

Wastewater from the edible oil industry as a potential source of lipase- and surfactant-producing actinobacteria

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Supplementary information

Lipase and esterase sequences annotated for strains BT3 and BT4

>BT3_putative_lipase_esterase

MGSSRASRPGRGRAGASRTLGRGPCTAEQGPAGPGVAPGPGPSWAGPGPGQGPTGPQYGRAEAAS
RAEEDDGGRSAERGGARGGGGELPVRAPGGGAGHHGGVVRPGPGPGGGLLRPARSGRGTGHAAG
RGGARRGVAGRARPAHLAVRGVPGGARVRGGERGVPAQRRAGRRLADTFDDIAAAFDALP
ELAAEAVPEADPGRTVLTGHSAGGHLALWAAARHVLPAGSPWRLPEAPAVRGVVALAPIADFAT
SAELNVCGGAFAQLLGEYEERLAHADPTALLPTGMATTLVQGTVDTEVPPAVAEAYADAATAA
GETPGFTLVGVDVGHFPLIDPASAACALVAEEIAQLAW

>BT3_putative_esterase

MSTMWQGCCLAHTDYFEMRSGGGHDYGIWVTPPGYDAAVAQAPVVYVLDGNWTVGLTAPLIVT
QLDPMQSIRPYIQVSVGYAGKEAEHWERLRNRDLVPPGEPIAKEYVDAVEMSVETGTTTRDQADA
YLAELSNSRGMFLDFTDDLHPRIARDWGAAPNGHGLFGYSYGGFLSLYAWLTRSTFFESVGAGS
PGVVDTSQVFARLQAMGDALPATRLHVTFNERELLGDIQNLAKNAATFLHRLTARGGPVTS
ALLHETHVTGLQASFLSYLRTCRAQ

>BT3_lipase

MQSTPRTGTTTPPTRRTRRLAGTAAVAAVVSLTTLSTPGAHAADNPYERGPAPTRASIEAPRG
PYAVSQTSSVLLVSGFGGGTIYYPTSTSDGTFGAVVVTPGFTATESSMAWLGPRLASQGFVFTIDT
LTTLDQPDSRGRQMLAALDYLTERSSARTRIDGTRLGVIGHSMGGGGTLEAAKSRLKAAIPLTPW
NLDKWTPEVTTPTLVVGADGDTVAPVATHAKPFYSTLPSTTDRAYLELNNATHFAPNISNTTIKY
SVSWLKRFIDDTRYEQFLCPLPEPDRDIEEYRGTCPSVADGRPLARPKWRTARFRTGLRTRNLPGM
TGEESALPTVRLHGRAPQLSRIRAWWHQPPAHRSAALLVAGEPGLGRTAVLRWAARALGADSTGH
LVAGPAPA

>BT3_esterase_lipase

MPAPCLVWFHGGGMVLGTPETDDARVSAYARDVGCVVVSAEYRPAEPHPVPVEDCYRALGW
TAGQAKALGVDPHRLAVGGISAGGGLAAATALLARDRGGPALAFQLLCPMLDDRNTTPSSREFS
RAVAWPRADNLFGWSALLGPLAGTGRVPPHAAPARAADLSGLPAASVDVGELEVFRDECARYAL
RLAEAGVPAELRLSPGAFHGFDFGILPQVTLSRRAAAEQVAALRRALGGC

>BT3_putative_esterase

MNDTAEATGHPAPDEQDPAPEPVAHVHGTVAPGYEPVRDAFARNFAQLGDRGAAVTVHRHGSPV
VDLWAGTRDHDSTAPWERGTAQVVHVSVTKGVSAAAALLLHQGRGLDLDAPVSTYWPEYAAEGK
ERTLVRHLLAHRAGVPVLDRLTPDEAAHPGTGAAAVAAQAPVWEPGTEHGYHAQTYSWLTGE
LVRRVTGISLGRYVAEEIAGPLGLDLWIGLPPAQKDRVGRSGAVSAPERGGGLRLRPRNVQDAYG
DPASLTRRAFDVDPADENSPAYHAAELPGANGIATAYALSRFYASLIGAVEQGPRLFAPATLAL
ARTVESEGPDRVLVVPTRFGPGFMLHGAASPLLAEGSFHGHPGRGGSGLGFADPESGVAFGYVTNGLQ
KTVTNDPRAQALVRAVRGVLCG

>BT3_putative_lipase

MASQLPPPPDPYLETAAKELAEATDPHPRIYEVPPAQGRDILAGLQSGEGVERPEVDEEWVTVDAG
QWGQVRTRIIRPKGATGPLPVFYIHGAGWVFGDENTHDLRFRELTGAGAAGVFPVYDRAPEAQ
YPTQVEQNYAVGQWVLQGAEHGLDTSRIA VTGESVGGAMSAVF AIMNKERGGIDLCGQVLLYP
VANADFGTPSYLQFAEGYYLTRDGMKWFWDQYAPNPAHRTEVYASPLQATTEQLRGLPPALVVT
DEADVLRDEGEAYAARLREAGVDVTAVRVAGMVHDFLLDSLRLDTRAANVARHLAIDALTKAL
HD

