :	- :								
ABG2_T_eme :	I : 857								
Fv3C :	- :								

FIG. 70E-2

***FIG. 70F***

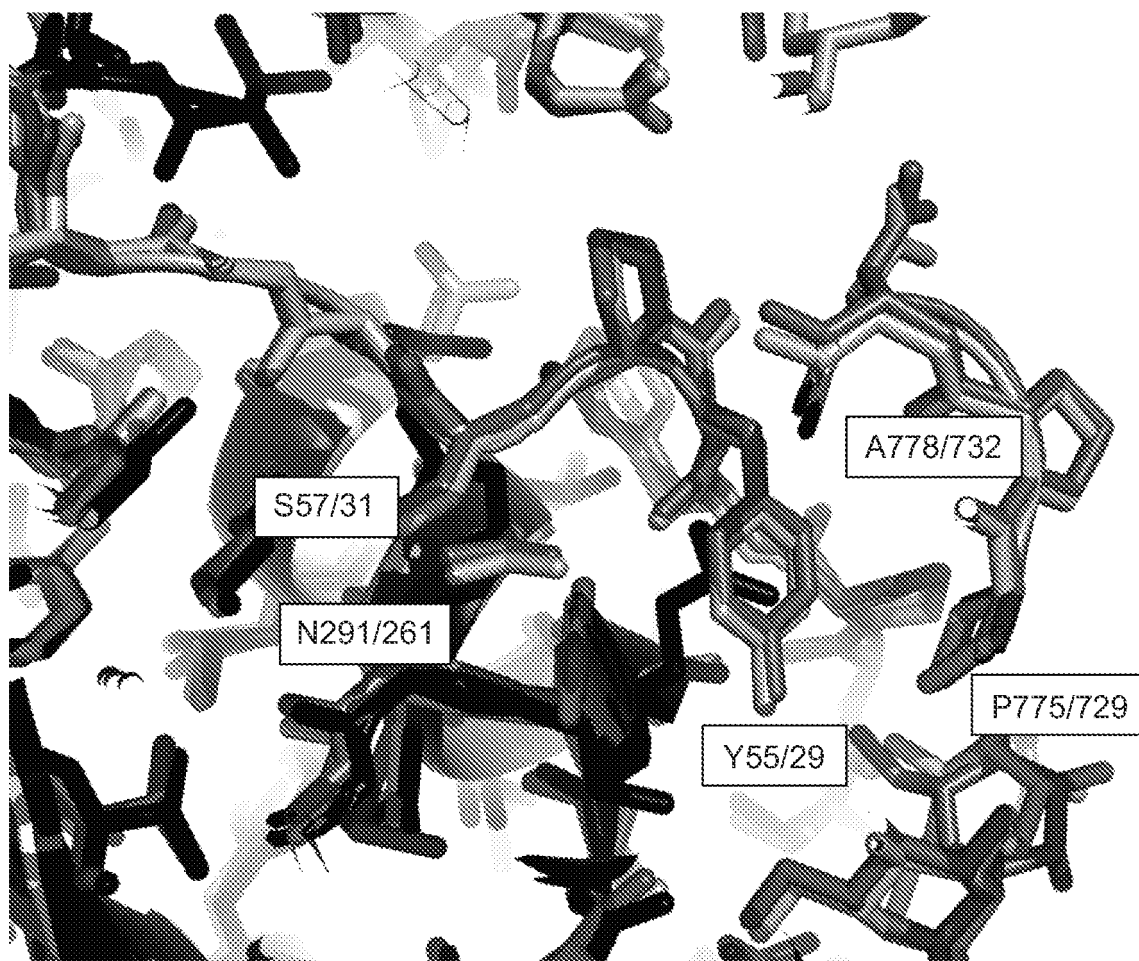


