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MDPI

SUPLEMMENTARY MATERIAL

Table S1. Antarctic strains with positive detection of β-galactosidase activity based on β-Bluo-Gal reduction detection.

Strain ID	Nearest taxa (based on 16S rARN BLASTn comparison)	B-galactosidase activity [a]	Agar diffusion [b]	Max. β-galactosidase activity (U/mL)
34 Sc	*Arthrobacter sp*	48 h		
26Sc	*Arthrobacter sp*	48 h		
5 Sc	*Arthrobacter cryoconiti*	48 h		182
36Pc	N/A			
7 Sc	N/A	48 h		
So 9.2	N/A			
22	N/A			
64	*Arthrobacter sp*			
28Pc	N/A			
64 pc	*Arthrobacter sp*			
Cep 68	N/A	48 h		
So 64.3	*Arthrobacter sp*	48 h		
So 64.1	*Sporosarcina psychrofila*	72 h		
So 5b	*Arthrobacter alpinus*	72 h		
So9b	*Arthrobacter scleromae*	48 h		246
98	*Arthrobacter psychrochitiniphilus*	48 h		119
So 8.10.10	Non cultivable	96h		
63	*Arthrobacter scleromae*			
c vic 80 A	N/A			
Yelcho 5	*Arthrobacter alpinus*			
S 6.10	N/A		+	
71	N/A			
31	N/A			
S 11.9	N/A			
Se 8.10.12	*Rahnella sp.*	48 h	+	2157
Sod3	N/A			
So 30.1	N/A			
C vic 62	N/A			
So 30	N/A			
S 11.3	*Serratia liquefaciens*	72 h		
75 Pc	*Arthrobacter sulfonivorans*			
C vic 28	N/A	48 h		
C vic 15	*Stenotrophomonas maltophilia*			
C vic 82	*Streptomonas sp.*	72 h		
Cp 7.27	N/A			
39 pc	N/A			
10 Scan	N/A	48 h		
C v 71	N/A			
28	Non cultivable			
S1.2	N/A			
So 1c	N/A			
So 5c	*Arthrobacter sp.*	96h		
CSo 30.1	N/A			
11.1 Pc	*Streptomonas sp.*			
1Pc	N/A	48 h		
6 Sca	N/A			
88	*Arthrobacter sp.*	48 h		
8 Sca	N/A			
C vic 68	N/A	48 h		
C vic 85	N/A			
75	*Arthrobacter sulfonivorans*			
49	N/A			
64 pc	*Arthrobacter sp.*			
23 Sc	N/A			
C vic 75	*Arthrobacter sulfonivorans*			

Cp 4.7	N/A	
Cp7.12	N/A	
Cp 50	N/A	
45	N/A	
So 30.3	N/A	
C vic prat	*Sphingobacterium faecium*	
C vic 12 r	*Serratia sp*	72 h
Yelcho 4	*Arthrobacter Psychrochitiniphilus*	48 h
11.12	N/A	72 h
35 Sc	*Arthrobacter sp.*	72h
52 Pc	N/A	72h
So 10b	*Arthrobacter scleromae*	72h
So 17 1c	*Stenotrophomonas rhizophila*	
Decet	N/A	
Se 4.02	N/A	
C vic 71	N/A	
So1d	N/A	
29 sc	N/A	
65	N/A	
33 Sc	*Arthrobacter sp.*	
92	No cultivable	72h
So 4.5	N/A	
58.5 pc	N/A	48 h
68	N/A	48 h
8 Sc	N/A	
91	*Arthrobacter sp.*	

N/A: No identified strains

a: highest color intensity detected; non-reported strains showed low activity (light blue color)

b: indicative of possible extracellular activity

Table S2. Alignment lengths and porcentage of identity between nine *Rahnella* species genomes including the Antarctic isolate Se8.10.12. by Average Nucleotide Identity (ANI) calculation using blastn method.