>BT3_putative_lipase

MLYSPGLQVSRTLGTATAIELASRGYVVVAVDHTYEAPAVEFPGGRVEPQQPMSGTGDLKKMVET
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YDDTDFLPVAREGLDRPFMLMGKPGQSHLVKASWRSFWDRSTGWKRDLSLTRGSHFSYTDASQSFV
PALDEHLDIPGPLREQYIGTVDPVRSTAAQRAYIAAFFDQHLRQRPQELLDGPAAHPEVRFVD

>BT3_putative_esterase

MSTSRRPTRRGVLKAAAGLTATTALGATSVLASASAAHAAGDGFGLRIVDRNESDARMWYYRFAT
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PAGWYSNPVSSNVGPRNWETFHIAQLLPWIDANFRTYAEYDGRAVSGFSMGGFGALKYAAKYYG
HFASVSSHSGPASLRRDAGLVTHWANVSSAAVELGGGTVYGAPLWDEARVSADNPVQRVESYRN
KRVFLVAGTSPDPVNWFDTVNETQVLAGQREFKSVLGAAGIPHEGHEVPGGHFVRPDLFIRDLDGI
VARLRKA

>BT3_putative_esterase

MCTVEIGGWADEGFGGVADVRENFDVFGELGTAVSVRAGGRPVELWGGVADERSGRPWDQE
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VSFGEITEWTPVVRAIEEQRLWEPGEAYEYHGHVFGFLVGEVIRITGLTPGRFFREAVGGPLGLRT
WIGLPAAERGLARLVEAEGRPAGDPQSLLMRIVTMNGALVFPGLEEPHGFNDPELLGTLPAGAG
AVASASGLAALYGA AVTGLDGGPRLSEETLDAVREVSAGPTWQGYDLGQRWGSGLLDSEPR
PMLGGRSFGNDGAGGQFAFGDDEFGVGFAVANRMIGHGDDRANRLITALRGSLKA

>BT3_putative_esterase_lipase

MPVLPGAEPYRHDGGPTGVLLCHGFTGTPQSMRPWAEDLAARGHTVSLPLPGHGTRWEDLQLT
GWQDWYAEVDRALGELLARCERYVAGLSMGGALALRLAARHGDAVRGVVVVNPANKVHGLS
AYALPAARHLVRTTKGLVSDIALEGSEEVGYHRVPLHAAHSLRNFFRLVDAELPQVTQPLLLRSR
DHVVPADSARVLGRVSSRDVTEILLQNSFHVATLDHDAPRVFEESAFLARTGANGADSRPEGEA
VSG

>BT4_putative_esterase

MSTMWQGCLAHTDYFEMRSGGGHDYGIWVTPPGHDAAVAQAPVVYVLDGNWTVGLTAPLIVT
QLDPMQSIQVYQVSVGYAGKEAEHWERLRNRDLVPPGEPIAKEYVDAVEMSVETGTTTRDQADA
YLAELSNSRGMFLDFTDDLHPRIARDWGAAPNGHGLFGYSYGGGLFSLYAWLTRSTFFESVGAGS

PGVVDTSQVFARLQAMGDALPATRLHVTFNERELLGDIQVYQNLAKNAATFLHRLTARGGPVTS
ALLHETHVTGLQASFLSYLRTCRAQ

>BT4_putative_esterase

MCTVEIGGWADEGFGGVADVDFRENFDFVFGELGTAVSVRAGGRPVELWGGVADERSGRPWDQE
TVVPVFSCAKGLVSIHAHLLAQQGRLLDAPVAAYWPEFAAEGKERITTRMVLGHRAGVPVLDRT
VSFGEITEWTPVVRAIEEQRPLWEPGEAYEYHGHVFGFLVGEVIRITGLTPGRFFREAVGGPLGLRA
WIGLPAAERGLARLVEAEGRPAGDPQSLLMRIVTMNGALVFPGLEEPHGFNDPELLGTPLGAG
AVASASGLAALYGA AVTGLDGGPRLLSEETLDAVREVSAGPTWQGYDLGQRWGSGLDSDGRPR
PMLGGRSFGNDGAGGQFAFGDDEFVGFAYVANRMIGHGDDRANRLITALRGSKA

>BT4_putative_lipase_esterase

MGAARSAAEREAEESSLFHPEAAPDTPVAYGPDQVDFYAPRGPGAAPGTPLVVVVHGA
WRAAHDRHLHISFPAFLAGRGFAVASVEYRRGNGGQVAGRWPDTFDDIAAFDALPELAAEAVP
EADPGRTVLTGHSAGGHLALWAAARHVLPAAGSPWRLPEAPAVRGVVALAPIADFATSALNVCG
GAFAQLLGEEYEERLAHADPTALLPTGMATTLVQGTVDTEVPPAVAEAYADAATAAGETPGFTLV
DGVGHFPLDPASAACALVAEEIAQLAW

