SUPPLEMENTAL DATA

Biochemical and structural characterization of a five-domain GH115- alpha-glucuronidase from the marine bacterium *Saccharophagus degradans* 2-40^T

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Running title: A five-domain GH115 α-glucuronidase

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SUPPLEMENTAL TABLES

Table S1. Protein representatives structurally related to SdeAgu115A and specific sub-domains.

PDB code	Z score	rmsd	lali (number of aligned residues)	nres (total number of residues)	% sequence identity in structurally consd. Regs.	Protein	Family	Organism
Whole enzyme								
4C90	53.1	2.4	656	822	41	α-Glucuronidase	GH115	*Bacteroides ovatus*
5BV3	38.3	2.1	713	759	31	α-Glucuronidase	GH115	*Bacteroides thetaiotaomicron*
2VUR	24.0	6.2	471	584	13	O-GlcNAcase	GH84	*Clostridium perfringens*
1K9E	22.6	4.7	469	671	14	α-Glucuronidase	GH67	*Bacillus stearothermophilus*
4H04	10.7	2.6	117	633	19	Lacto- *N*-biosidase	GH20	*Bifidobacterium bifidum*
Domain A								
4C90	22.8	1.5	160	811	36	α-Glucuronidase	GH115	*Bacteroides ovatus*
5BV3	19.0	1.4	140	759	25	α-Glucuronidase	GH115	*Bacteroides thetaiotaomicron*
1H41	14.0	2.2	124	700	19	α-Glucuronidase	GH67	*Cellvibrio japonicus*
1K9D	12.4	2.5	118	670	15	α-Glucuronidase	GH67	*Geobacillus stearothermophilus*
3GH7	11.0	2.5	117	506	17	Beta-N-acetylhexosaminidase	GH20	*Paenibacillus sp.*
4H04	10.7	2.2	1.0	633	19	Lacto- *N*-biosidase	GH20	*Bifidobacterium bifidum*
2YDQ	10.3	2.5	114	579	20	O-GlcNAcase	GH84	*Clostridium perfringens*

PDB code	**Z score**	**rmsd**	**lali (number of aligned residues)**	**nres (total number of residues)**	**% sequence identity in structurally consd. Regs.**	**Protein**	**Family**	**Organism**
Domain B (Catalytic domain)								
4C90	37.4	1.3	285	822	54	α-Glucuronidase	GH115	*Bacteroides ovatus*
2EPK	15.2	3.7	239	613	9	N-acetyl-beta-D-glucosaminidase	GH20	*Streptococcus gordonii*
3S6T	15.0	3.4	242	575	12	N-acetyl-beta-D-glucosaminidase	GH20	*Ostrinia furnacalis*
2CBI	14.9	3.2	231	584	10	O-GlcNAcase (OGA),	GH84	*Clostridium perfringens*
1K9D	13.8	4	242	670	13	α-Glucuronidase	GH67	*Geobacillus stearothermophilus*
Domain C								
4C90	25.0	0.9	174	811	29	α-Glucuronidase	GH115	*Bacteroides ovatus*
5BV3	14.9	1.8	154	759	25	α-Glucuronidase	GH115	*Bacteroides thetaiotaomicron*
4P3F	7.2	3.4	112	193	5	SRP68 RNA-binding domain	-	*Homo sapiens*
2EPN	7.1	3.9	146	623	5	N-acetyl-beta-D-glucosaminidase	GH20	*Streptococcus gordonii*
1YWT	6.8	3.7	111	222	5	14-3-3σ protein	-	*Homo sapiens*
Domain C$^+$								
1L4I	10.3	2.6	95	189	12	S pilus periplasmic chaperone SfaE	-	*Escherichia coli*
3BWU	10.3	2.5	95	200	12	Chaperone protein fimC	-	*Escherichia coli*
3ZMR	10.1	2.8	87	469	17	Bacon-domain in BoGH5A(endo – xyloglucanase)	-	*Bacteroides ovatus*

PDB code	Z score	rmsd	lali (number of aligned residues)	nres (total number of residues)	% sequence identity in structurally consd. Regs.	Protein	Family	Organism
					Domain D			
4C90	21.4	2.1	167	811	26	α-Glucuronidase	GH115	*Bacteroides ovatus*
5BV3	13.9	2.0	132	759	17	α-Glucuronidase	GH115	*Bacteroides thetaiotaomicron*
4CRR	13.1	1.8	112	124	16	C-terminal CBM6 in a GH16 laminarianse	CBM6	*Zobellia galactanivorans*
2CDO	12.7	2.2	117	137	12	CBM6 in a beta-agarase	CBM6	*Saccharophagus degradans*
3ZM8	12.3	2.3	119	444	11	C-CBM35 in GH26 endo-β-1,4-mannanase (PaMan26A)	CBM35	*Podospora anserina*

