

Supplementary material to: Draft genome of *Thermomonospora* sp. CIT 1 (Thermomonosporaceae) and *in silico* evidence of its functional role in filter cake biomass deconstruction

Table S3 - Identifications of enzymes with activity on carbohydrate structures present in the draft genome CIT 1 recovered from metagenomic sequencing of filter cake. Predictions were performed with dbCAN online, following for blastp confirmation against the non-redundant NCBI protein database of the occurrence of predicted protein-like sequence deposition.

ORF LENGTH	Search results for dbCAN conserved domains		BLASTP RESULTS				
	CAZy FAMILY	ID CAZy	ENZYME NAME (NCBI)	QUERY COVER	E-VALUE	IDENTITY	ACCESSION
747	AA2.hmm	peroxidase (EC 1.11.1.-)	catalase/peroxidase HPI	100	0.00E+00	100	WP_012852289
786	AA3.hmm	glucose-methanol-choline (GMC)	glucose-methanol-choline oxidoreductase	100	0.00E+00	100	ACY97563
520	AA3.hmm	glucose-methanol-choline (GMC)	mycofactocin system GMC family oxidoreductase MftG	99	0.00E+00	99	WP_012852714
582	AA3.hmm	glucose-methanol-choline (GMC)	GMC family oxidoreductase	100	0.00E+00	99	WP_012854558
531	AA3_2.hmm	glucose-methanol-choline (GMC)	choline dehydrogenase	100	0.00E+00	100	WP_012854223
533	AA4.hmm	vanillyl-alcohol oxidase (EC 1.1.3.38)	FAD-binding oxidoreductase	99	0.00E+00	99	WP_012852156
209	AA6.hmm	1,4-benzoquinone reductase (EC. 1.6.5.6)	NAD(P)H:quinone oxidoreductase type IV	100	4.00E-152	100	WP_012850533
187	AA6.hmm	1,4-benzoquinone reductase (EC. 1.6.5.6)	NAD(P)H-dependent oxidoreductase	100	9.00E-86	69	WP_067443322
152	AA6.hmm	1,4-benzoquinone reductase (EC. 1.6.5.6)	flavodoxin	99	6.00E-104	100	WP_012853676
178	AA6.hmm	1,4-benzoquinone reductase (EC. 1.6.5.6)	NADPH-dependent oxidoreductase	100	3.00E-124	99	WP_012855187
457	AA7.hmm	1_	FAD-binding oxidoreductase	100	0.00E+00	100	WP_012850500
441	AA7.hmm	-	FAD-linked oxidoreductase	100	0.00E+00	100	WP_012852047
378	AA7.hmm	-	FAD linked oxidase domain-containing protein	100	0.00E+00	99	WP_012852317
459	AA7.hmm	-	FAD-binding oxidoreductase	100	0.00E+00	99	WP_012853068

ORF LENGTH	Search results for dbCAN conserved domains		BLASTP RESULTS				
	CAZy FAMILY	ID CAZy	ENZYME NAME (NCBI)	QUERY COVER	E-VALUE	IDENTITY	ACCESSION
502	AA7.hmm	-	FAD-binding oxidoreductase	92	0.00E+00	99	WP_012853288
482	AA7.hmm	-	FAD-binding oxidoreductase	100	0.00E+00	99	WP_012853594
411	AA7.hmm	-	FAD-binding oxidoreductase	100	0.00E+00	99	WP_012853595
188	AA10.hmm	lytic polysaccharide monooxygenases (LPMOs)	chitin-binding domain 3 protein	100	8.00E-109	90	ACZ00089
159	CBM2.hmm	CBM2	cellulose-binding family II	100	2.00E-109	100	WP_012853764
447	CBM2.hmm	CBM2	cellulose-binding family II	99	0.00E+00	99	ACY99074
335	CBM13.hmm	-	hypothetical protein Tcur_3315	100	0.00E+00	99	ACY98853
1430	CBM32.hmm	-	coagulation factor 5/8 type domain protein	100	0.00E+00	99	ACY99521
532	CBM32.hmm	-	phosphopeptide-binding protein	100	0.00E+00	100	WP_012855260
498	CBM35.hmm	CBM35+GH43	glycoside hydrolase family 43	100	0.00E+00	99	WP_012851007
918	CBM44.hmm	-	PKD domain-containing protein	100	0.00E+00	99	WP_012851385
701	CBM48.hmm	-	glycogen debranching enzyme GlgX	100	0.00E+00	100	WP_012852133
736	CBM48.hmm	-	1,4-alpha-glucan-branching protein	100	0.00E+00	99	WP_012853921
680	CBM48.hmm	-	glycogen debranching protein	100	0.00E+00	99	WP_012854434
280	CE1.hmm	esterase	esterase	100	0.00E+00	99	WP_012851583
288	CE1.hmm	esterase	esterase	100	0.00E+00	100	WP_012850408
284	CE1.hmm	esterase	alpha/beta hydrolase fold protein	100	0.00E+00	99	ACY97135
347	CE1.hmm	esterase	alpha/beta hydrolase	91	0.00E+00	99	WP_012852003
362	CE1.hmm	-	hypothetical protein	100	0.00E+00	99	WP_052305466
309	CE1.hmm	esterase	alpha/beta hydrolase fold protein	72	9.00E-154	99	WP_012852600
278	CE1.hmm	cinnamoyl esterase (EC 3.1.1.-)	putative lipoprotein	100	0.00E+00	99	WP_012854167
292	CE1.hmm	cinnamoyl esterase (EC 3.1.1.-)	lipase	100	0.00E+00	99	WP_012850775
263	CE1.hmm	esterase	alpha/beta hydrolase	100	0.00E+00	100	WP_012854209

