

SUPPLEMENTARY ONLINE DATA

Structure and activity of the cold-active and anion-activated carboxyl esterase OLEI01171 from the oil-degrading marine bacterium *Oleispira antarctica*

Sofia LEMAK*†, Anatoli TCHIGVINTSEV*†, Pierre PETIT*†, Robert FLICK*†, Alexander U. SINGER*†, Greg BROWN*†, Elena EVDOKIMOVA*†, Olga EGOROVA*†, Claudio F. GONZALEZ‡, Tatyana N. CHERNIKOVA§†, Michail M. YAKIMOV¶†, Michael KUBE||†¹, Richard REINHARDT||†², Peter N. GOLYSHIN§†, Alexei SAVCHENKO*† and Alexander F. YAKUNIN*†³

*Department of Chemical Engineering and Applied Chemistry, Banting and Best Department of Medical Research, University of Toronto, Toronto, ON M5G 1L6, Canada, †The MAMBA (Marine Metagenomics for New Biotechnological Applications) and BEEM (Bioproducts and Enzymes from Environmental Metagenomes) Scientific Consortium, ‡Department of Microbiology and Cell Science, University of Florida, Gainesville, FL 32611-0700, U.S.A., §School of Biological Sciences, University of Bangor, Gwynedd LL57 2UW, U.K., ¶Institute for Coastal Marine Environment, CNR (Consiglio Nazionale delle Ricerche), Messina 98122, Italy, and ||Max-Planck Institute for Molecular Genetics, D-14195 Berlin-Dahlem, Germany

Table S1 The number of the surface-located charged residues (calculated using a cut-off value 2 Å²) in the structures of homologous PF00746 esterases from psychrophilic and mesophilic organisms

Protein ID	Total number of amino acids	Percentage of sequence identity with OLEI01171	Number of the surface-located residues				Total amino acids
			Aspartic acid	Glutamic acid	Arginine	Lysine	
OLEI01171	280	100	11	17	11	10	49
<i>Ps. haloplanktis</i> FGH	280	65	12	10	2	15	39
Atu1476	277	48	15	21	14	11	61
<i>Saccharomyces cerevisiae</i> FGH	299	43	17	15	8	20	60

¹ Present address: Department Phytomedicine, Humboldt-Universität zu Berlin, D-14195 Berlin, Germany

² Present address: Max-Planck Genome Centre Cologne, Max-Planck Institute for Plant Breeding Research, D-50829, Cologne, Germany

³ To whom correspondence should be addressed (email a.iakounine@utoronto.ca).

Co-ordinates and structure factors of the OLEI01171 complexes with Cl⁻ or Br⁻ have been deposited in the PDB under the accession codes 3I6Y and 3S8Y respectively.

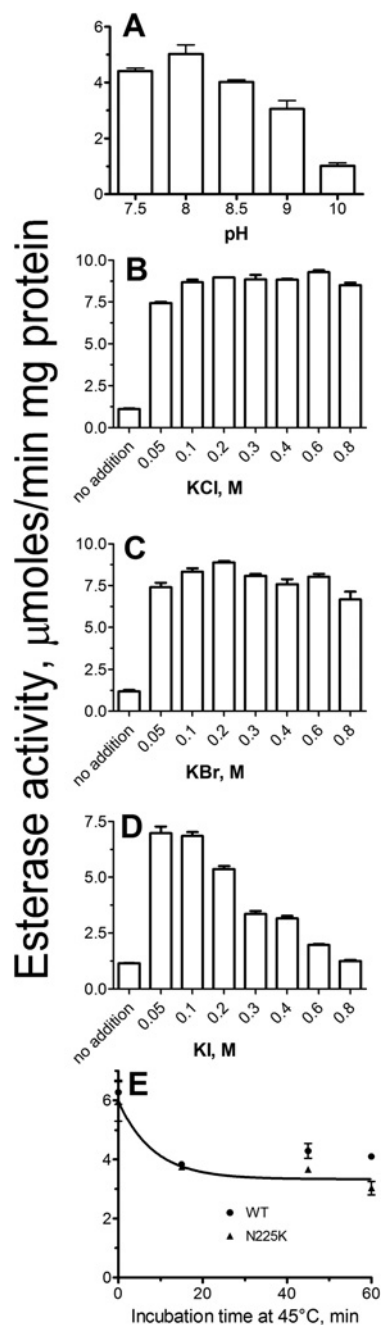


Figure S1 Hydrolysis of α -naphthyl acetate by OLEI01171 as a function of pH (A), KCl concentration (B), KBr concentration (C), KI concentration (D) and pre-incubation time at 45°C (E)

The reaction mixtures contained 2 mM α -naphthyl acetate and 1 μg of OLEI01171, and the assay temperature was 15°C.

