Thermophilic carboxylesterases from hydrothermal vents of the volcanic island of Ischia active on synthetic and biobased polymers and mycotoxins

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ABSTRACT

Hydrothermal vents have a widespread geographical distribution and are of high interest for investigating microbial communities and robust enzymes for various industrial applications. We examined microbial communities and carboxylesterases of two terrestrial hydrothermal vents of the volcanic island of Ischia (Italy) predominantly composed of Firmicutes (*Geobacillus* and *Brevibacillus* spp.), *Proteobacteria* and *Bacteroidota*. High-temperature enrichment cultures with the polyester plastics polyhydroxybutyrate (PHB) and polylactic acid (PLA) resulted in an increase of *Thermus* and *Geobacillus* spp., and to some extent, *Fontimonas* and *Schleiferia* spp. The screening at 37-70ºC of metagenomic fosmid library from above enrichment cultures resulted in identification and successful production in *Escherichia coli* of three hydrolases (IS10, IS11 and IS12), all derived from yet uncultured Chloroflexota and showing low sequence identity (33-56%) to characterized enzymes. Enzymes exhibited maximal esterase activity at temperatures 70-90ºC, with IS11 showing the highest thermostability (90% activity after 20 min incubation at 80ºC). IS10 and IS12 were highly substrate-promiscuous and hydrolysed all 51 monoester substrates tested. Enzymes were active with polyesters (PLA and polyethylene terephthalate model substrate, 3PET) and mycotoxin T-2 (IS12). IS10 and IS12 had a classical α/β hydrolase core domain with a serine hydrolase catalytic triad (Ser155, His280, and Asp250) in the hydrophobic active sites. The crystal structure of IS11 resolved at 2.92 Å revealed the presence of the N-terminal β-lactamase-like domain and C-terminal lipocalin domain. The catalytic cleft of IS11 includes catalytic residues Ser68, Lys71, Tyr160, and Asn162, whereas the lipocalin domain encloses the catalytic cleft like a lid contributing to substrate binding. Thus, this study has identified novel thermotolerant carboxylesterases with a broad substrate range including polyesters and mycotoxins for potential applications in biotechnology.

IMPORTANCE

High-temperature-active microbial enzymes are important biocatalysts for many industrial applications including recycling of synthetic and biobased polyesters increasingly used in textiles, fibres, coatings and adhesives. Here, we have discovered three novel thermotolerant carboxylesterases (IS10, IS11 and IS12) from high-temperature enrichment cultures from the Ischia hydrothermal vents incubated with biobased polymers. The identified metagenomic enzymes originated from uncultured Chloroflexota and showed low sequence similarity to known carboxylesterases. Active sites of IS10 and IS12 had the largest "effective volumes" among the characterized prokaryotic carboxylesterases and exhibited high substrate promiscuity, including hydrolysis of polyesters and mycotoxin T-2 (IS12). Though less promiscuous compared to IS10 and IS12, IS11 had a higher thermostability with high temperature optimum (80-90 ºC) for activity, hydrolysed polyesters, and its crystal structure revealed an unusual lipocalin domain likely involved in substrate binding. The polyesterase activity in these enzymes makes them attractive candidates for further optimisation and potential application in plastics recycling.