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	CAZy FAMILY	ID CAZy	ENZYME NAME (NCBI)	QUERY COVER	E-VALUE	IDENTITY	ACCESSION
364	CE1.hmm	esterase	alpha/beta hydrolase	100	0.00E+00	100	WP_012854576
374	CE1.hmm	esterase	putative esterase	100	0.00E+00	100	ACY96221
253	CE2.hmm	-	SGNH/GDSL hydrolase family protein	100	0.00E+00	99	WP_012851045
343	CE3.hmm	-	GDSL family lipase	100	0.00E+00	100	WP_012851417
267	CE4.hmm	-	polysaccharide deacetylase	100	0.00E+00	99	WP_012851516
341	CE4.hmm	-	polysaccharide deacetylase	100	0.00E+00	99	ACY97622
375	CE4.hmm	-	polysaccharide deacetylase	100	0.00E+00	98	WP_012853180
285	CE4.hmm	-	polysaccharide deacetylase family protein	100	0.00E+00	100	WP_012853293
264	CE4.hmm	-	polysaccharide deacetylase	100	0.00E+00	99	WP_012853908
234	CE4.hmm	-	polysaccharide deacetylase	100	4.00E-168	100	ACZ00196
275	CE4.hmm	-	polysaccharide deacetylase family protein	100	0.00E+00	99	WP_012855020
235	CE5.hmm	cutinase (EC 3.1.1.74)	cutinase family protein	100	5.00E-164	99	WP_012851874
241	CE5.hmm	cutinase (EC 3.1.1.74)	cutinase	100	4.00E-175	99	ACY97091
176	CE5.hmm	cutinase (EC 3.1.1.74)	cutinase family protein	100	6.00E-123	99	WP_012851879
410	CE9.hmm	N-acetylglucosamine 6-phosphate deacetylase (EC 3.5.1.25)	N-acetylglucosamine-6-phosphate deacetylase	100	0.00E+00	99	WP_012854344
349	CE10.hmm	esterase	Alpha/beta hydrolase fold-3 domain protein	100	0.00E+00	100	ACY96637
335	CE10.hmm	esterase	alpha/beta hydrolase	100	0.00E+00	100	WP_012851463
692	CE10.hmm	-	S9 family peptidase	100	0.00E+00	99	WP_012851498
703	CE10.hmm	-	S9 family peptidase	100	0.00E+00	100	WP_012851705
593	CE10.hmm	cinnamoyl esterase (EC 3.1.1.-)	Esterase/lipase-like protein	100	0.00E+00	99	ACY97597
317	CE10.hmm	esterase	alpha/beta hydrolase	100	0.00E+00	100	WP_012852810