FIG. 70G

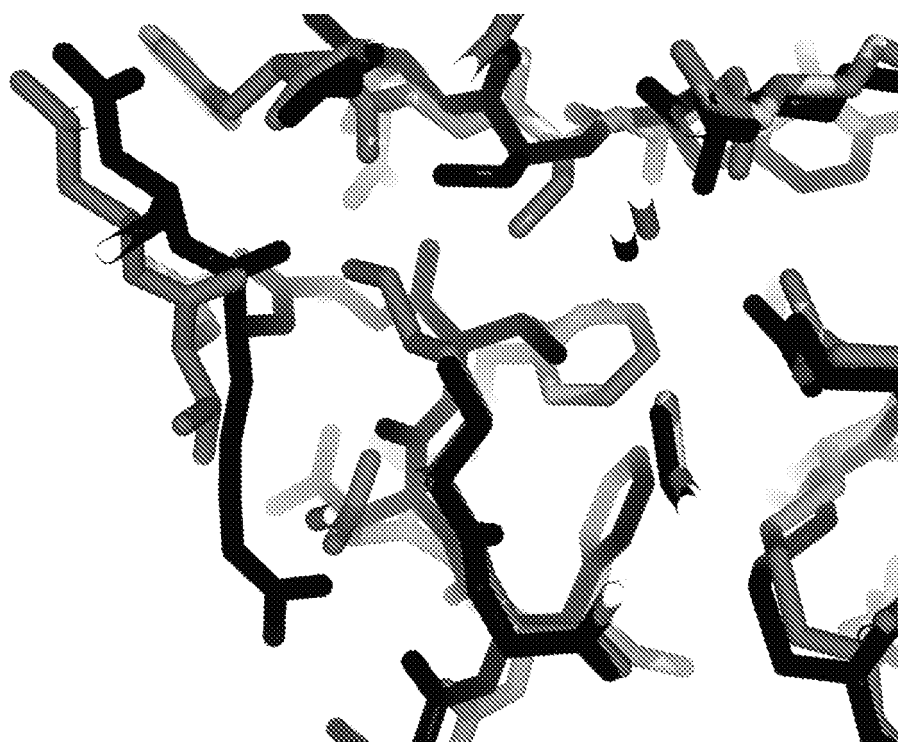
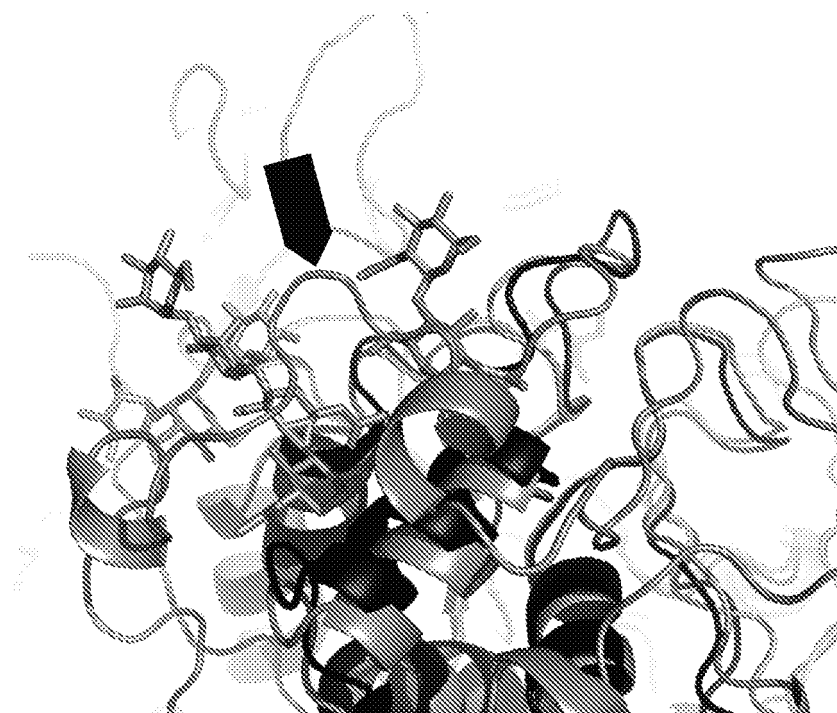
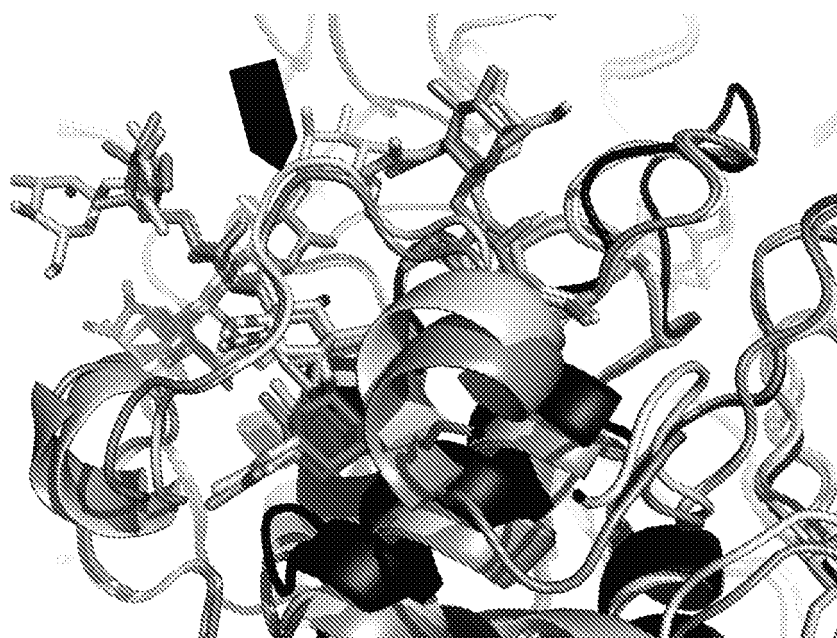