INTRODUCTION

Environmental microbial communities and microorganisms represent an enormous reserve of biochemical diversity and enzymes for fundamental research and applications in biotechnology (1,2). However, the vast majority of environmental microbes have never been grown and characterised in the laboratory (3,4). The metagenomic approach has emerged as a strategic way to study unculturable microorganisms and their enzymes using various computational and experimental methods (5-7). Metagenomics includes shotgun sequencing of microbial DNA purified from a selected environment, high-throughput screening of metagenomic expression libraries (functional metagenomics), profiling of RNAs and proteins produced by a microbial community (meta-transcriptomics and meta-proteomics), and identification of metabolites and metabolic networks of a microbial community (meta-metabolomics) (8). Global DNA sequencing efforts and several large-scale metagenome sampling projects revealed the vast sequence diversity in environmental metagenomes and microbial genomes, as well as the presence of numerous unknown or poorly characterised genes (9-12). For example, a high-throughput project focused on carbohydrate-active enzymes has identified over 27,000 related genes and demonstrated the presence of glycoside hydrolase activity in 51 out of 90 tested proteins (13). Other large scale metagenomic projects include the Sargasso Sea sampling (over one million new genes discovered), the Global Ocean Survey (over six million genes), and human gut microbiome (over three million genes) (9-12). Thus, through the advent of metagenomics, we are starting to generate insights into the rich microbial worlds thriving in different environments. Nevertheless, a recent analysis of metagenome screening studies suggested that all representative types of environmental habitats (terrestrial, marine, and freshwater) are under-sampled and under-investigated (14). It is estimated that total number of microbial cells is 10^{30}, whereas the natural protein universe exceeds 10^{12} proteins indicating that our knowledge of proteins and biochemical diversity on Earth is very limited (15-17). Therefore, the determination of protein function or enzyme activity for millions of genes of unknown function and biochemically uncharacterised proteins represents one of the main challenges of the postgenomic biology.

The approaches of experimental metagenomics include meta-transcriptomics, meta-proteomics, metabolomics, and enzyme screening (6,7,17-19). Activity-based screening of metagenome gene libraries represents a direct way for tapping into the metagenomic resource of novel enzymes. This approach involves expressing genes from metagenomic DNA fragments in *Escherichia coli* cells and assaying libraries of clones on agar plates for enzymatic activities using chromogenic or insoluble substrates (18). Importantly, this approach offers the possibility to identify novel families of enzymes with no sequence similarity to known enzymes. Screening of metagenome gene libraries from different terrestrial, marine, and freshwater environments has already expanded the number of new enzymes including novel nitrilases, glycoside hydrolases, carboxyl esterases, and laccases (14,20,21).

Carboxylesterases (EC 3.1.1.1) are a diverse group of hydrolytic enzymes catalyzing the cleavage and formation of ester bonds, which represent the third largest group of industrial biocatalysts (after amylases and proteases). Many esterases show a wide substrate range and high regio- and stereo-selectivity making them attractive biocatalysts for applications in

pharmaceutical, cosmetic, detergent, food, textile, paper and biodiesel industries (22,23). Most of known carboxylesterases belong to the large protein superfamilies of α/β hydrolases and β-lactamases and have been classified into 16 families based on sequence analysis (22,24,25). A significant number of these enzymes have been characterised both biochemically and structurally, because they are of high interest for biotechnological applications (22,23,26). Screening of metagenome gene libraries and genome mining has greatly expanded the number of novel carboxylesterases including enzymes active against aryl esters or polymeric esters (polyesterases) (21-23,26,27). However, the increasing demand for environmentally friendly industrial processes has stimulated research on the discovery of new enzymes and their application as biocatalysts to meet the challenges of a circular bioeconomy (28,29). The global enzyme market is expected to grow from $8.18 billion in 2015 to $17.50 billion by 2024 (28). However, the majority of known enzymes are originated from mesophilic organisms, which have limited stability under harsh industrial conditions including high temperatures, extreme pH, solvents, and salts (30,31). Thus, the discovery of robust enzymes including carboxylesterases and engineering of more active variants represent the key challenges for the development of future biocatalytic processes. Extremophilic microorganisms are an attractive source of industrial biocatalysts, because they evolved robust enzymes that function under extreme conditions (high/low temperatures, high/low pH, salts) (14,26,30,32). In addition, extremophilic enzymes found in one environment are typically also tolerant to other extreme conditions making them attractive biocatalysts for various applications including depolymerization of natural and synthetic polymers (32-35).