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	CAZy FAMILY	ID CAZy	ENZYME NAME (NCBI)	QUERY COVER	E-VALUE	IDENTITY	ACCESSION
323	CE10.hmm	esterase	alpha/beta hydrolase	100	0.00E+00	100	WP_012852854
489	CE10.hmm	-	peptidase S15	100	0.00E+00	99	WP_012852916
546	CE10.hmm	carboxyl esterase (EC 3.1.1.3)	carboxylesterase family protein	100	0.00E+00	99	WP_012850644
234	CE10.hmm	esterase	alpha/beta hydrolase fold-3 domain-containing protein	100	2.00E-158	100	WP_012853073
668	CE10.hmm	-	S9 family peptidase	100	0.00E+00	100	WP_012853613
343	CE10.hmm	esterase	alpha/beta hydrolase	100	0.00E+00	99	WP_012854310
364	CE10.hmm	esterase	alpha/beta hydrolase	100	0.00E+00	100	WP_012854576
362	CE10.hmm	esterase	alpha/beta hydrolase	99	0.00E+00	99	WP_083789919
587	CE10.hmm	-	S9 family peptidase	100	0.00E+00	99	WP_012855196
303	CE14.hmm	mycothiol S-conjugate amidase (EC 3.5.1.-)	mycothiol conjugate amidase Mca	100	0.00E+00	100	ACY96652
297	CE14.hmm	N-acetyl-1-D-myo-inositol-2-amino-2-deoxy- α -D-glucopyranoside deacetylase (EC 3.5.1.89)	1D-myo-inositol 2-acetamido-2-deoxy-alpha-D-glucopyranoside deacetylase	100	0.00E+00	100	WP_012851500
271	CE14.hmm	N-acetyl-1-D-myo-inositol-2-amino-2-deoxy- α -D-glucopyranoside deacetylase (EC 3.5.1.89)	GlcNAc-PI de-N-acetylase	100	0.00E+00	100	WP_041441415
482	GH1.hmm	β -glucosidase (EC 3.2.1.21)	beta-glucosidase	100	0.00E+00	100	WP_012852091
471	GH1.hmm	β -glucosidase (EC 3.2.1.21)	beta-glucosidase	100	0.00E+00	100	WP_012852534
447	GH1.hmm	β -glucosidase (EC 3.2.1.21)	beta-glucosidase	100	0.00E+00	99	WP_012855073
543	GH3.hmm	-	glycoside hydrolase family 3 domain-containing protein	100	0.00E+00	100	WP_012854338
427	GH4.hmm	-	glycoside hydrolase family 4	100	0.00E+00	99	WP_012854171
626	GH5_43.hmm	endoglycoceramidase (EC 3.2.1.123)	endoglycosylceramidase	98	0.00E+00	99	WP_012851730
409	GH6.hmm	-	glycoside hydrolase family 6	100	0.00E+00	99	WP_012852096
701	GH13_11.hmm	-	glycogen debranching enzyme GlgX	100	0.00E+00	100	WP_012852133
680	GH13_11.hmm	-	glycogen debranching protein	100	0.00E+00	99	WP_012854434
613	GH13_16.hmm	-	maltose alpha-D-glucosyltransferase	100	0.00E+00	99	WP_083790013

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	CAZy FAMILY	ID CAZy	ENZYME NAME (NCBI)	QUERY COVER	E-VALUE	IDENTITY	ACCESSION
661	GH13_3.hmm	α -1,4-glucan: phosphate α -maltosyltransferase (EC 2.4.99.16)	alpha-1,4-glucan-maltose-1-phosphate maltosyltransferase	100	0.00E+00	99	WP_012853902
550	GH13_30.hmm	α -amylase (EC 3.2.1.1)	alpha-amylase	100	0.00E+00	99	WP_012852097
736	GH13_9.hmm	branching enzyme (EC 2.4.1.18)	1,4-alpha-glucan-branching protein	100	0.00E+00	99	WP_012853921
629	GH15.hmm	-	glycoside hydrolase family 15 protein	100	0.00E+00	100	WP_012853541
484	GH15.hmm	-	glycoside hydrolase family 15	100	0.00E+00	100	WP_012854532
272	GH23.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012851447
352	GH23.hmm	-	NLP/P60 protein	99	0.00E+00	100	WP_012851472
378	GH23.hmm	peptidoglycan lyase (EC 4.2.2.n1) also known in the literature as peptidoglycan lytic transglycosylase	lytic transglycosylase domain-containing protein	100	0.00E+00	99	WP_012852049
246	GH23.hmm	-	hypothetical protein	100	8.00E-180	99	WP_012852903
266	GH23.hmm	peptidoglycan lyase (EC 4.2.2.n1) also known in the literature as peptidoglycan lytic transglycosylase	transglycosylase domain-containing protein	100	0.00E+00	100	WP_012851352
297	GH25.hmm	-	glycoside hydrolase family 25	100	0.00E+00	100	WP_012852705
371	GH25.hmm	-	glycoside hydrolase family 25	100	0.00E+00	99	WP_012850936
334	GH26.hmm	β -mannanase (EC 3.2.1.78)	beta-mannanase-like protein	100	0.00E+00	99	WP_012854497
335	GH26.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012851356
506	GH26.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012851387
465	GH30.hmm	-	hypothetical protein	100	0.00E+00	99	WP_012853919
973	GH33.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012853982
498	GH43_30.hmm	-	glycoside hydrolase family 43	100	0.00E+00	99	WP_012851007
331	GH43_5.hmm	arabinanase (EC 3.2.1.99)	arabinan endo-1,5-alpha-L-arabinosidase	100	0.00E+00	100	WP_012853142
456	GH63.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012852353
440	GH63.hmm	-	hypothetical protein	100	0.00E+00	99	WP_012853510