>BT4_lipase

MQSTPRTGTTTTPPTRTRTRRLAGTAAVA AVVSLTTLSTPGAHAADNPYERGPAPTRASIEAPRG
PYAVSQTSVSLLVSGFGGGTIYYPTSTSDGTFGAVVVTPGFTATESSMAWLGPRLASQGFVFTIDT
LTTLDQPDSRGRQMLAALDYLTERSSARTRIDGTRLGVIGHSMGGGGTLEAAKSRLKAAIPLTPW
NLDKTWPEVTTPTLVVGADGDTVAPVATHAKPFYSTLPSTTDRAYLELNNATHFAPNISNTTIKY
SVSWLKRFIDDTRYEQFLCPLPEPDRDIEEYRGTCPSVADGRPLARPKWRTARFRTGLRTRNLPGM
TGEESALPTVRLHGRAPQLSRIRAWWHQPPAHRSAALLVAGEPGLGRTAVLRWAARALGADSTGH
LVAGRPPPHQDV

>BT4_esterase_lipase

MVSAEYRPAPEHPVPVEDCYRALGWTAGQAKALGVDPHRLAVGGISAGGGLAAATALLARD
RGGPALAFQLLCPMLDDRNTTPSSREFSRAVAWPRADNLFGWSALLGPLAGAGRVPPHAAPAR
AADLSGLPAASVDVGELEVRDECARYALRLAEAGVPAELRLSPGAFHGFDFGALPQVTLSSRAAA
EQVAALRRALGGC

>BT4_putative_esterase

MSTSRPTRRGVLKAAAGLTATTALGATSVLASASAAHAAGDGFGLRIVDRNESDARMWYYRFAT
DAIGWDPGVNVLLPDGYHAGGRRYPVLYLFHGGGTGQDFITFDRMGIRAWTAGKPLIVVMPDGG
PAGWYSNPVSSNVGPRNWETFHIAQLLPWIDANFRTYAEYDGRAVSGFSMGGFGALKYAAKYYG
HFASVSSHSGPASLRDAGLVTHWANVSSAAVELGGGTVYGAPLWDEARVSADNPVQRVESYRN
KRVFLVAGTSPDPVNWFDTVNETQVLQAGQREFKSVLGAAGIPHEGHEVPGGHFVRPDLFIRDLGI
VARLRKA

>BT4_putative_esterase_lipase

MPVLPGAEPYRHDGGPTGVLLCHGFTGTPQSMRPWAEDLAARGHTVSLPLLPGHGTRWEDLQLT
GWQDWYAEVDRLGELLARCERYVAGLSMGGALALRLAARHGDAVRGVVVVNPANKVHGLS
AYALPAARHLVRTTKGLVSDIALEGSEEVGYHRVPLHAAHSLRNFFRLVDAELPQVTQPLLLRSR
DHVPPADSARVLGRVSSRDVTEILLQNSFHVATLDHDA PRVFEESSAFLARTGANGADSRPEGEA
VSG

>BT4_putative_esterase

MNDTAEATGHPAPDEQDPAPPEPVAHVHGTVA PGYEPVRDAFARNFAQLGDRGAAVTVHRHGSPV
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ERTLVRHLLAHRAGVPVLD RPLTPDEAAHPGTGAAAVAAQAPVWEPGTEHGYHAQTYSWLTGE
LVRRVTGISLGRYVAEEIAGPLGLDLWIGLPPAQKDRVGRSGAVSAPERGGGLRLRPRRNVQDAYG
DPASLTRRAFDVADPPADENSPAYHAAELPGANGIATAYALSRFYASLIGAVEQGPRLFAPATLAL
ARTVESEGPDRVLVVPTRFGPGFMLHGAASPLLAEGSFGHPGRGGS LGFADPESGVAFGYVTNGLQ
KTVTNDPRAQALVRAVRGV LQG

>BT4_putative_lipase

MLYSPGLQVSRTLGTATAIELASRGYVVVA VDHTYEAPAVEFPGGRVEPQQPMSGTGDLKKMVET
RVGDTRFVLDQLATGRGLPERLGKALDLERVGMYGHSGGGATAAEAMRVDRRIDAGINMDGTLQ
YDDTDFLPVAREGLDRPFMLMGKPGQSHLVKASWRSFWDRSTGWKRDL SLTRGSHFSYTDAQSFV
PALDEHLDIPGPLREQYIGTVDPVRSTAAQRAYIAAFFDQH LRQRPQELLDGPSAAHPEVRFVD

>BT4_putative_lipase

MASQLPPPPDPYLETAAKELAEATD PHPRIYEVPPAQGRDILAGLQSGEGVERPEVDEEWVTVDAG
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YPTQVEQNYAVGQWVLQHGAEHGLDTSRIAVTGESVGGAMSAVF AIMNKERGGIDLKGQVLLYP
VANADFGTPSYLQFAEGYYLTRDGMKWFWDQYAPNPAHRTEVYASPLQATTEQLRGLPPALVVT
DEADVLRDEGEAYAARLREAGVDVTAVRVAGMVHDFLLDSL RDTAANVARHLAIDALTKAL
HD

Supplementary Table S1: Lipases and esterases detected within the annotated genomes of BT3 and BT4. Export signals were detected through SignalP-5.0 analysis.