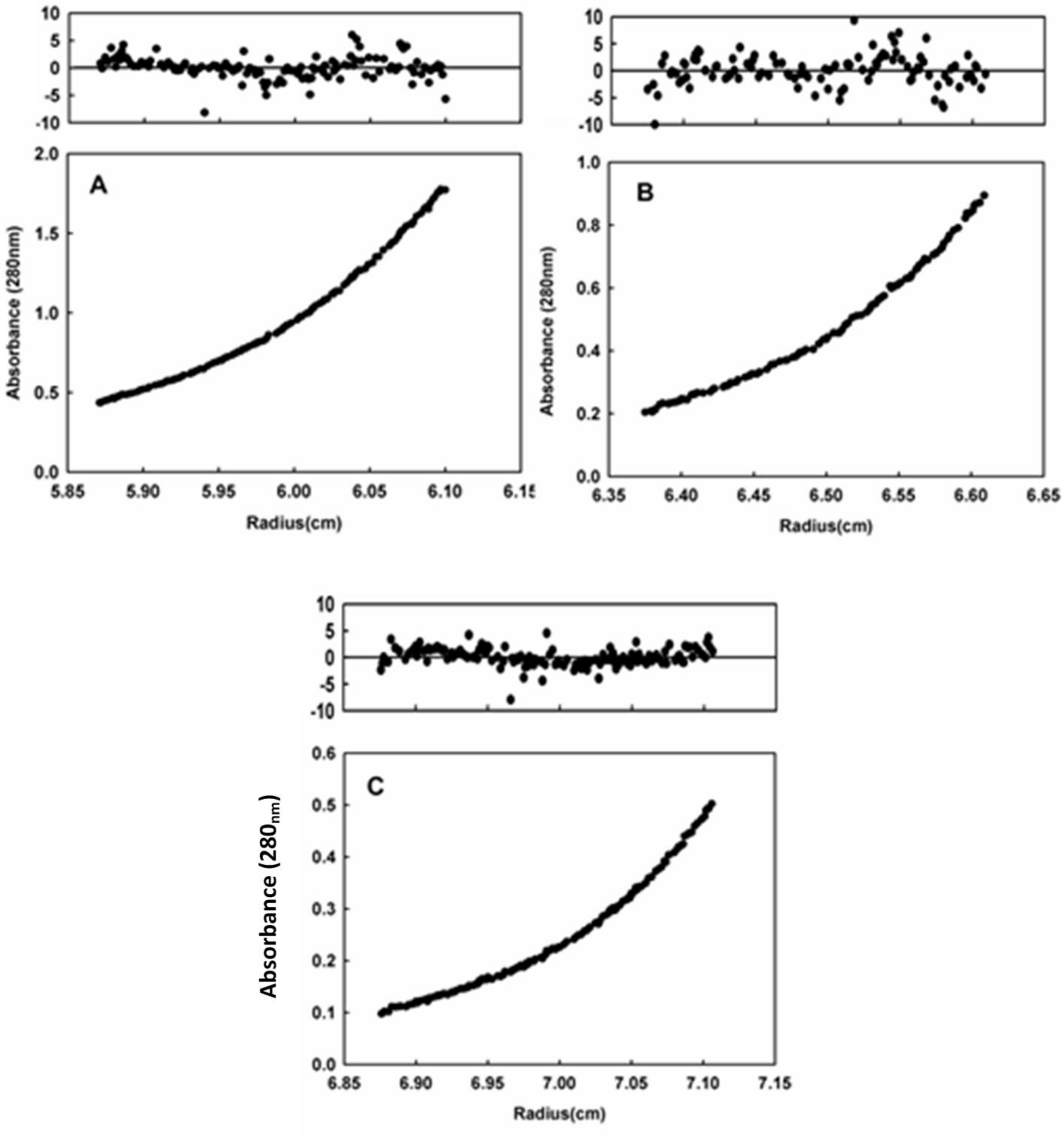

Fig. S1 Equilibrium analytical ultracentrifugation analysis to probe the oligomeric state of SdeAgu115A. The equilibrium profile and the residuals of the fit for the data obtained at 20°C for SdeAgu115A at concentration of 5.9 µM (A); 3.0 µM (B); 1.5 µM (C) in 20 mM HEPES buffer pH7.0 containing 300 mM NaCl. The rotor speed for the displayed data was 7000 rpm in a Beckman Optima XL-A analytical ultracentrifuge. The weight-average molecular weight of native SdeAgu115A was determined to be 189±3.9 kD.