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	CAZy FAMILY	ID CAZy	ENZYME NAME (NCBI)	QUERY COVER	E-VALUE	IDENTITY	ACCESSION
810	GH65.hmm	-	glycoside hydrolase family 65 protein	100	0.00E+00	100	WP_012853146
794	GH65.hmm	-	glycoside hydrolase family 65 protein	100	0.00E+00	99	WP_012853851
717	GH77.hmm	amylomaltase or 4- α -glucanotransferase (EC 2.4.1.25)	4-alpha-glucanotransferase	100	0.00E+00	99	WP_012851713
303	GH117.hmm	-	hypothetical protein	93	0.00E+00	99	WP_012851745
214	GH135.hmm	-	Zn-dependent hydrolase	100	7.00E-155	100	WP_012854286
400	GT1.hmm	-	glycosyltransferase	99	0.00E+00	96	WP_012852871
380	GT1.hmm	-	protein of unknown function DUF1205	100	0.00E+00	100	ACY98322
380	GT1.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012853119
418	GT1.hmm	-	glycosyltransferase	100	0.00E+00	99	WP_012855060
946	GT2.hmm	-	CDP-glycerol--poly(glycerophosphate) glycerophosphotransferase	100	0.00E+00	99	WP_012851579
807	GT2.hmm	-	AMP-dependent synthetase and ligase	100	0.00E+00	99	ACY97654
248	GT2.hmm	-	polyprenol monophosphomannose synthase	100	1.00E-178	100	WP_012852699
487	GT2.hmm	-	glycosyl transferase family 2	100	0.00E+00	99	ACY97924
238	GT2.hmm	-	glycosyltransferase family 2 protein	100	2.00E-172	99	WP_012853905
337	GT2.hmm	-	glycosyltransferase family 2 protein	100	0.00E+00	99	WP_012853907
246	GT2.hmm	-	glycosyl transferase family 2	100	3.00E-178	99	ACY99186
268	GT2.hmm	-	glycosyl transferase family 2 protein	99	0.00E+00	100	WP_012854307
1072	GT2.hmm	-	glycosyltransferase family 2 protein	100	0.00E+00	99	WP_012854382
305	GT2.hmm	-	glycosyltransferase family 2 protein	100	0.00E+00	100	WP_012854405
1148	GT2.hmm	-	CDP-glycerol--poly(glycerophosphate) glycerophosphotransferase	100	0.00E+00	99	WP_012854410
317	GT2.hmm	-	glycosyltransferase family 2 protein	100	0.00E+00	99	WP_012854417

