

Supplementary materials

“Genome wide analysis of PL7 family alginate lyases in the genus *Zobellia*”

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Submitted to Molecules.

Table S1. List of accession numbers for genomes used in phylogenomic analysis.

Strain	GenBank Accession No.
<i>Zobellia uliginosa</i> DSM 2061 ^T	FTOB000000000.1
<i>Zobellia galactanivorans</i> DsiJ ^T	FP476056.1
<i>Zobellia galactanivorans</i> OII3	MWRZ000000000.1
<i>Zobellia</i> sp. Asnod1-F08	JADDXT000000000.1
<i>Zobellia</i> sp. Asnod2-B02-B	JADDXS000000000.1
<i>Zobellia</i> sp. Asnod2-B07-B	JADDXR000000000.1
<i>Zobellia</i> sp. Asnod3-E08-A	JADDXQ000000000.1
<i>Zobellia laminariae</i> KMM 3676 ^T	RCNS000000000.1
' <i>Zobellia barbeyronii</i> ' KMM 6746 ^T	JACATN000000000.1*
<i>Zobellia amurskyensis</i> KMM 3526 ^T	RCNR000000000.1
<i>Zobellia amurskyensis</i> MAR 2009 138	JQMD000000000.1
<i>Zobellia russellii</i> KMM 3677 ^T	JACSOI000000000.1*
<i>Arenibacter latericius</i> DSM 15913 ^T	AUKX000000000.1
<i>Maribacter sedimenticola</i> DSM 19840 ^T	FZNV000000000.1

*Unpublished data

Table S2. Identity matrix of catalytic domains from PL7 alginate lyases identified in *Zobellia* genomes.**Table S3.** Identifiers of PL7 and adjacent genes included in loci I–VI.

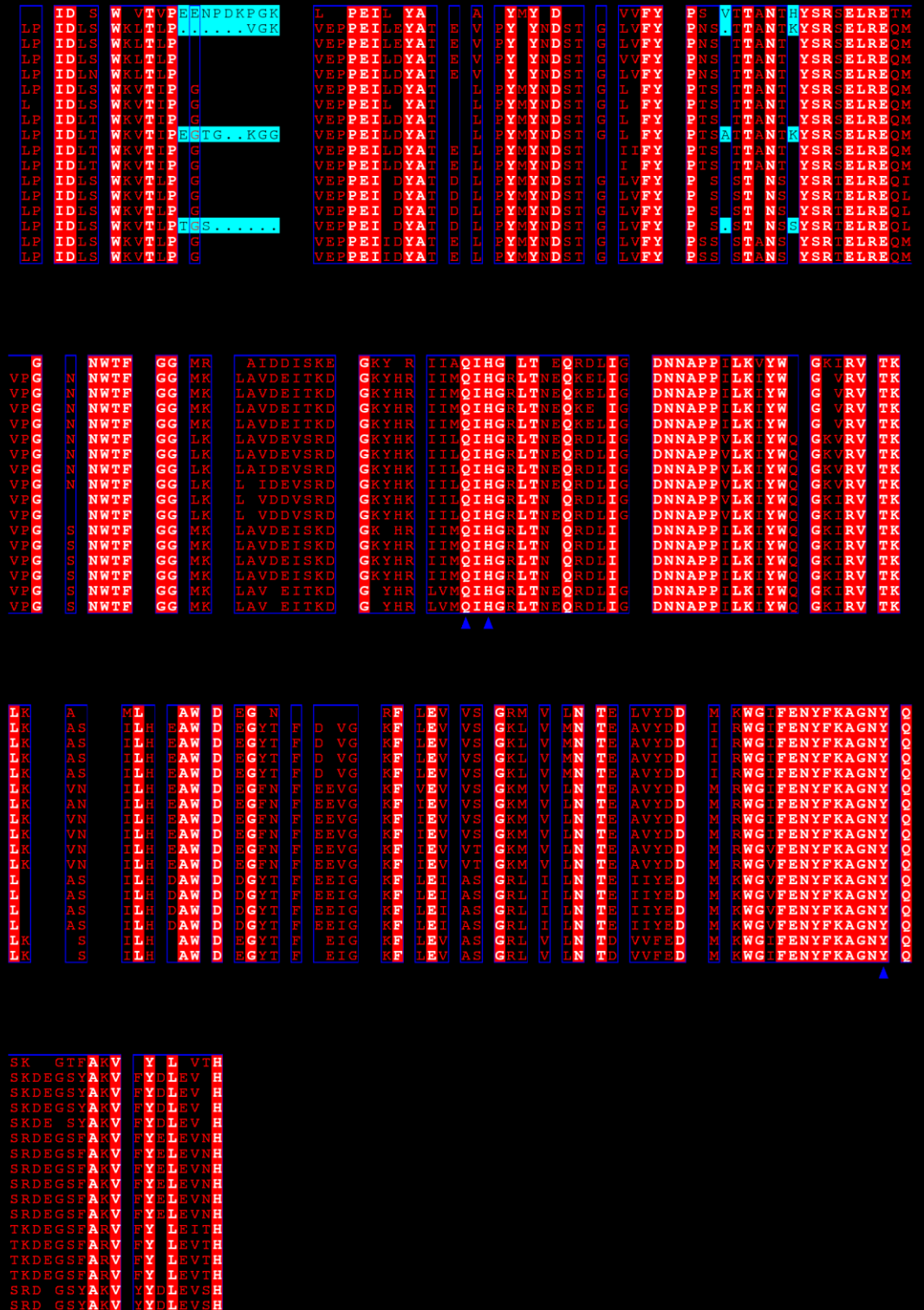


Figure S2. Structure-based sequence alignment of PL7 alginate lyases from subfamily SF6. The sequences are aligned using known structure, FlAlaA from *Flavobacterium* sp. UMI-01 (PDB ID: 5Y33). The secondary structures are shown above the alignment. Conserved amino acids in white letters highlighted on the red background are identical and those in red letters are similar. α -Helices are represented as schematically, and β -turns are marked with TT. Blue triangles indicate the conserved residues involved in the catalytic machinery. The differences between in-paralogs, which were colored in ribbon representations of superimpositions are highlighted by cyan background.