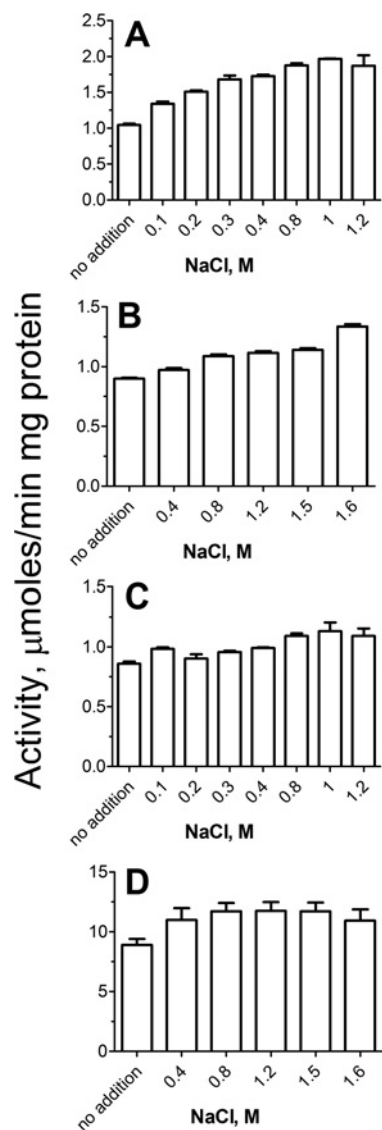


Figure S2 Effect of NaCl on esterase activity of Atu1476 (A), SMc01273 (B), *E. coli* YeiG (C) and *E. coli* BioH (D)

The reaction mixtures contained 2 mM naphthyl acetate and 1 μg of purified enzyme.

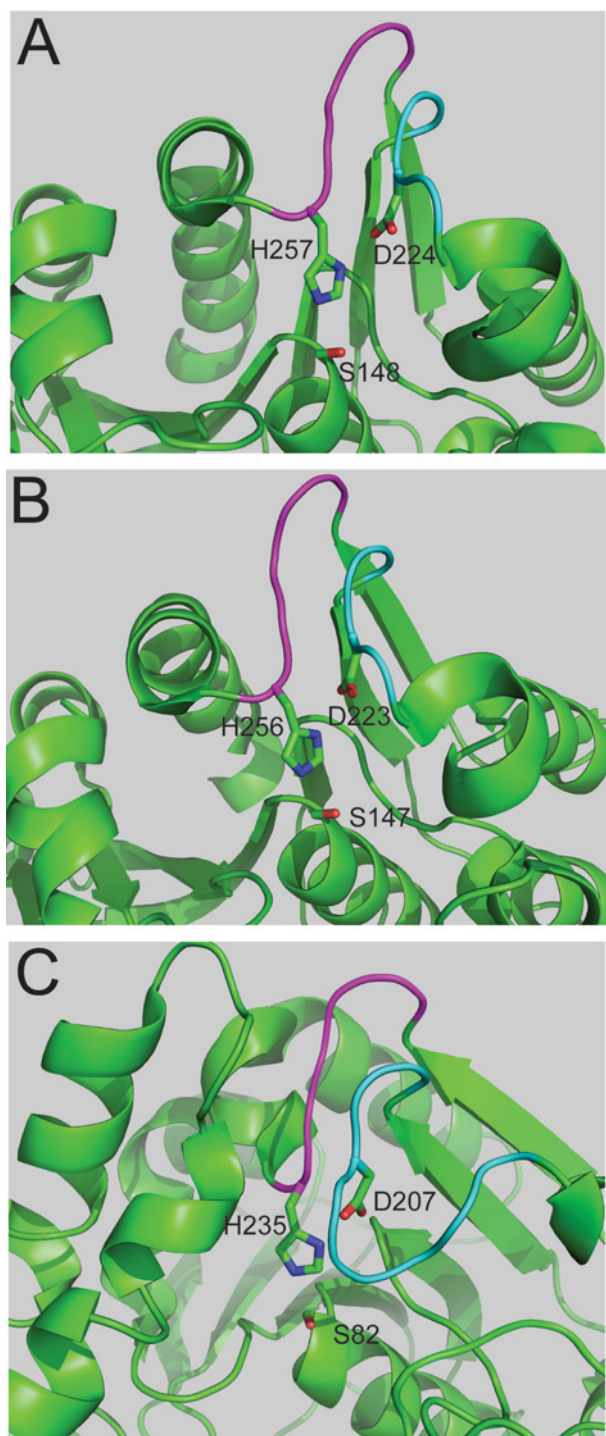


Figure S3 The active site histidine residue loop of OLEI01171 and other structurally characterized esterases

(A) OLEI01171. (B) *PhFGH*. (C) *E. coli* BioH. Side chains of the catalytic triad residues are shown as sticks and labelled, whereas the histidine loop is coloured in magenta.