Strain	Lipase/Esterase	BLASTp top hit	SignalP likelihood
BT3	Putative lipase/esterase	<i>Streptomyces</i> alpha/beta hydrolase	0.67 (other)
	Putative esterase/lipase	<i>Streptomyces</i> alpha/beta hydrolase	0.97 (other)
	Lipase	<i>Streptomyces</i> diene lactone hydrolase	0.60 (TAT)
	Esterase/lipase	<i>Streptomyces</i> alpha/beta hydrolase	0.70 (other)
	Putative esterase	<i>Streptomyces</i> serine hydrolase	0.96 (other)
	Putative lipase	<i>Streptomyces</i> alpha/beta hydrolase	0.98 (other)
	Putative lipase	<i>Streptomyces</i> lipase	0.88 (other)
	Putative esterase	<i>Streptomyces</i> esterase	0.93 (TAT)
	Putative esterase	<i>Streptomyces</i> beta-lactamase	0.98 (other)
	Putative esterase	<i>Streptomyces</i> alpha/beta hydrolase	0.96 (other)
BT4	Putative esterase	<i>Streptomyces</i> alpha/beta hydrolase	0.97 (other)
	Putative esterase	<i>Streptomyces</i> beta-lactamase	0.98 (other)
	Putative lipase/esterase	<i>Streptomyces</i> alpha/beta hydrolase	0.96 (other)
	Lipase	<i>Streptomyces</i> diene lactone hydrolase	0.60 (TAT)
	Esterase/lipase	<i>Streptomyces</i> alpha/beta hydrolase	0.82 (other)
	Putative esterase	<i>Streptomyces</i> esterase	0.93 (TAT)
	Putative esterase/lipase	<i>Streptomyces</i> alpha/beta hydrolase	0.97 (other)
	Putative esterase	<i>Streptomyces</i> serine hydrolase	0.96 (other)
	Putative lipase	<i>Streptomyces</i> lipase	0.88 (other)
	Putative lipase	<i>Streptomyces</i> alpha/beta hydrolase	0.98 (other)

TAT = Twin arginine translocation signal peptide

Supplementary Table S2: Biosynthetic gene clusters detected within the genome sequences of *Streptomyces* sp. BT3 and *Streptomyces* sp. BT4.

Biosynthetic gene cluster	BT3 (number of clusters present)	BT4 (number of clusters present)
Butyrolactone	1	1
Ectoine	1 1x 100% match: ectoine	1 1x 100% match: ectoine
Lanthipeptide class III	2	2
Lasso peptide	1	1
Linear azol(in)e-containing peptides (LAP)	1	1
Non-ribosomal peptide synthetase (NRPS)	20 1x 100% match: rhizomide A/B/C	16
NRPS-like	4	3
NRPS/RRE-containing	-	1
NRPS/T1PKS	3	2
RRE-element containing cluster (RRE-containing)	2	-
Other unspecified ribosomally synthesised and post-translationally modified peptide product (RiPP) cluster (RiPP-like)	2	2
Siderophore	3 1x 100% match: desferrioxamin	3 1x 100% match: desferrioxamin
Terpene	8 1x 100% match: geosmin	6 1x 100% match: geosmin
Trans-AT-PKS	-	1
Type 1 Polyketide synthase (T1PKS)	23 1x 100% match: 1-heptadecene	24 1x 100% match: 1-heptadecene
T1PKS/terpene	-	1
Type 3 Polyketide synthase (T3PKS)	1	1

Supplementary Table S3: CAzymes predicted to be present in the genomes of *Streptomyces* sp. BT3 and *Streptomyces* sp. BT4 (predicted by dbCAN2). Only CAzymes predicted by all three algorithms are listed.