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	CAZy FAMILY	ID CAZy	ENZYME NAME (NCBI)	QUERY COVER	E- VALUE	IDENTIT Y	ACCESSION
324	GT2.hmm	-	glycosyltransferase family 2 protein	100	0.00E+00	99	WP_012854425
537	GT2.hmm	-	glycosyl transferase family 2	100	0.00E+00	100	ACY99713
418	GT2.hmm	-	polysaccharide synthesis protein GtrA	100	0.00E+00	100	WP_012850821
306	GT2.hmm	-	glycosyl transferase	100	0.00E+00	100	WP_012851004
658	GT2.hmm	-	glycosyltransferase family 2 protein	100	0.00E+00	99	WP_012851015
321	GT2.hmm	-	glycosyltransferase family 2 protein	100	0.00E+00	100	WP_012851019
1176	GT2.hmm	-	CDP-glycerol:glycerophosphate glycerophosphotransferase	98	0.00E+00	99	WP_012851021
430	GT2.hmm	-	glycosyl transferase family 2	100	0.00E+00	100	ACY96562
294	GT2.hmm	-	glycosyltransferase family 2 protein	100	0.00E+00	99	WP_012851375
390	GT4.hmm	-	glycosyltransferase family 4 protein	100	0.00E+00	100	WP_012851578
380	GT4.hmm	-	group 1 glycosyl transferase protein	100	0.00E+00	99	WP_012852245
388	GT4.hmm	-	glycosyltransferase family 1 protein	100	0.00E+00	100	WP_012852452
381	GT4.hmm	-	glycosyl transferase group 1	100	0.00E+00	100	ACY97742
425	GT4.hmm	-	glycosyltransferase family 4 protein	100	0.00E+00	96	WP_012852806
381	GT4.hmm	-	glycosyl transferase	100	0.00E+00	100	WP_012853078
374	GT4.hmm	-	glycosyltransferase family 1 protein	100	0.00E+00	100	WP_012853385
456	GT4.hmm	-	glycosyltransferase family 1 protein	99	0.00E+00	99	WP_012853975
381	GT4.hmm	-	glycosyltransferase family 1 protein	100	0.00E+00	99	WP_012854306
359	GT4.hmm	-	glycosyl transferase	100	0.00E+00	98	WP_012854404
418	GT4.hmm	-	glycosyltransferase family 4 protein	100	0.00E+00	100	WP_012854550
401	GT4.hmm	-	glycosyltransferase family 4 protein	92	0.00E+00	99	WP_012851010
403	GT4.hmm	-	D-inositol-3-phosphate glycosyltransferase	100	0.00E+00	100	WP_012851072
404	GT4.hmm	-	glycosyltransferase family 1 protein	100	0.00E+00	99	WP_012850472
283	GT14.hmm	-	glycosyl transferase family 14	100	0.00E+00	99	WP_012851388

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	CAZY FAMILY	ID CAZY	ENZYME NAME (NCBI)	QUERY COVER	E-VALUE	IDENTITY	ACCESSION
470	GT20.hmm	α,α -trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.15)	Alpha,alpha-trehalose-phosphate synthase (UDP-forming)	100	0.00E+00	100	ACY97534
493	GT20.hmm	trehalose-6-P phosphatase (EC 3.1.3.12)	trehalose-6-phosphate synthase	100	0.00E+00	99	WP_012851175
259	GT26.hmm	-	glycosyltransferase	100	0.00E+00	100	WP_012851389
364	GT28.hmm	UDP-GlcNAc: Und-PP-MurAc-pentapeptide β -N-acetylglucosaminyltransferase (EC 2.4.1.227)	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	100	0.00E+00	100	WP_012853252
863	GT35.hmm	-	DUF3417 domain-containing protein	100	0.00E+00	100	WP_012853901
496	GT39.hmm	-	hypothetical protein	100	0.00E+00	99	WP_012853866
533	GT39.hmm	-	phospholipid carrier-dependent glycosyltransferase	99	0.00E+00	100	WP_012851342
561	GT39.hmm	-	hypothetical protein	100	0.00E+00	99	WP_012851347
1189	GT51.hmm	-	glycosyl transferase family 51	99	0.00E+00	93	ACY96851
762	GT51.hmm	murein polymerase (EC 2.4.1.129)	peptidoglycan glycosyltransferase	98	0.00E+00	100	WP_012855218
817	GT51.hmm	murein polymerase (EC 2.4.1.129)	penicillin-binding protein	91	0.00E+00	99	WP_012855252
796	GT51.hmm	-	glycosyl transferase family 51	97	0.00E+00	99	WP_012851396
401	GT76.hmm	-	hypothetical protein Tcur_4954	99	0.00E+00	99	ACZ00470
236	GT81.hmm	-	glycosyl transferase family 2	100	6.00E-162	99	WP_012850508
350	GT81.hmm	-	glycosyl transferase family 2	95	0.00E+00	99	ACY98049
257	GT83.hmm	-	mechanosensitive ion channel family protein	100	5.00E-175	99	WP_012854384
504	GT83.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012854498
746	GT83.hmm	-	glycosyl transferase	100	0.00E+00	99	WP_012850819
691	GT83.hmm	-	glycosyl transferase family 39	100	0.00E+00	94	WP_012850820
500	GT83.hmm	-	hypothetical protein	100	0.00E+00	99	WP_012851348
429	GT87.hmm	-	DUF2029 domain-containing protein	100	0.00E+00	100	WP_012850510
404	GT94.hmm	-	glycosyltransferase family 1	100	0.00E+00	99	WP_012850472