FIG. 70H

**FIG. 70I (a)****FIG. 70I (b)**

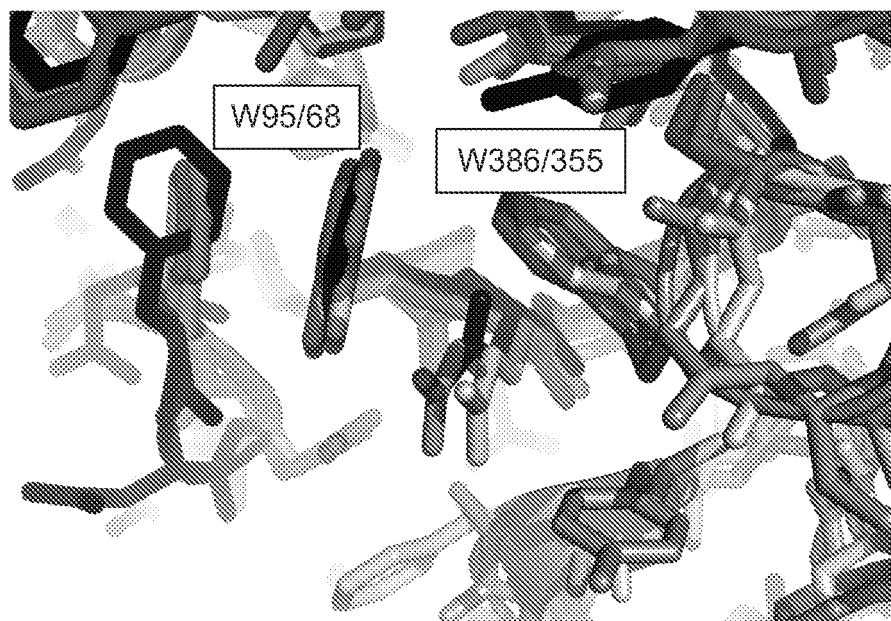
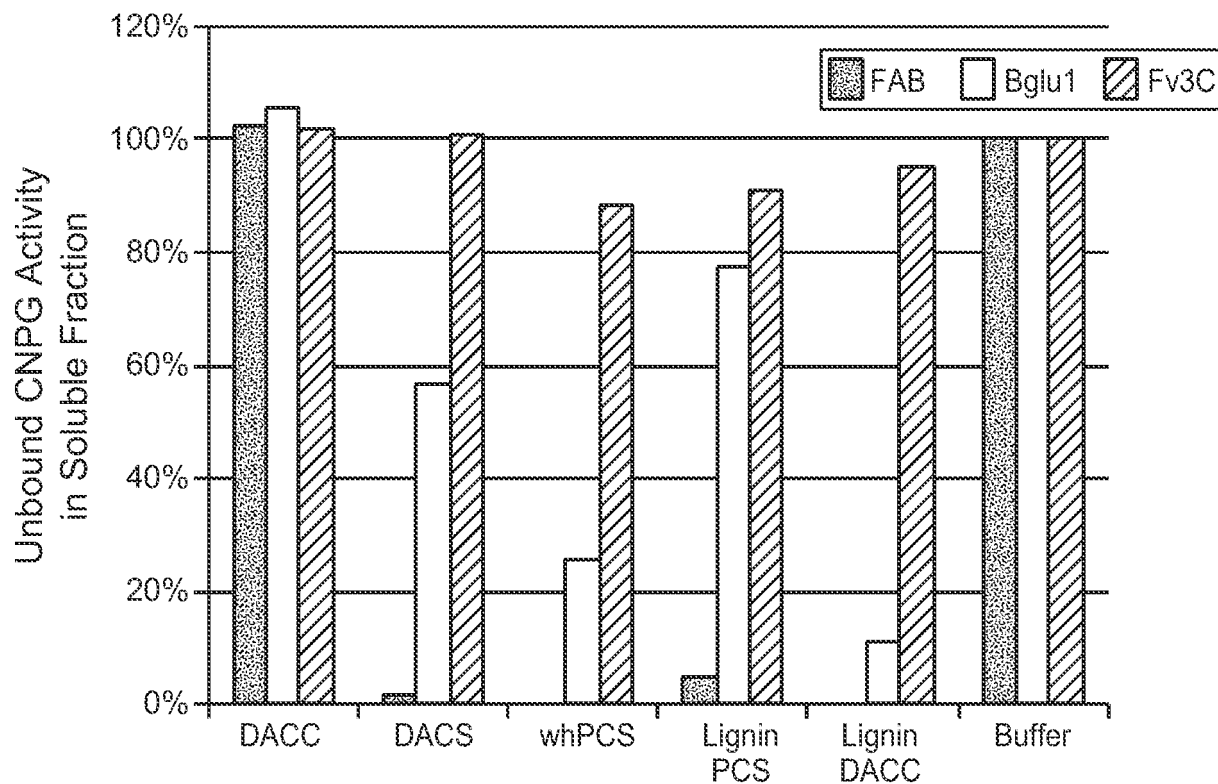


