

Table S1. Entire result of similarity search for major proteins in *G. japonicas* 12-2^T culture supernatant using the Protein BLAST algorithm.

Band	Queried sequence	Hit protein			Homology	
		Protein name	Protein ID	Subjected sequence	Identity (%)	Positive (%)
A	GPEAHPWTWW	Hypothetical protein [<i>Gilvimarinus chinensis</i>]	WP_020208830.1	⁴⁴² VDEANTWSWT ⁴⁵¹	40	60
		Putative α -glucosidase [<i>Saccharophagus degradans</i>]	WP_011468976.1	³²⁵ KPGAASWSWW ³²⁴	50	70
		Endoxylanase [<i>Aeromonas caviae</i>]	BAA13641.1	¹⁶⁸ PDYAHEWTWW ¹⁷⁷	70	70
		Glucuronoxylanase [<i>Streptomyces</i> sp. SBT349]	WP_049570278.1	¹⁸⁸ PDYAHEWTWW ¹⁹⁷	70	70
		Glucuronoxylanase [<i>Paenibacillus riograndensis</i>]	WP_046505123.1	¹⁷² PDYAHTWTWW ¹⁸¹	70	70
B	WPPAGDYNWE	Agarase [<i>Gilvimarinus agarilyticus</i>]	WP_041522726.1	⁵¹⁵ VPTAGNYNVS ⁵²⁴	50	70
		β -Glucanase [<i>Saccharophagus degradans</i>]	WP_011467926.1	²⁸¹ WPDVGNYNAY ²⁸⁸	50	70
		1,4- β -xylanase [<i>Oceanobacillus</i> sp. <i>Castelsardo</i>]	WP_082918135.1	²⁹⁵ WPPSGEYNTE ³⁰²	70	90

		α -glucosidase [<i>Maricaulis</i> sp. W15]	WP_083635023.1	¹⁸⁶ WTPAGDYNRY ¹⁵³	70	70
		Glycoside hydrolase family 2 [<i>Opitutaceae</i> bacterium TSB47]	WP_068772578.1	¹³¹ KPPDIAGDYN ¹⁴⁰	70	70
C	GQEV LGVFSE	Hypothetical protein [<i>Gilvimarinus polysaccharolyticus</i>]	WP_049722783.1	¹⁴²⁵ DQEILEIFME ¹⁴³⁴	50	80
		Hypothetical protein [<i>Saccharophagus degradans</i>]	WP_011466768.1	²³⁰ LQEV---FSE ²³⁶	60	70
		Glycoside hydrolase [<i>Marinimicrobia</i> bacterium 46_47]	KUK56294.1	⁴⁹² GQEV L-MFSE ⁵⁰⁰	80	80
		Glycoside hydrolase family 2 protein [<i>Rhizobium leguminosarum</i>]	WP_018072003.1	¹⁰⁴ GQEV L--FSE ¹¹¹	80	80
		Glycoside hydrolase family 2 protein [<i>Burkholderia</i> sp. Leaf177]	WP_056364617.1	⁵⁹³ AEVMGEVFSE ⁶⁰³	70	70
D	WEAEEYE AWE	Glycoside hydrolase family 2 [<i>Gilvimarinus polysaccharolyticus</i>]	WP_049721000.1	⁷⁵ WAA-EYE-WW ⁸²	60	60
		Endoglucanase	WP_011469469.1	²¹⁵ WESE EYQERT ²²⁴	50	60

		[<i>Saccharophagus degradans</i>]				
		Glycoside hydrolase family 15 protein [<i>Phycoccus</i> sp. Soil748]	WP_056884386.1	²⁰⁷ WEATEY-AWE ²¹⁵	80	80
		Glycoside hydrolase [<i>Zunongwangia mangrovi</i>]	WP_092542741.1	¹⁹⁶ DLVEEYEAWE ²⁰⁵	70	80
		β -galactosidase [<i>Actinomyces odontolyticus</i>]	WP_003792996.1	⁶⁵⁵ WEA-EYEAAS ⁶⁶³	70	70
E	GQQQAWVAEQ	Agarase [<i>Gilvamarinus polysaccharolyticus</i>]	WP_049721026.1	⁵⁴ AQQQGWLTAQ ⁶³	50	80
		Hypothetical protein [<i>Saccharophagus degradans</i>]	WP_011469776.1	¹⁷⁹ DQQQKWVDEW ¹⁸⁸	60	60
		α/β -hydrolase [<i>Serratia marcescens</i>]	WP_004932055.1	²²² WQQQAFVAEQ ²³¹	80	90
		Glycosyl hydrolase [<i>Chitinophaga sancti</i>]	WP_072364398.1	⁷⁴² EAQQAWVAEP ⁷⁵¹	70	70
		Glycoside hydrolase family 31 protein [<i>Fischerella</i> sp. PCC 9339]	WP_026081578.1	⁸¹² CLQQAWVDEQ ⁸²¹	70	70
F	AHWPNVVWW	Glycosyl hydrolase [<i>Gilvamarinus agarilyticus</i>]	WP_041522559.1	¹⁶¹ AHWQDAWSLV ¹⁷⁰	40	80
		Endolytic transglycosylase [<i>Saccharophagus degradans</i>]	WP_011468115.1	⁶⁹ IEWPKVWVLY ⁷⁸	50	70