ANIb Porcentage Identity

	R.variigena	R.sp_ERMR1	R.sp_Y9602	R.victoriana	R.woolbedingensis	**Antarctic_strain-Se81012**	R.bruchi	R.inusitata	R.aquatilis
R.variigena	100,000%	85,151%	87,967%	87,824%	90,925%	**84,390%**	90,776%	84,149%	87,894%
R.sp_ERMR1	85,191%	100,000%	85,172%	85,464%	85,011%	**84,691%**	84,910%	84,471%	85,140%
R.sp_Y9602	87,979%	85,128%	100,000%	88,788%	87,408%	**84,374%**	87,181%	84,067%	99,575%
R.victoriana	87,850%	85,395%	88,794%	100,000%	87,211%	**84,683%**	87,097%	84,548%	88,804%
R.woolbedingensis	90,922%	84,926%	87,306%	87,157%	100,000%	**84,314%**	93,323%	84,079%	87,288%
Antarctic_strain-Se81012	**84,443%**	**84,732%**	**84,390%**	**84,708%**	**84,438%**	**100,000%**	**84,246%**	**99,047%**	**84,340%**
R.bruchi	90,678%	84,847%	87,121%	86,972%	93,317%	**84,099%**	100,000%	83,889%	87,068%
R.inusitata	84,156%	84,473%	84,077%	84,510%	84,134%	**99,042%**	83,983%	100,000%	84,029%
R.aquatilis	87,864%	85,145%	99,532%	88,811%	87,370%	**84,307%**	87,109%	84,034%	100,000%

ANIb Alingment Lengths

	R.variigena	R.sp_ERMR1	R.sp_Y9602	R.victoriana	R.woolbedingensis	**Antarctic_strain-Se81012**	R.bruchi	R.inusitata	R.aquatilis
R.variigena	5499108.0	3838651.0	4181097.0	4283792.0	4016795.0	**3559437.0**	4149954.0	3773432.0	4165937.0
R.sp_ERMR1	3810085.0	5530672.0	3851166.0	3831249.0	3770733.0	**3512016.0**	3834676.0	3700932.0	3840761.0
R.sp_Y9602	4173062.0	3864328.0	5614252.0	4339729.0	3909444.0	**3589950.0**	3968411.0	3809407.0	5247245.0
R.victoriana	4276676.0	3852733.0	4345330.0	5563295.0	3916929.0	**3558522.0**	4015161.0	3762187.0	4342022.0
R.woolbedingensis	4018336.0	3763544.0	3928272.0	3901674.0	5457431.0	**3526755.0**	4364029.0	3761374.0	3912419.0
Antarctic_strain-Se81012	**3550583.0**	**3497099.0**	**3576406.0**	**3539610.0**	**3517166.0**	**4704828.0**	**3607730.0**	**4215481.0**	**3536186.0**
R.bruchi	4121409.0	3792488.0	3950430.0	4005238.0	4361003.0	**3596944.0**	5501702.0	3832222.0	3943148.0
R.inusitata	3730309.0	3655198.0	3786768.0	3723719.0	3729523.0	**4194551.0**	3809462.0	4910561.0	3772326.0
R.aquatilis	4151938.0	3830309.0	5266460.0	4340385.0	3919960.0	**3539061.0**	3971400.0	3796544.0	5656799.0

Table S3. Quality evaluation of the three-dimensional models of *Rahnella inusitata* Se8.10.12 β-galactosidases

Protein	Structure state	QMEAN4 Value	Ramachandran graphic (PROCHECK)	
			A	B
Se.8.10.12 Lac-Z	SWISS-MODEL Output	-1.04	1	8
	YASARA Output	0.07	1	5
Se.8.10.12 BglY	SWISS-MODEL Output	-0.69	1	4
	YASARA Output	0.08	1	3
Se.8.10.12 EbgA	SWISS-MODEL Output	-3.02	1	10
	YASARA Output	-2.63	1	7