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327	PL1.hmm	pectate lyase (EC 4.2.2.2)	pectate lyase	100	0.00E+00	99	WP_012852783
676	PL22_1.hmm	-	hypothetical protein	100	0.00E+00	99	WP_086014605

¹ The name of the enzyme differs between the CAZy databases and non-redundant NCBI proteins.

Table S4 - Identifications of enzymes with activity on carbohydrate structures present in the circular genome of *Thermomonospora curvata* DSM 43183 (Thermomonosporaceae). Predictions were performed with dbCAN online, following for blastp confirmation against the non-redundant NCBI protein database of the occurrence of predicted protein-like sequence deposition.

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	CAZy FAMILY	ID CAZy	ENZYME NAME (NCBI)	QUERY COVER	E-VALUE	IDENTITY	ACCESSION
517	AA3.hmm	glucose-methanol-choline (GMC)	mycofactocin system GMC family oxidoreductase MftG	100	0.00E+00	100	WP_012852714
528	AA4.hmm	vanillyl-alcohol oxidase (EC 1.1.3.38)	FAD-binding oxidoreductase	99	0.00E+00	76	WP_067912508
209	AA6.hmm	1,4-benzoquinone reductase (EC. 1.6.5.6)	NAD(P)H dehydrogenase (quinone)	99	4.00E-128	88	SEG76937
186	AA6.hmm	1,4-benzoquinone reductase (EC. 1.6.5.6)	NAD(P)H-dependent FMN reductase	100	2.00E-84	70	SEG82383
411	AA7.hmm	glycolate oxidase (EC 1.1.3.15)	glycolate oxidase FAD binding subunit	98	0.00E+00	77	SEG60993
482	AA7.hmm	glycolate oxidase (EC 1.1.3.15)	glycolate oxidase	100	0.00E+00	88	SEG60983
459	AA7.hmm	¹ -	FAD-binding oxidoreductase	99	0.00E+00	72	WP_091378734
212	AA10.hmm	lytic polysaccharide monooxygenases (LPMOs)	chitin-binding protein	100	7.00E-86	73	WP_079318887
505	CBM35.hmm	CBM35	CBM35+GH43	96	3.00E-172	57	SEG79516
943	CBM44.hmm	-	PKD domain containing protein	95	0.00E+00	66	WP_083597587
736	CBM48.hmm	-	1,4-alpha-glucan branching enzyme	98	0.00E+00	86	SEF80265
92	CBM48.hmm	-	hypothetical protein	98	7.00E-45	75	WP_030510813
292	CE1.hmm	cinnamoyl esterase (EC 3.1.1.-)	lipase	100	0.00E+00	100	WP_012850775