CAzymes predicted	<i>Streptomyces</i> sp. BT3	<i>Streptomyces</i> sp. BT4
Auxiliary activity family 3 cellobiose dehydrogenase; glucose 1-oxidase; aryl alcohol oxidase; alcohol oxidase; pyranose oxidase	AA3 (1)	AA3 (1)
Auxiliary activity family 10 Copper-dependent lytic polysaccharide monooxygenases (LPMOs); some proteins have been shown to act on chitin, others on cellulose; lytic cellulose monooxygenase (C1-hydroxylating); lytic cellulose monooxygenase (C4-dehydrogenating); lytic chitin monooxygenase; lytic xylan monooxygenase / xylan oxidase (glycosidic bond-cleaving)	AA10 (3)	AA10 (3)
Carbohydrate-binding module family 2 This module has been found to bind cellulose, chitin or xylan	CBM2 (2)	CBM2 (2)
Carbohydrate-binding module family 3 Binds to cellulase; one report of binding to chitin	CBM3 (1)	CBM3 (1)
Carbohydrate-binding module 6 The cellulose-binding function has been demonstrated in one case on amorphous cellulose and β -1,4-xylan. Some of these modules also bind β -1,3-glucan, β -1,3-1,4-glucan, and β -1,4-glucan.	CBM6 (2)	CBM6 (2)
Carbohydrate-binding module 13 Often found in association with xylanase	CBM13 (4)	CBM13 (4)
Carbohydrate-binding module family 20 Starch-binding CBM, strongly interacts with cyclodextrins	CBM20 (1)	CBM20 (1)
Carbohydrate-binding module family 32 Binds galactose and lactose, polygalacturonic acid, and LacNAc (β -D-galactosyl-1,4- β -D-N-acetylglucosamine)	CBM32 (3)	CBM32 (2)

CAzymes predicted	<i>Streptomyces</i> sp. BT3	<i>Streptomyces</i> sp. BT4
Carbohydrate-binding module family 35 Binds to xylan, mannoooligosacchardies, β -galactan	CBM35 (1)	CBM35 (1)
Carbohydrate-binding module family 42 Found mostly at the C-terminus of GH54 catalytic domains; binds to arabinofuranose	CBM42 (1)	CBM42 (1)
Carbohydrate-binding module family 48 Glycogen-binding module usually in association with GH13 modules	CBM48 (1)	CBM48 (2)
Carbohydrate esterase family 1 acetyl xylan esterase; cinnamoyl esterase; feruloyl esterase; carboxylesterase; S-formylglutathione hydrolase; diacylglycerol O-acyltransferase; trehalose 6-O-mycolyltransferase	CE1 (1)	CE1 (1)
Carbohydrate esterase family 4 acetyl xylan esterase; chitin deacetylase; chitooligosaccharide deacetylase; peptidoglycan GlcNAc deacetylase; peptidoglycan N-acetylmuramic acid deacetylase	CE4 (3)	CE4 (3)
Carbohydrate esterase family 7 acetyl xylan esterase; cephalosporin-C deacetylase	CE7 (1)	CE7 (1)
Carbohydrate esterase family 9 N-acetylglucosamine 6-phosphate deacetylase; N-acetylglucosamine 6-phosphate deacetylase	CE9 (1)	CE9 (1)
Carbohydrate esterase family 14 N-acetyl-1-D-myo-inositol-2-amino-2-deoxy- α -D-glucopyranoside deacetylase; diacetylchitobiose deacetylase; mycothiol S-conjugate amidase	CE14 (2)	CE14 (2)
Glycoside hydrolase family 1	GH1 (4)	GH1 (4)

CAzymes predicted	<i>Streptomyces</i> sp. BT3	<i>Streptomyces</i> sp. BT4
β-glucosidase; β-galactosidase; β-mannosidase; β-glucuronidase; β-xylosidase; β-D-fucosidase; phlorizin hydrolase; exo-β-1,4-glucanase; 6-phospho-β-galactosidase; 6-phospho-β-glucosidase; strictosidine β-glucosidase; lactase; amygdalin β-glucosidase; prunasin β-glucosidase; vicianin hydrolase; raucaffricine β-glucosidase; thioglucosidase; β-primeverosidase; isoflavonoid 7-O-β-apiosyl-β-glucosidase; ABA-specific β-glucosidase; DIMBOA β-glucosidase; β-glycosidase; hydroxyisourate hydrolase; β-rutinosidase /α-L-rhamnose-(1,6)-β-D-glucosidase		
Glycoside hydrolase family 2 β-galactosidase; β-mannosidase; β-glucuronidase; α-L-arabinofuranosidase; mannosylglycoprotein endo-β-mannosidase; exo-β-glucosaminidase; α-L-arabinopyranosidase; β-galacturonidase; β-xylosidase; β-D-galactofuranosidase; β-glucosidase	GH2 (2)	GH2 (2)
Glycoside hydrolase family 3 β-glucosidase; xylan 1,4-β-xylosidase; β-glucosylceramidase; β-N-acetylhexosaminidase; α-L-arabinofuranosidase; glucan 1,4-β-glucosidase; isoprimeverose-producing oligoxyloglucan hydrolase; coniferin β-glucosidase; exo-1,3-1,4-glucanase; β-N-acetylglucosaminide phosphorylases; β-1,2-glucosidase; β-1,3-glucosidase; xyloglucan-specific exo-β-1,4-glucanase / exo-xyloglucanase	GH3 (5)	GH3 (6)
Glycoside hydrolase family 4 maltose-6-phosphate glucosidase; α-glucosidase; α-galactosidase; 6-phospho-β-glucosidase; α-glucuronidase; α-galacturonase; palatinase	GH4 (2)	GH4 (2)
Glycoside hydrolase family 5	GH5 (0)	GH5 (1)