A: Residues in disallowed regions, B: Residues in generously allowed regions

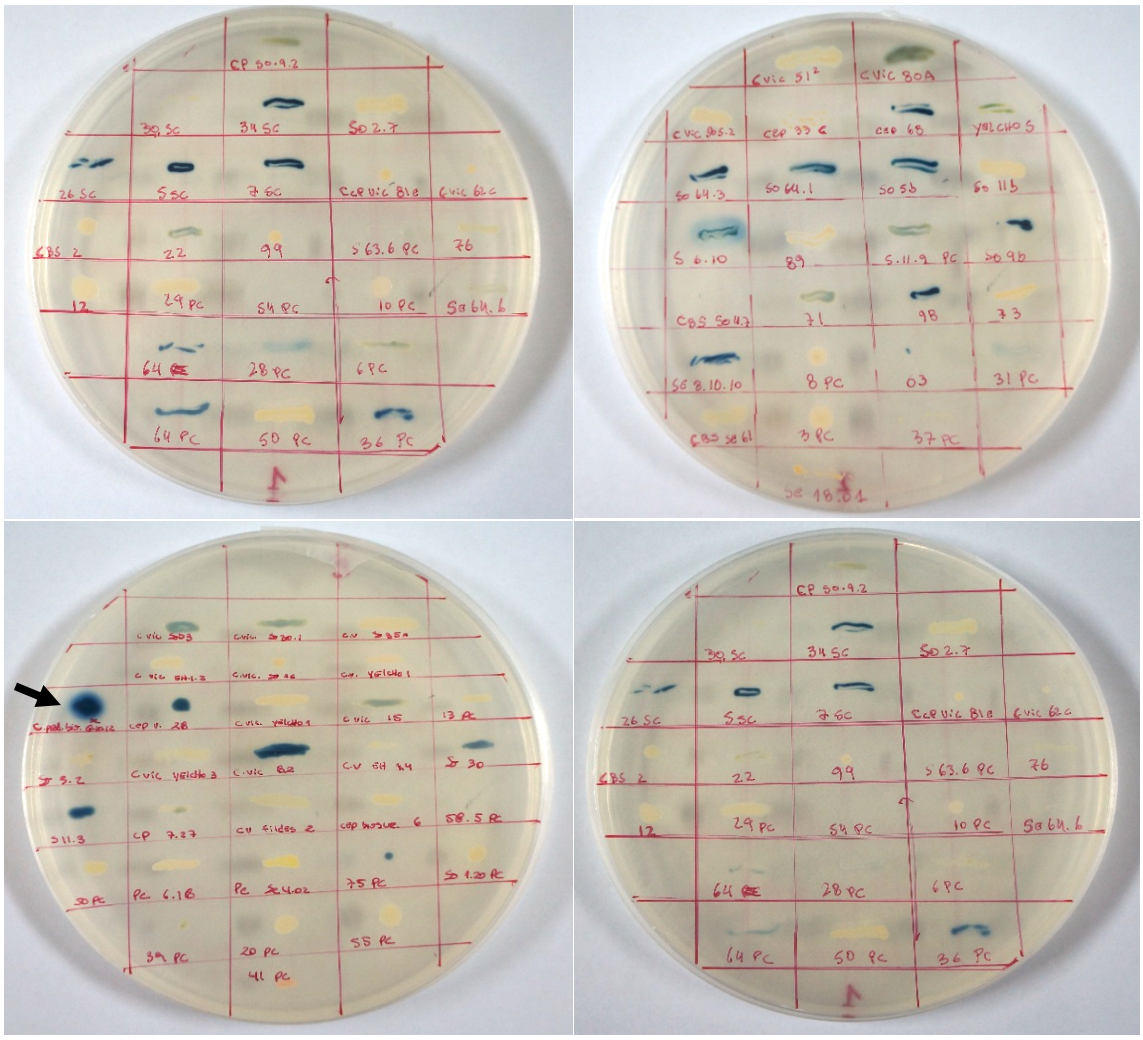

Figure S1. Example of β-galactosidase producing Antarctic strains determined in Lactose Agar using β-Bluo-Gal as an indicator of the β-galactosidase activity (blue stripes showing positive activity). Selected strain Se 8.10.12 as promising β-galactosidase enzyme producer is marked with an arrow.

