

**Table S5.** List of NCBI GenBank/RefSeq accession numbers for glycoside hydrolases (GHs) in *Celeribacter* genomes.

Category (CAZy GH family)	Predicted function	Identity within <i>Celeribacter</i> genomes (%)														
	(EC number)	PS-C1	P73 <sup>T</sup>	TSPH2	IMCC12053 <sup>T</sup>	LH4	DSM27375 <sup>T</sup>	DSM26471 <sup>T</sup>	DSM100434 <sup>T</sup>	NH195 <sup>T</sup>	ZXM137 <sup>T</sup>	G3M19	ASW11-22	EaN35-2	B30	HF31
Cellulose- degrading enzyme (GH1)																

PS-C1: Strain PS-C1; EaN35-2: *Celeribacter naphthalenivorans* EaN35-2; HF31: *Celeribacter* sp. HF31; NH195<sup>T</sup>: *Celeribacter ethanolicus* NH195<sup>T</sup> [27]; TSPH2: *Celeribacter ethanolicus* TSPH2 [30]; ZXM137<sup>T</sup>: *Celeribacter halophilus* ZXM137<sup>T</sup>; G3M19: *Celeribacter halophilus* G3M19; DSM100434<sup>T</sup>: *Celeribacter persicus* DSM100434<sup>T</sup> [26]; DSM26471<sup>T</sup>: *Celeribacter neptunius* DSM26471<sup>T</sup> [19]; ASW11-22: *Celeribacter* sp. ASW11-22; P73<sup>T</sup>: *Celeribacter indicus* P73<sup>T</sup> [16,24]; B30: *Celeribacter baekdonensis* B30; DSM27375<sup>T</sup>: *Celeribacter baekdonensis* DSM27375<sup>T</sup>; LH4: *Celeribacter baekdonensis* LH4 [32]; IMCC12053<sup>T</sup>: *Celeribacter marinus* IMCC12053<sup>T</sup> [25,31]. Characteristics scored as: -, absence. <sup>T</sup> type strain.

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		PS-C1	P73 <sup>T</sup>	TSPH2	IMCC12053 <sup>T</sup>	LH4	DSM27375 <sup>T</sup>	DSM26471 <sup>T</sup>	DSM100434 <sup>T</sup>	NH195 <sup>T</sup>	ZXM137 <sup>T</sup>	G3M19	ASW11-22	EaN35-2	B30	HF31	
Hemicellulose-degrading enzyme																	
	(GH2)	β-mannosidase (3.2.1.25)	-	-	WP_0968 05090.1	-	CP02847 5.1_1194	WP_0746458 74.1	-	WP_107815347.1 1	LRUC010000 45.1_116	-	-	-	-	AMR K0100 0004.1 _168	-
	(GH26)	β-1,3-xylanase (3.2.1.32)	WP_219785 562.1	-	-	-	-	-	-	-	-	-	-	-	-	-	WP_1 676002 67.1
	(GH36)	α-galactosidase (3.2.1.22)	-	-	-	-	-	-	-	-	-	LRUD0100 0026.1_120	JAHKPE0 10000030.1 _96	-	-	-	-
	(GH43)	β-xylosidase (3.2.1.37)	-	-	-	WP_06221493 9.1	-	-	-	-	-	-	-	-	-	-	-
	(GH51)	α-L- arabinofuranosidase (3.2.1.55)	-	-	-	-	-	-	-	-	-	-	-	-	JAIVLK010 000001.1_5 88	-	-

PS-C1: Strain PS-C1; EaN35-2: *Celeribacter naphthalenivorans* EaN35-2; HF31: *Celeribacter* sp. HF31; NH195<sup>T</sup>: *Celeribacter ethanolicus* NH195<sup>T</sup> [27]; TSPH2: *Celeribacter ethanolicus* TSPH2 [30]; ZXM137<sup>T</sup>: *Celeribacter halophilus* ZXM137<sup>T</sup>; G3M19: *Celeribacter halophilus* G3M19; DSM100434<sup>T</sup>: *Celeribacter persicus* DSM100434<sup>T</sup> [26]; DSM26471<sup>T</sup>: *Celeribacter neptunius* DSM26471<sup>T</sup> [19]; ASW11-22: *Celeribacter* sp. ASW11-22; P73<sup>T</sup>: *Celeribacter indicus* P73<sup>T</sup> [16,24]; B30: *Celeribacter baekdonensis* B30; DSM27375<sup>T</sup>: *Celeribacter baekdonensis* DSM27375<sup>T</sup>; LH4: *Celeribacter baekdonensis* LH4 [32]; IMCC12053<sup>T</sup>: *Celeribacter marinus* IMCC12053<sup>T</sup> [25,31]. Characteristics scored as: -, absence. <sup>T</sup> type strain.

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Starch- degrading enzyme (GH13)	$\alpha$ -amylase (3.2.1.1)	-	-	-	-	-	-	-	-	-	LRUD0100JAHKPE	-	-	AMR	-	
											0012.1_184 0100000			K0100		
											31.1_875			0009.1 _1		
(GH13)	Oligo-1,6-glucosidase (3.2.1.10)	-	-	-	-	-	-	-	-	-	-	-	-	AMR	-	
														K0100		
														0009.1 _2		
(GH13)	$\alpha$ -glucosidase (3.2.1.20)	WP_219784 593.1	WP_043871 237.1	WP_0968 05181.1	WP_06221566 0.1	CP02847 5.1_717	WP_143026706 1	WP_090058665 1	WP_107816651 1	LRUC0100 0045.1_116	LRUD0100JAHKPE 0054.1_143	WP_2245041 0100000 13.1_156	JAIVLK01 52.1	0000002.1 309	AMR K0100	WP_1 67600 630.1 _183

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