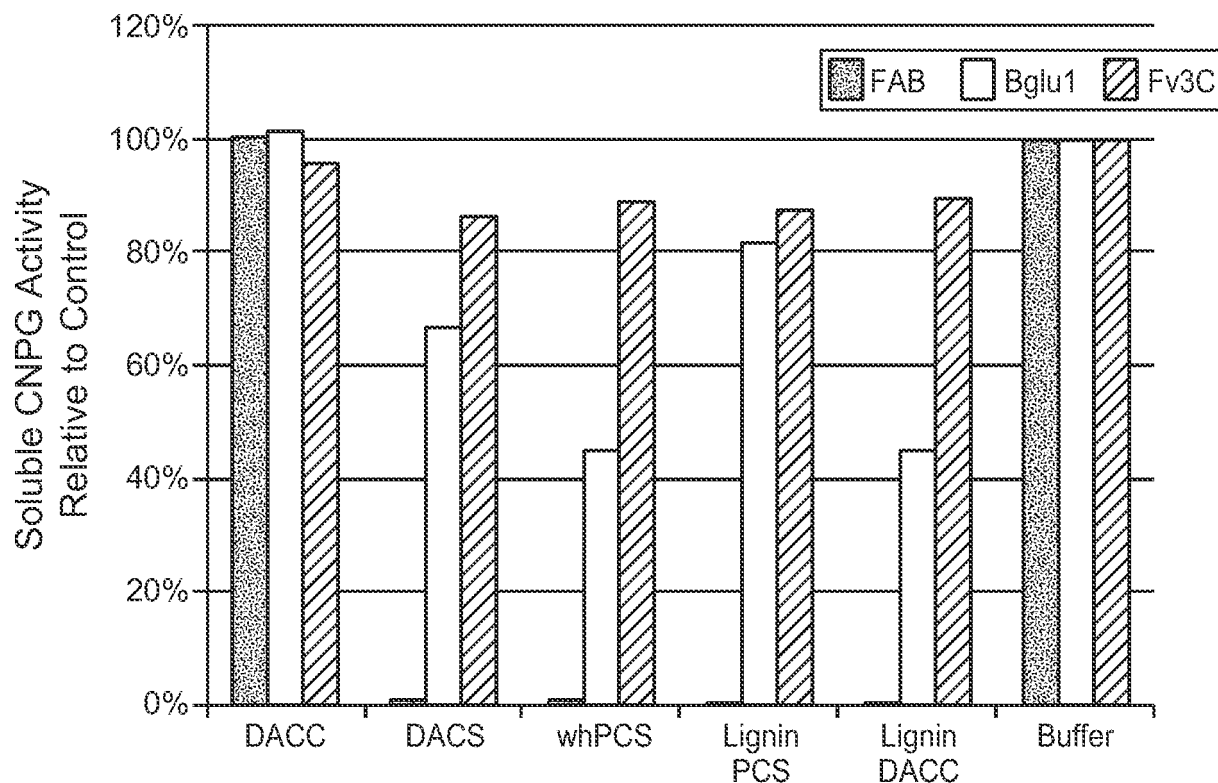
FIG. 70J

110 / 111

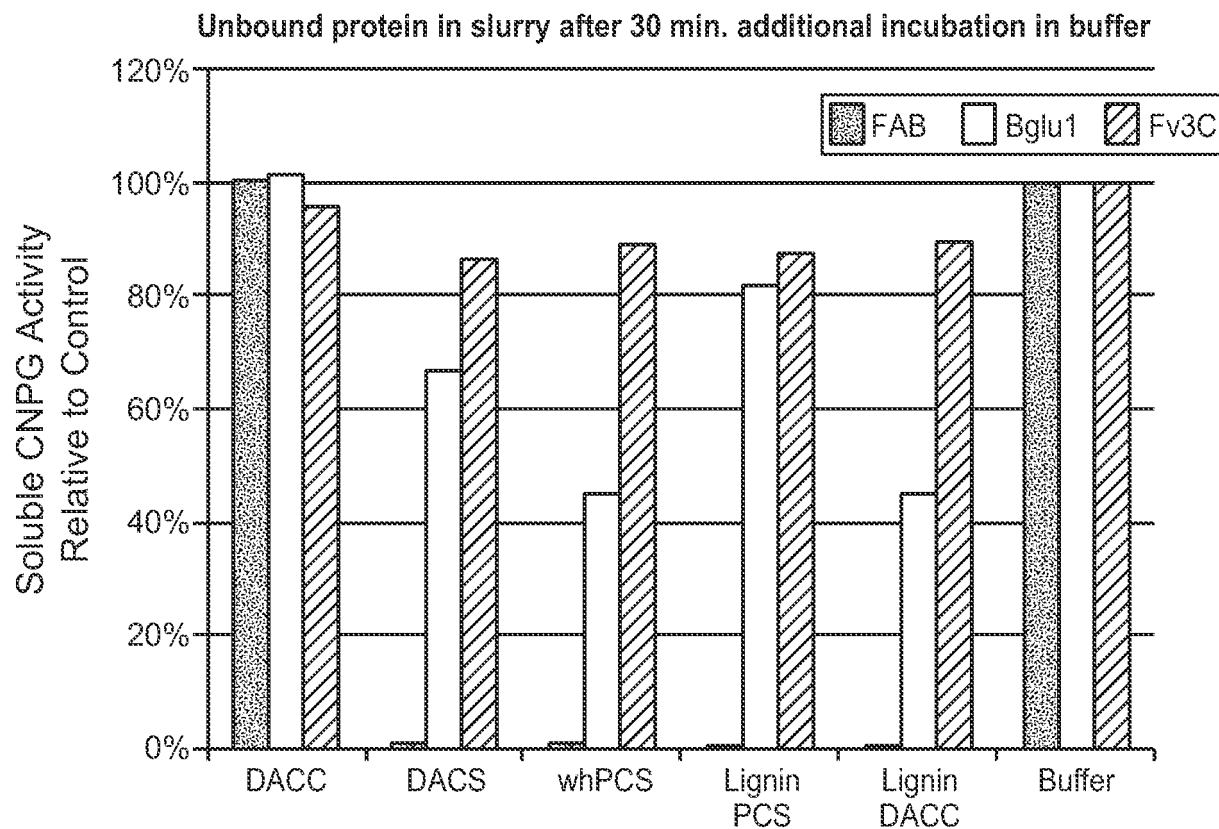
Unbound proteins in soluble fraction (supernatant) following 50°C incubation for 44 hrs.

**FIG. 71A**

Total protein (bound and unbound) protein in slurry following 50°C incubation for 44 hrs.

**FIG. 71B**

111 / 111

**FIG. 71C**