		α/β -hydrolase [<i>Burkholderia</i> sp. AU6039]	WP_089474706.1	⁵³⁷ AHWPNVSVDM ⁵⁴⁶	70	80
		O-Glycosyl hydrolase [<i>Bacillus caseinilyticus</i>]	SDX99039.1	²⁷⁰ AGW-NMWVWW ²⁷⁸	70	70
		Glycoside hydrolase 68 family protein [<i>Burkholderia cepacia</i>]	WP_048245367.1	⁹⁶ LINPNVWWD ¹⁰⁵	50	80
G	ALQELTQWWA	Glycoside hydrolase [<i>Gilvimarinus agarilyticus</i>]	WP_041522066.1	¹⁸⁶ ELGNELNAYWA ¹⁹⁵	50	70
		Hypothetical protein [<i>Saccharophagus degradans</i>]	WP_011467694.1	⁹⁹ DWQGLTQHWA ¹⁰⁸	60	70
		Glycoside hydrolase [<i>Paenibacillus</i> sp. SSG-1]	OXL87686.1	¹⁶⁰ ALEEVVQWWA ¹⁶⁹	70	80
		α -galactosidase [<i>Paenibacillus</i> sp. XY044]	WP_094593668.1	¹⁶⁴ ALEEVVQWWA ¹⁷³	70	80
		Glycoside hydrolase [<i>Alteromonadaceae</i> sp. XY-R5]	WP_082925239.1	²⁶ AVQELTDWDK ³⁴	60	70
H	APKWKIWKWW	Hypothetical protein [<i>Gilvimarinus agarilyticus</i>]	WP_052480823.1	¹⁴³ QPTWNIWEYH ¹⁵²	40	40
		Glycosyltransferase [<i>Saccharophagus degradans</i>]	WP_011466623.1	²⁰⁶ VTKWNYWKLW ²¹⁵	50	70
		Glycoside hydrolase-16 protein [<i>Millionella massiliensis</i>]	WP_071135132.1	³¹ APKWKLIWKD ⁴⁰	80	80
		Glycosyltransferase-2 protein	WP_087732789.1	²⁷⁷ APLWKRWKWV ²⁸⁶	70	70

		[<i>Paraburkholderia piptadeniae</i>]				
		α/β -hydrolase [<i>Enterobacter asburiae</i>]	WP_080973630.1	²⁶³ APWWKIWKET ²⁷²	70	70
I	WGGTAEWVWV	Hypothetical protein [<i>Gilvimarinus agarilyticus</i>]	WP_041521566.1	²⁵ VGLTGDWTWV ³⁴	50	90
		Hypothetical protein [<i>Saccharophagus degradans</i>]	WP_011470232.1	³⁵⁷ WSGETYAWVWP ³⁶⁷	50	60
		α -mannosidase [<i>Butyrivibrio fibrisolvens</i>]	WP_027215840.1	¹⁰² GTHRAEWVWV ¹¹¹	80	80
		Exo- β -1,3-glucanase [<i>Pseudomonas</i> sp. GM18]	EJM15586.1	³⁸⁷ TRFTSEWVWV ³⁹⁶	60	80
		Glycoside hydrolase [<i>Alteromonas</i> sp. TMED35]	OUX88559.1	²⁷ W--TAEWIWA ³³	60	80
J	AQEGQWWWWH	Glycoside hydrolase [<i>Gilvimarinus agarilyticus</i>]	WP_041523242.1	⁵¹¹ LCEGSDWFWWF ⁵²¹	50	80
		Endo-1,4- β -xylanase [<i>Saccharophagus degradans</i>]	WP_011469110.1	⁸¹ PQMGEWRWQD ⁸⁸	40	60
		Endoglucanase [<i>Opitutaceae</i> bacterium TAV1]	EIP96695.1	¹⁰⁵⁸ IHHGRWWWWI ¹⁰⁶⁷	60	80
		Glycoside hydrolase-43 protein [<i>Pseudoxanthomonas suwonensis</i>]	WP_051464569.1	³¹¹ AQDGQWWALF ³²⁰	60	70

		Glycoside hydrolase [<i>Paeniglutamicibacter gangotriensis</i>]	WP_007271102.1	¹¹ VREGQWWWQR ²⁰	60	90
K	AQPGTAGETG	Hypothetical protein [<i>Gilvimarinus agarilyticus</i>]	WP_041524321.1	¹⁹ AQPTTTDETE ²⁸	60	60
		Polysaccharide lyase-6 protein [<i>Saccharophagus degradans</i>]	WP_011468739.1	⁴¹⁹ AQSGTADNLI ⁴²⁴	50	70
		Chitinase [<i>Pseudoalteromonas ruthenica</i>]	WP_022946955.1	⁹⁷⁶ AQP GTGGDTG ⁹⁸⁵	80	100
		α/β -hydrolase [<i>Pseudonocardia</i> sp. MH-G8]	WP_094925796.1	¹¹³ AQP GTAGEPR ¹²²	80	80
		Endoglucanase [<i>Cellulosilyticum ruminicola</i>]	ACZ98593.1	¹⁷⁶ AQP GSAVAGETA ¹⁸⁶	70	90
L	AQTGTAGTIG	Hypothetical protein [<i>Gilvimarinus agarilyticus</i>]	WP_041523910.1	¹³³ AKAGTTGTAIG ¹⁴³	70	70
		Hypothetical protein [<i>Saccharophagus degradans</i>]	WP_011468796.1	⁴⁸ SQSG---GTIG ⁵⁴	60	70
		Endoglucanase [<i>Cellulomonas cellasea</i>]	KGM02499.1	⁶⁸⁷ AQTGTAVTAT ⁶⁹⁶	70	90
		Cell wall hydrolase [<i>Methylobacterium extorquens</i>]	WP_015857198.1	³⁶¹ NDVG TAGTIG ³⁷⁰	70	70
		β -Glucosidase [<i>Paenibacillus taichungensis</i>]	WP_094937581.1	⁷⁰⁴ SQTGTEGTIT ⁷¹³	70	70