CAzymes predicted	<i>Streptomyces</i> sp. BT3	<i>Streptomyces</i> sp. BT4
endo- β -1,4-glucanase / cellulase; endo- β -1,4-xylanase; β -glucosidase; β -mannosidase; β -glucosylceramidase; glucan β -1,3-glucosidase; exo- β -1,4-glucanase / cellodextrinase; glucan endo-1,6- β -glucosidase; mannan endo- β -1,4-mannosidase; cellulose β -1,4-cellobiosidase; steryl β -glucosidase; endoglycoceramidase; chitosanase; β -primeverosidase; xyloglucan-specific endo- β -1,4-glucanase; endo- β -1,6-galactanase; β -1,3-mannanase; arabinoxylan-specific endo- β -1,4-xylanase; mannan transglycosylase; lichenase / endo- β -1,3-1,4-glucanase; β -glycosidase; endo- β -1,3-glucanase / laminarinase; β -N-acetylhexosaminidase; chitosanase; β -D-galactofuranosidase; β -galactosylceramidase; β -rutinosidase / α -L-rhamnose-(1,6)- β -D-glucosidase; α -L-arabinofuranosidase; glucomannan-specific endo- β -1,4-glucanase		
Glycoside hydrolase family 6 endoglucanase; cellobiohydrolase; lichenase / endo- β -1,3-1,4-glucanase	GH6 (4)	GH6 (3)
Glycoside hydrolase family 10 endo-1,4- β -xylanase; endo-1,3- β -xylanase; tomatinase; xylan endotransglycosylase; endo- β -1,4-glucanase	GH10 (1)	GH10 (1)
Glycoside hydrolase family 13	GH13 (10)	GH13 (10)

CAzymes predicted	<i>Streptomyces</i> sp. BT3	<i>Streptomyces</i> sp. BT4
α -amylase; pullulanase; cyclomaltodextrin glucanotransferase; cyclomaltodextrinase; trehalose-6-phosphate hydrolase; oligo- α -glucosidase; maltogenic amylase; neopullulanase; α -glucosidase; maltotetraose-forming α -amylase; isoamylase; glucodextranase; maltohexaose-forming α -amylase; maltotriose-forming α -amylase; branching enzyme; trehalose synthase; 4- α -glucanotransferase; maltopentaose-forming α -amylase; amylosucrase; sucrose phosphorylase; malto-oligosyltrehalose trehalohydrolase; isomaltulose synthase; malto-oligosyltrehalose synthase; amylo- α -1,6-glucosidase; α -1,4-glucan: phosphate α -maltosyltransferase; amino acid transporter; [retaining] sucrose 6(F)-phosphate phosphorylase; [retaining] glucosylglycerol phosphorylase; Glucosylglycerate phosphorylase; [retaining] sucrose α -glucosidase; oligosaccharide α -4-glucosyltransferase; [retaining] α -amylase		
Glycoside hydrolase family 15 glucoamylase; glucodextranase; α,α -trehalase; dextran dextrinase	GH15 (2)	GH15 (1)
Glycoside hydrolase family 16 xyloglucan:xyloglucosyltransferase; keratan-sulfate endo-1,4- β -galactosidase; endo-1,3- β -glucanase / laminarinase; endo-1,3(4)- β -glucanase; licheninase; β -agarase; κ -carrageenase; xyloglucanase; endo- β -1,3-galactanase; [retaining] β -porphyranase; hyaluronidase; endo- β -1,4-galactosidase; chitin β -1,6-glucanosyltransferase; β -transglycosidase; β -glycosidase; β -carrageenase	GH16 (1)	GH16 (1)
Glycoside hydrolase family 18 chitinase; lysozyme; endo- β -N-acetylglucosaminidase; peptidoglycan hydrolase with endo- β -N-acetylglucosaminidase specificity; Nod factor hydrolase; xylanase inhibitor; concanavalin B; narbonin	GH18 (3)	GH18 (5)
Glycoside hydrolase family 19 Chitinase; lysozyme	GH19 (3)	GH19 (3)