365	CE1.hmm	-	hypothetical protein	99	0.00E+00	99	WP_052305466
341	CE1.hmm	S-formylglutathione hydrolase (EC 3.1.2.12)	S-formylglutathione hydrolase FrmB	99	0.00E+00	78	SEG71481
284	CE1.hmm	esterase	alpha/beta hydrolase	100	0.00E+00	99	WP_041439411
336	CE1.hmm	-	polyhydroxybutyrate depolymerase	96	2.00E-171	76	SEF89583
317	CE1.hmm	esterase	Pimeloyl-ACP methyl ester carboxylesterase	100	0.00E+00	85	SEG14212
285	CE4.hmm	-	polysaccharide deacetylase family protein	100	0.00E+00	100	WP_012855020
267	CE4.hmm	-	polysaccharide deacetylase	100	0.00E+00	100	WP_012851516
264	CE4.hmm	-	polysaccharide deacetylase	100	0.00E+00	100	WP_012853908
285	CE4.hmm	-	polysaccharide deacetylase family protein	100	0.00E+00	100	WP_012853293
241	CE5.hmm	cutinase (EC 3.1.1.74)	cutinase	100	9.00E-176	100	ACY97091
234	CE10.hmm	esterase	alpha/beta hydrolase fold-3 domain-containing protein	100	2.00E-158	100	WP_012853073
349	CE10.hmm	-	hypothetical protein	98	0.00E+00	99	WP_083789966
497	CE10.hmm	-	peptidase S15	100	0.00E+00	100	WP_012852916
668	CE10.hmm	-	S9 family peptidase	100	0.00E+00	100	WP_012853613
343	CE10.hmm	esterase	alpha/beta hydrolase	100	0.00E+00	100	WP_012854310
317	CE10.hmm	esterase	alpha/beta hydrolase	100	0.00E+00	99	WP_083789919
335	CE10.hmm	esterase	alpha/beta hydrolase	100	0.00E+00	100	WP_012851463
303	CE14.hmm	mycothiol S-conjugate amidase (EC 3.5.1.-)	mycothiol conjugate amidase Mca	97	0.00E+00	100	WP_041439331
271	CE14.hmm	N-acetyl-1-D-myo-inositol-2-amino-2-deoxy- α -D-glucopyranoside deacetylase (EC 3.5.1.89)	GlcNAc-PI de-N-acetylase	100	0.00E+00	100	WP_041441415
297	CE14.hmm	N-acetyl-1-D-myo-inositol-2-amino-2-deoxy- α -D-glucopyranoside deacetylase (EC 3.5.1.89)	1D-myo-inositol 2-acetamido-2-deoxy- α -D-glucopyranoside deacetylase	100	0.00E+00	100	WP_012851500
411	GH1.hmm	β -glucosidase (EC 3.2.1.21)	β -glucosidase	100	0.00E+00	100	WP_012852534
447	GH1.hmm	β -glucosidase (EC 3.2.1.21)	β -glucosidase	100	0.00E+00	100	WP_012855073
427	GH4.hmm	-	glycoside hydrolase family 4	100	0.00E+00	100	WP_012854171

618	GH5_43.hmm	glucosylceramidase (EC 3.2.1.45)	endoglycosylceramidase	100	0.00E+00	100	WP_012851730
419	GH6.hmm	-	glycoside hydrolase family 6	100	0.00E+00	100	WP_012852096
601	GH13_16.hmm	-	maltose α -D-glucosyltransferase	100	0.00E+00	99	WP_083790013
684	GH13_3.hmm	α -1,4-glucan: phosphate α -maltosyltransferase (EC 2.4.99.16)	α -1,4-glucan--maltose-1-phosphate maltosyltransferase	100	0.00E+00	100	WP_012853902
736	GH13_9.hmm	-	1,4- α -glucan-branching protein	100	0.00E+00	100	WP_012853921
629	GH15.hmm	-	glycoside hydrolase family 15	100	0.00E+00	100	WP_012853541
484	GH15.hmm	-	glycoside hydrolase family 15	100	0.00E+00	100	WP_012854532
378	GH23.hmm	peptidoglycan lyase (EC 4.2.2.n1) also known in the literature as peptidoglycan lytic transglycosylase; chitinase (EC 3.2.1.14)	lytic transglycosylase catalytic subunit	100	0.00E+00	100	WP_012852049
349	GH23.hmm	-	NLP/P60 protein	100	0.00E+00	100	WP_012851472
266	GH23.hmm	peptidoglycan lyase (EC 4.2.2.n1) also known in the literature as peptidoglycan lytic transglycosylase; chitinase (EC 3.2.1.14)	transglycosylase domain-containing protein	100	0.00E+00	100	WP_012851352
272	GH23.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012851447
380	GH25.hmm	-	glycoside hydrolase family 25	100	0.00E+00	100	WP_012850936
297	GH25.hmm	-	glycoside hydrolase family 25	100	0.00E+00	100	WP_012852705
335	GH26.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012851356
334	GH26.hmm	β -mannanase (EC 3.2.1.78)	beta-mannanase-like protein	100	0.00E+00	100	WP_012854497
465	GH30.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012853919
505	GH43_30.hmm	-	glycoside hydrolase family 43	100	0.00E+00	100	WP_012851007
456	GH63.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012852353
807	GH65.hmm	-	glycoside hydrolase family 65	100	0.00E+00	100	WP_012855093
810	GH65.hmm	-	glycosyl hydrolase	100	0.00E+00	100	WP_012853146
794	GH65.hmm	-	glycoside hydrolase family 65	100	0.00E+00	100	WP_012853851
717	GH77.hmm	amylomaltase or 4- α -glucanotransferase (EC 2.4.1.25)	4- α -glucanotransferase	100	0.00E+00	100	WP_012851713
283	GH117.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012851745