Hydrothermal vents are extreme environments located in tectonically active sites, which are classified as terrestrial and marine (deep-sea and shallow-sea) systems (36). Hydrothermal vents are characterised by harsh physico-chemical conditions (high temperature and low pH) and are known as source of thermophilic microbes and enzymes with biotechnological importance. Although terrestrial hydrothermal vents have relatively easy access, they remain under-investigated compared to (sub)marine hydrothermal vents. To provide insights into microbial diversity of terrestrial hydrothermal vents, we analysed the natural microbial communities of two thermophilic hydrothermal vents located on the volcanic island of Ischia (Italy), as well as the effect of polyester plastic addition on these microbial communities using barcoded DNA sequencing of extracted DNA. Using activity-based metagenomic approach, we screened fosmid libraries for carboxylesterase activity using tributyrine agar plates, identified 14 unique fosmids encoding putative hydrolases, from which three soluble carboxylesterases (IS10, IS11, and IS12) were recombinantly produced in *E. coli* and biochemically characterised including substrate range and stability using both monoester and polyester substrates. The crystal structure of IS11 was resolved to reveal the N-terminal β-lactamase-like serine hydrolase domain connected to the C-terminal lipocalin domain. The active site of IS11 accommodated the conserved catalytic residues Ser68, Lys71, Tyr160, and Asn162, as well as numerous hydrophobic residues potentially involved in substrate binding. Structural models of IS10 and IS12 revealed classical α/β hydrolase domains with a catalytic serine hydrolase triad (Ser155, His280, Asp250), multiple hydrophobic residues in their active sites with the largest "effective volumes" reported for prokaryotic carboxylesterases.

MATERIALS AND METHODS

Environmental sampling sites and enrichment cultures. Sediment samples with water were collected in September 2018 from the geothermal areas of the volcanic island of Ischia (the Gulf of Naples, Italy). The samples were taken from the Cavascura hydrothermal springs (40.70403 13.90502): IS1 (pH 8.5, 45ºC) and IS2 (pH 7.0, 55ºC) and from the sandy fumaroles of Maronti beach near St Angelo (40.70101 13.89837): IS3 (pH 4.5, 75ºC) and IS4 (pH 5.0, 75ºC). For each sample, triplicate enrichment cultures were established containing different polymers or plastics as substrates, polylactic acid film (PLA, poly-D,L-lactide, M_w 10,000-18,000 Da), PLA polyhydroxybutyrate (PHB) and a commercial compostable polyester blend (P3, Blend) were kindly provided by the Biocomposites Centre, Bangor University, UK. Plastic films were cut (3 mm x 20 mm), washed in 70% ethanol and air-dried before adding to samples. For IS1 and IS2 cultures, modified DSMZ medium 1374 (https://bacmedia.dsmz.de/medium/1374) was used, which contained (g L^{-1}): NaCl, 1; $MgCl_2 \cdot 6H_2O$, 0.4; KCl, 0.1; NH_4Cl, 0.25; KH_2PO_4, 0.2; Na_2SO_4, 4; $NaHCO_3$, 0.1; $CaCl_2 \cdot 2H_2O$, 0.5. The medium was adjusted to pH 7.5 with 10N NaOH. For IS3 and IS4 cultures, modified DSMZ medium 88 (https://bacmedia.dsmz.de/medium/88) was used, which contained (g L^{-1}): $(NH_4)_2SO_4$, 1.3; KH_2PO_4, 0.28; $MgSO_4 \cdot 7H_2O$, 0.25; $CaCl_2 \cdot 2H_2O$, 0.07. The medium was adjusted to pH 4.5 with 10N H_2SO_4. Additionally, the trace element solution SL-10 (from DSMZ medium 320 https://bacmedia.dsmz.de/medium/320) was added at 1:1000 (vol/vol) to both media. Enrichment cultures contained 0.5 g of sample sediment and 0.25 g of a polymer in 10 mL of growth medium. The cultures were incubated at 50 °C (IS1-IS2) or 75 °C (IS3-IS4) with slow agitation (30 rpm) for 4 days, then culture aliquots (20% of the volume of enrichment cultures) were transferred to a fresh medium and incubated for 11 days under the same conditions (Table S1).