CAzymes predicted	<i>Streptomyces</i> sp. BT3	<i>Streptomyces</i> sp. BT4
Glycoside hydrolase family 20 β -hexosaminidase; lacto-N-biosidase; β -1,6-N-acetylglucosaminidase; β -6-SO ₃ -N-acetylglucosaminidase	GH20 (2)	GH20 (2)
Glycoside hydrolase family 23 (lysozyme type G, peptidoglycan lyase, chitinase)	GH23 (3)	GH23 (3)
Glycoside hydrolase family 25 Lysozyme	GH25 (3)	GH25 (3)
Glycosyl hydrolase family 32 invertase; endo-inulinase; β -2,6-fructan 6-levanbiohydrolase; endo-levanase; exo-inulinase; fructan β -(2,1)-fructosidase/1-exohydrolase; fructan β -(2,6)-fructosidase/6-exohydrolase; sucrose:sucrose 1-fructosyltransferase; fructan:fructan 1-fructosyltransferase; sucrose:fructan 6-fructosyltransferase; fructan:fructan 6G-fructosyltransferase; levan fructosyltransferase; [retaining] sucrose:sucrose 6-fructosyltransferase (6-SST); cycloinulo-oligosaccharide fructanotransferase	GH32 (1)	GH32 (2)
Glycoside hydrolase family 33 sialidase or neuraminidase; trans-sialidase; anhydrosialidase; Kdo hydrolase; 2-keto-3-deoxynononic acid hydrolase / KDNase	GH33 (1)	GH33 (1)
Glycoside hydrolase family 43 β -xylosidase; α -L-arabinofuranosidase; xylanase; α -1,2-L-arabinofuranosidase; exo- α -1,5-L-arabinofuranosidase; [invertig] exo- α -1,5-L-arabinanase; β -1,3-xylosidase; [invertig] exo- α -1,5-L-arabinanase; [invertig] endo- α -1,5-L-arabinanase; exo- β -1,3-galactanase; β -D-galactofuranosidase	GH43 (1)	GH43 (1)
Glycoside hydrolase family 46 chitosonase	GH46 (1)	GH46 (1)
Glycoside hydrolase family 55	GH55 (1)	GH55 (1)

CAzymes predicted	<i>Streptomyces</i> sp. BT3	<i>Streptomyces</i> sp. BT4
exo- β -1,3-glucanase; endo- β -1,3-glucanase		
Glycoside hydrolase family 62 α -L-arabinofuranosidase	GH62 (1)	GH62 (0)
Glycoside hydrolase family 63 processing α -glucosidase; α -1,3-glucosidase; α -glucosidase; mannosylglycerate α -mannosidase / mannosylglycerate hydrolase; glucosylglycerate hydrolase	GH63 (1)	GH63 (1)
Glycoside hydrolase family 64 β -1,3-glucanase	GH64 (1)	GH64 (1)
Glycoside hydrolase family 65 α , α -trehalase; maltose phosphorylase; trehalose phosphorylase; kojibiose phosphorylase; trehalose-6-phosphate phosphorylase; nigerose phosphorylase; 3-O- α -glucopyranosyl-L-rhamnose phosphorylase; 2-O- α -glucopyranosylglycerol: phosphate β -glucosyltransferase; α -glucosyl-1,2- β -galactosyl-L-hydroxylysine α -glucosidase; 1,3- β -oligoglucan phosphorylase	GH65 (4)	GH65 (3)
Glycoside hydrolase family 77 amylomaltase or 4- α -glucanotransferase	GH77 (1)	GH77 (1)
Glycoside hydrolase family 81 endo- β -1,3-glucanase	GH81 (1)	GH81 (1)
Glycoside hydrolase family 84 (N-acetyl β -glucosaminidase; hyaluronidase; [protein]-3-O-(GlcNAc)-L-Ser/Thr β -N-acetylglucosaminidase	GH84 (2)	GH84 (2)
Glycoside hydrolase family 87 mycodextranase; α -1,3-glucanase	GH87 (1)	GH87 (1)
Glycoside hydrolase family 114 endo- α -1,4-polygalactosaminidase	GH114 (1)	GH114 (1)
Glycoside hydrolase family 158	GH158 (1)	GH158 (1)

CAzymes predicted	<i>Streptomyces</i> sp. BT3	<i>Streptomyces</i> sp. BT4
endo- β -1,3-glucanase		
<p>Glycosyltransferase family 1</p> <p>(UDP-glucuronosyltransferase; zeatin O-β-xylosyltransferase; 2-hydroxyacylsphingosine 1-β-galactosyltransferase; N-acylsphingosine galactosyltransferase; flavonol 3-O-glucosyltransferase; anthocyanidin 3-O-glucosyltransferase; sinapate 1-glucosyltransferase; indole-3-acetate β-glucosyltransferase; flavonol L-rhamnosyltransferase; sterol glucosyltransferase; UDP-Glc: 4-hydroxybenzoate 4-O-β-glucosyltransferase; zeatin O-β-glucosyltransferase; limonoid glucosyltransferase; UDP-GlcA: baicalein 7-O-β-glucuronosyltransferase; UDP-Glc: chalcone 4'-O-β-glucosyltransferase; ecdysteroid UDP-glucosyltransferase; salicylic acid β-glucosyltransferase; anthocyanin 3-O-galactosyltransferase; anthocyanin 5-O-glucosyltransferase; dTDP-β-2-deoxy-L-fucose: α-L-2-deoxyfucosyltransferase; UDP-β-L-rhamnose: α-L-rhamnosyltransferase; zeaxanthin glucosyltransferase; UDP-Glc: flavone-6-C-glucosyltransferase; UDP-Glc: cinnamate β-glucosyltransferase; UDP-Glc: hydroxycinnamic acid O-β-glucosyltransferase; UDP-Glc: cinnamoyl O-β-glucosyltransferase; UDP-Arap: flavone-C-arabinosyltransferase</p>	GT1 (3)	GT1 (3)
<p>Glycosyltransferase family 2</p> <p>cellulose synthase; chitin synthase; dolichyl-phosphate β-D-mannosyltransferase; dolichyl-phosphate β-glucosyltransferase; N-acetylglucosaminyltransferase; N-acetylgalactosaminyltransferase; hyaluronan synthase; chitin oligosaccharide synthase; β-1,3-glucan synthase; β-1,4-mannan synthase; β-mannosylphosphodecaprenol-mannooligosaccharide α-1,6-mannosyltransferase; UDP-Galf: rhamnopyranosyl-N-acetylglucosaminyl-PP-decaprenol β-1,4/1,5-galactofuranosyltransferase; UDP-Galf: galactofuranosyl-galactofuranosyl-rhamnosyl-N-acetylglucosaminyl-PP-decaprenol β-1,5/1,6-galactofuranosyltransferase; dTDP-L-Rha: N-acetylglucosaminyl-PP-decaprenol α-1,3-L-rhamnosyltransferase; alternating β-1,3/4-N-acetylmannan synthase</p>	GT2 (6)	GT2 (5)

