

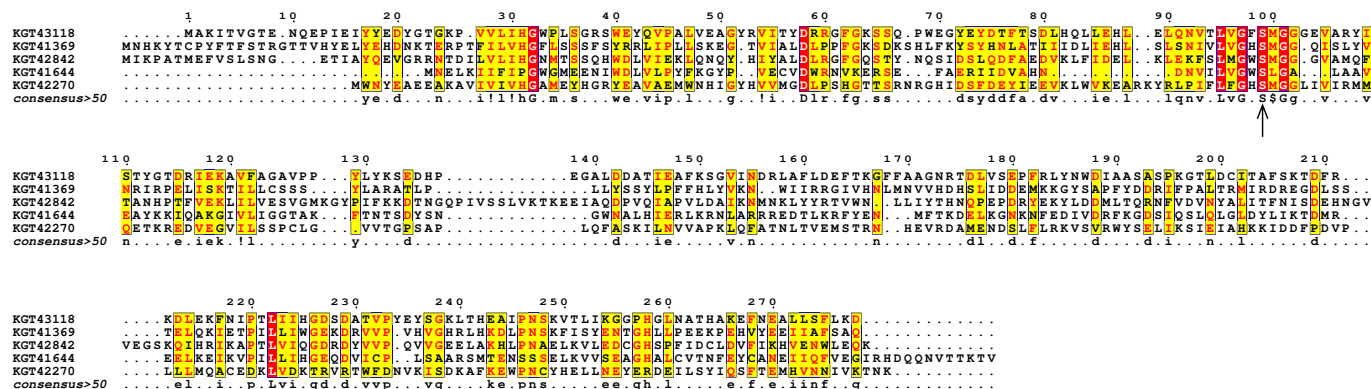


Figure S1. Multiple sequence alignment of A/B hydrolase superfamily proteins on *B. cereus* tsu1 genome. Multiple sequence alignment of A/B hydrolase proteins were performed using ClustalW followed by online-based ESPript 3.0. The consensus sequences between 3-oxoadipate enol-lactonase (KGT42842) and A/B hydrolase enzymes on *B. cereus* tsu1 genome are highlighted in yellow and pink boxes. The lipase-box like sequence (GXSSXG) and the serine site that are important for the PHB-hydrolyzing activity were detected on these A/B hydrolase proteins.