DNA extraction and 16S rRNA amplicon sequencing. Prior to DNA extraction, the enrichment cultures (9 mL each) were vortexed and biomass was collected by centrifugation at 10,000 rcf for 10 min at 4°C. The pellets were resuspended in 250 µL of sterile phosphate-buffered saline (PBS, pH 7.5) and transferred to 1.5 mL tubes. High molecular weight DNA was obtained using the ZymoBIOMICS DNA Miniprep Kit (Zymo Research, Irvine, Ca, USA) in accordance with manufacturer's instructions. Finally, DNA was eluted with 50 µL of nuclease free water. The quality of extracted DNA was assessed by gel electrophoresis, and DNA concentration was estimated using Qubit™ 4.0 Fluorometer dsDNA BR Assay Kit (Life Technologies, USA). The Illumina-compatible libraries of hypervariable V4 region of 16S rRNA gene were prepared by single PCR with dual-indexing primer system with heterogeneity spacer as described previously (37). Modified forward primer F515 (5'-GTGBCAGCMGCCGCGGTAA-3') and reverse R806 prokaryotic primer (5'-GGACTACHVGGGTWTCTAAT-3') were used. PCR reactions were performed using MyTaq™ Red DNA Polymerase (Bioline) in a Bio-Rad® thermocycler with the following program: 95 °C for 2 min for denaturation followed by 30 cycles at 95 °C for 45 s, 50 °C for 60 s, 72 °C for 30 s, with a final elongation at 72 °C for 3 min. PCR products of approximately 440 bp were visualised by gel electrophoresis and gel-purified using the QIAEX II Gel

202 Extraction Kit® (QIAGEN). The purified barcoded amplicons were quantified by Qubit™
203 dsDNA BR Assay Kit (Life Technologies, USA), pooled in equimolar amounts and sequenced
204 on Illumina MiSeq™ platform (Illumina Inc., San Diego, CA, USA) using paired-end 250 bp
205 reads at the Centre for Environmental Biotechnology (Bangor, UK). Sequencing reads were
206 processed and analysed as previously described (38).

207 All statistical analysis was conducted using R programming environment (39) *prcomp* function
208 and in-house scripts for graphical design.

209

210 **Preparation of the Ischia metagenome library from polyester enrichment cultures.** High
211 molecular weight DNA extracted from all enrichment cultures was combined in equimolar
212 amount and used to prepare the metagenomic fosmid library 'IS_Lib2' using the
213 CopyControl™ Fosmid Library pCC2FOS Production Kit (Epicentre Technologies, Madison,
214 USA). DNA was end-repaired to generate blunt-ended 5'-phosphorylated fragments according
215 to manufacturer's instructions. Subsequently, DNA fragments in the range of 30-40 kbp were
216 resolved by gel electrophoresis (2 V cm^{-1} overnight at 4 °C) and recovered from 1% low
217 melting point agarose gel using GELase 50X buffer and GELase enzyme (Epicentre). Nucleic
218 acid fragments were then ligated to the linearized CopyControl pCC2FOS vector following the
219 manufacturer's instructions. After the in vitro packaging into the phage lambda (MaxPlax™
220 Lambda Packaging Extract, Epicentre), the transfected phage T1-resistant EPI300™-T1R *E.*
221 *coli* cells were spread on Luria-Bertani (LB) agar medium containing 12.5 µg/ml
222 chloramphenicol and incubated at 37 °C overnight to determine the titre of the phage particles.
223 The resulting library had estimated titre of $1x10^4$ non-redundant fosmid clones. For long-term
224 storage, *E. coli* colonies were washed off from the agar surface using liquid LB medium
225 containing 20% (v/v) sterile glycerol and the aliquots were stored at −80 °C.

226 **Activity-based screening of the polyester enrichment metagenome library for esterase**
227 **activity.** The metagenomic library IS_Lib2 was screened for carboxylesterase/lipase activity
228 as follows. The fosmid library was grown on LB agar plates containing 12.5 µg/ml
229 chloramphenicol at 37°C overnight to yield single colonies. Then, 3,456 clones were arrayed
230 in 9 x 384-well microtitre plates and cultivated at 37 °C in LB medium supplemented with 12.5
231 µg/ml chloramphenicol. After overnight growth, replica plating was used to transfer the clones
232 onto the surface of large LB agar square plates (245 mm x 245 mm) containing 12.5 µg/ml
233 chloramphenicol, 2 ml/L fosmid autoinduction solution (Epicentre), each plate supplemented
234 with 0.3% (v/v) tributyrin (Sigma-Aldrich, Gillingham, UK). The original microtitre plates
235 were stored at -80 °C with the addition of 20% (vol/vol) glycerol to enable the isolation of
236 positive clones after the functional screenings. After an initial overnight growth at 37°C, the
237 LB agar plates were incubated for 48 hours at 37, 50 or 70 °C. Positive hits were confirmed by
238 re-testing of the corresponding fosmid clones taken from the original microtitre plate.