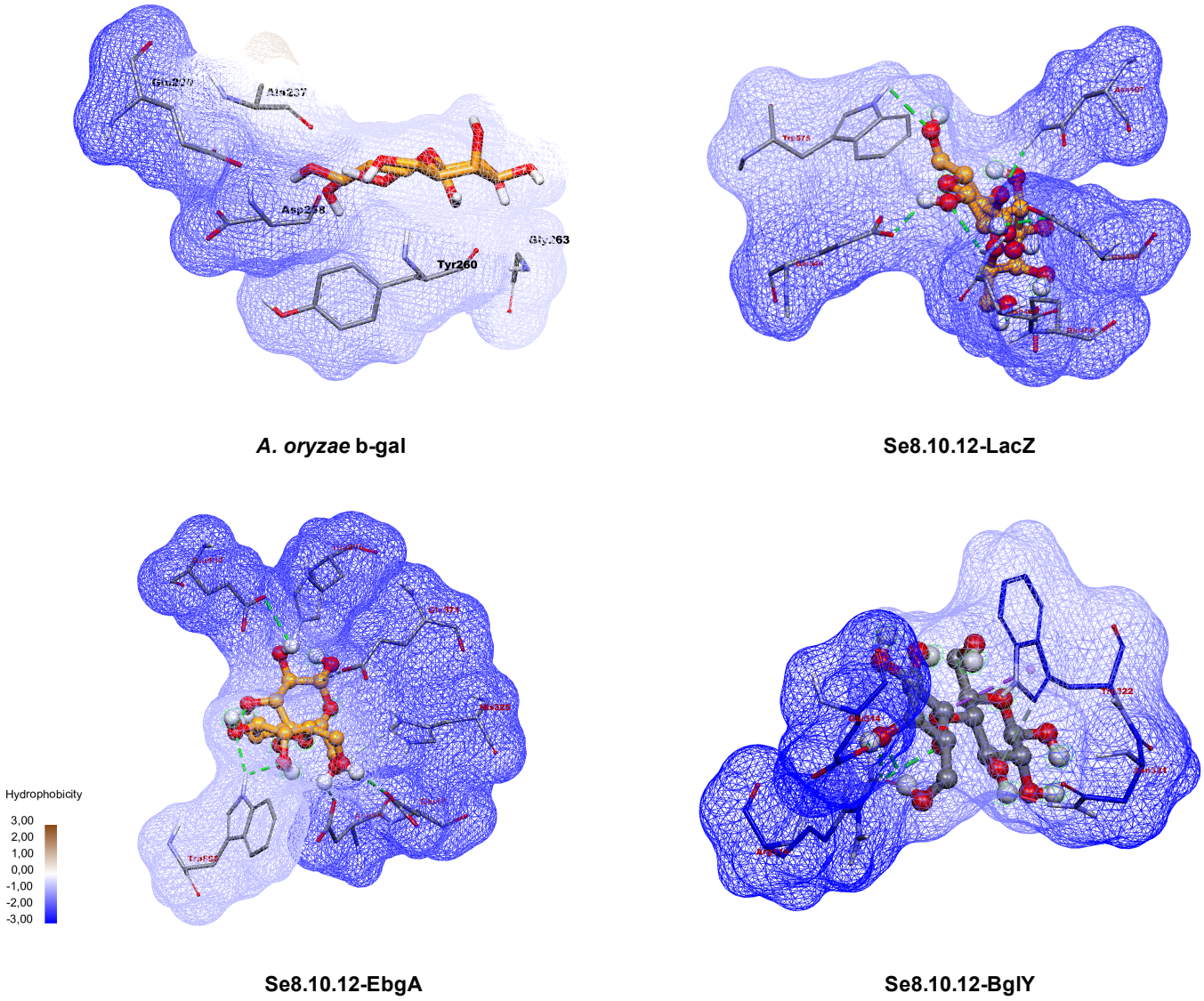

Figure S2. The hydrophobicity of the active site in docking analysis of β-galactosidases.