380	GT1.hmm	-	DUF1205 domain-containing protein	98	0.00E+00	100	WP_083789857
418	GT1.hmm	-	glycosyltransferase	100	0.00E+00	100	WP_012855060
272	GT2.hmm	-	glycosyltransferase family 2 protein	100	0.00E+00	100	WP_012853905
337	GT2.hmm	-	glycosyltransferase family 2 protein	100	0.00E+00	100	WP_012853907
157	GT2.hmm	-	CDP-glycerol:glycerophosphate glycerophosphotransferase	100	0.00E+00	100	WP_012851021
248	GT2.hmm	-	polyprenol monophosphomannose synthase	100	1.00E-178	100	WP_012852699
807	GT2.hmm	-	Acyl-CoA synthetase (AMP-forming)/AMP-acid ligase II	97	0.00E+00	86	SEG89133
301	GT2.hmm	-	glycosyltransferase family 2 protein	100	0.00E+00	100	WP_012851375
537	GT2.hmm	-	glycosyl transferase family 2	87	0.00E+00	99	WP_041442530
306	GT2.hmm	-	glycosyl transferase	95	0.00E+00	90	SEG79500
321	GT2.hmm	-	glycosyltransferase family 2 protein	100	0.00E+00	100	WP_012851019
315	GT2.hmm	-	glycosyl transferase	100	0.00E+00	100	WP_012851009
1148	GT2.hmm	-	CDP-glycerol-- poly(glycerophosphate) glycerophosphotransferase	100	0.00E+00	100	WP_012854410
658	GT2.hmm	-	glycosyl transferase	100	0.00E+00	100	WP_012851015
430	GT2.hmm	-	glycosyltransferase family 2 protein	98	0.00E+00	100	WP_083789964
381	GT4.hmm	-	glycosyl transferase	100	0.00E+00	100	WP_012853078
388	GT4.hmm	-	glycosyltransferase family 1 protein	100	0.00E+00	100	WP_012852452
381	GT4.hmm	-	glycosyltransferase family 1 protein	98	0.00E+00	99	WP_041441526
443	GT4.hmm	-	glycosyltransferase family 4 protein	100	0.00E+00	100	WP_012852806
431	GT4.hmm	-	D-inositol-3-phosphate glycosyltransferase	100	0.00E+00	100	WP_012851072
452	GT4.hmm	-	glycosyltransferase family 1 protein	100	0.00E+00	100	WP_012853975

404	GT4.hmm	-	glycosyltransferase family 1 protein	100	0.00E+00	100	WP_012850472
290	GT14.hmm	-	glycosyl transferase family 14	100	0.00E+00	100	WP_012851388
470	GT20.hmm	α,α -trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.15)	trehalose-6-phosphate synthase	100	0.00E+00	99	WP_083789822
595	GT39.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012851347
773	GT51.hmm	-	glycosyl transferase family 51	100	0.00E+00	100	WP_012851396
265	GT81.hmm	-	glycosyl transferase family 2	100	0.00E+00	100	WP_012850508
504	GT83.hmm	-	hypothetical protein	100	0.00E+00	100	WP_012854498
429	GT87.hmm	-	DUF2029 domain-containing protein	100	0.00E+00	100	WP_012850510
404	GT94.hmm	-	glycosyltransferase family 1 protein	100	0.00E+00	100	WP_012850472
327	PL1.hmm	pectate lyase (EC 4.2.2.2)	pectate lyase	100	0.00E+00	100	WP_012852783
616	PL22_1.hmm	-	hypothetical protein	100	0.00E+00	99	WP_086014605

¹ The name of the enzyme differs between the CAZy databases and non-redundant NCBI proteins.