CAzymes predicted	<i>Streptomyces</i> sp. BT3	<i>Streptomyces</i> sp. BT4
<p>Glycosyltransferase family 4</p> <p>sucrose synthase; sucrose-phosphate synthase; α-glucosyltransferase; lipopolysaccharide N-acetylglucosaminyltransferase; phosphatidylinositol α-mannosyltransferase; GDP-Man: Man1GlcNAc2-PP-dolichol α-1,3-mannosyltransferase; GDP-Man: Man3GlcNAc2-PP-dolichol/Man4GlcNAc2-PP-dolichol α-1,2-mannosyltransferase; digalactosyldiacylglycerol synthase; 1,2-diacylglycerol 3-glucosyltransferase; diglucosyl diacylglycerol synthase; trehalose phosphorylase; NDP-Glc: α-glucose α-glucosyltransferase / α,α-trehalose synthase; GDP-Man: Man2GlcNAc2-PP-dolichol α-1,6-mannosyltransferase; UDP-GlcNAc: 2-deoxystreptamine α-N-acetylglucosaminyltransferase; UDP-GlcNAc: ribostamycin α-N-acetylglucosaminyltransferase; UDP-Gal α-galactosyltransferase; UDP-Xyl α-xylosyltransferase; UDP-GlcA α-glucuronyltransferase; UDP-Glc α-glucosyltransferase; UDP-GalNAc: GalNAc-PP-Und α-1,3-N-acetylgalactosaminyltransferase; UDP-GalNAc: N,N'-diacetylbaucosaminyl-PP-Und α-1,3-N-acetylgalactosaminyltransferase; ADP-dependent α-maltose-1-phosphate synthase</p>	GT4 (6)	GT4 (6)
<p>Glycosyltransferase family 9</p> <p>lipopolysaccharide N-acetylglucosaminyltransferase; heptosyltransferase</p>	GT9 (1)	GT9 (2)
<p>Glycosyltransferase family 20</p> <p>α,α-trehalose-phosphate synthase [UDP-forming]; Glucosylglycerol-phosphate synthase; trehalose-6-P phosphatase; [retaining] GDP-valeniol: validamine 7-phosphate valeniolyltransferase</p>	GT20 (1)	GT20 (1)
<p>Glycosyltransferase family 28</p> <p>1,2-diacylglycerol 3-β-galactosyltransferase; 1,2-diacylglycerol 3-β-glucosyltransferase; UDP-GlcNAc: Und-PP-MurAc-pentapeptide β-N-acetylglucosaminyltransferase; digalactosyldiacylglycerol synthase</p>	GT28 (2)	GT28 (2)
<p>Glycosyltransferase family 35</p>	GT35 (1)	GT35 (1)

CAzymes predicted	<i>Streptomyces</i> sp. BT3	<i>Streptomyces</i> sp. BT4
glycogen or starch phosphorylase		
Glycosyltransferase family 39 (Dol-P-Man: protein α -mannosyltransferase)	GT39 (1)	GT39 (1)
Glycosyltransferase family 51 Murein polymerase	GT51 (4)	GT51 (3)
Glycosyltransferase family 81 NDP-Glc: glucosyl-3-phosphoglycerate synthase; NDP-Man: mannosyl-3-phosphoglycerate synthase; ADP-Glc: glucosyl-2-glycerate synthase; mannosyl-3-phosphoglycerate synthase / [retaining] GDP-Man: 3-phosphoglycerate α -mannosyltransferase	GT81 (1)	GT81 (1)
Glycosyltransferase family 87 (polyprenol-P-Man: α -1,2-mannosyltransferase)	GT87 (3)	GT87 (3)
Polysaccharide lyase family 31 endo- β -1,4-glucuronan lyase; poly(β -mannuronate) lyase / M-specific alginate lyase	PL31 (1)	PL31 (1)