239 **Sequencing and analysis of metagenomic fragments.** Positive fosmid clones were
240 cultivated in 100 mL LB medium containing 12.5 µg/ml chloramphenicol and 2 ml/L fosmid
241 autoinduction solution (Epicentre) at 37°C overnight. Biomass was collected by centrifuging

242 at 5,000 rpm for 30 min and fosmid DNA was extracted from the pellet using the QIAGEN
243 Plasmid Midi Kit (QIAGEN) following the manufacturer's instructions. Approximate size of
244 the cloned fragments was assessed on agarose gel electrophoresis after double endonuclease
245 digestion with *Xba*I and *Xho*I (New England Biolabs, Ipswich, MA, USA). The Sanger
246 sequencing of the termini of inserted metagenomic fragments of each purified fosmid was done
247 at Macrogen Ltd. (Amsterdam, The Netherlands) using standard pCC2FOS sequencing primers
248 (Epicentre). Non-redundant fosmids were selected, their DNA concentrations were quantified
249 by Qubit™ 4.0 Fluorometer dsDNA BR Assay Kit (Invitrogen), pooled in equimolar amounts
250 and prepared for Illumina MiSeq® sequencing. Pooled DNA was fragmented using the
251 Bioruptor Pico Sonicator (Diagenode, Denville, NJ, USA) with parameters adjusted to obtain
252 400-600 bp fragments. The fragment library was prepared using the NebNext Ultra II DNA
253 Library preparation kit (New England Biolabs, Ipswich, MA, USA) according to the
254 manufacturer's instructions. The obtained library was sequenced on MiSeq® platform
255 (Illumina, San Diego, USA) using a microflow cell 300-cycles V2 sequencing kit. Obtained
256 paired end reads were subjected to quality filtering, trimming and assembly as previously
257 described (40). Gene prediction and primary functional annotation were performed using the
258 MetaGeneMark annotation software (http://opal.biology.gatech.edu) (41). Translated protein
259 sequences were annotated using BLAST searches of UniProt and the non-redundant GenBank
260 databases (42). Multiple sequence alignments were generated using MUSCLE application (43)
261 and visualised on Geneious v.9 (Biomatters, New Zealand). The Neighbour-Joining and
262 maximum likelihood trees were constructed in MEGA X (44) using the settings for the Poisson
263 model and homogenous patterning between lineages. The bootstrapping was performed with
264 1,000 pseudoreplicates.

265 **Gene cloning, expression and purification of selected proteins.** Selected gene candidates
266 were amplified by PCR in a T100 Thermal Cycler (Bio-Rad) using Herculase II Fusion Enzyme
267 (Agilent, Cheadle, UK) with oligonucleotide primer pairs incorporating pET-46 Ek/LIC vector
268 adapters (Merck, Darmstadt, Germany). PCR products were then purified and cloned into the
269 above pET-46 Ek/LIC vectorharbouring an N-terminal 6xHis tag, as described by the
270 manufacturer. The DNA inserts in the resulting plasmids were verified by Sanger sequencing
271 at Macrogen Ltd. (Amsterdam, The Netherlands) and then transformed into *E. coli* BL21(DE3)
272 for recombinant protein expression. *E. coli* BL21(DE3) cultures harbouring pET-46 Ek/LIC
273 were grown on LB medium to mid-log growth phase (OD_{600} 0.7-0.8), induced with isopropyl-
274 β-d-thiogalactopyranoside (IPTG, 0.5 mM) and incubated at 20°C overnight. Cells were
275 disrupted by sonication as reported earlier (45) and recombinant proteins were purified using
276 metal-chelate affinity chromatography on Ni-NTA His-bind columns. Protein size and purity
277 were assessed using denaturing gel electrophoresis (SDS-PAGE), and protein concentration
278 was measured by Bradford assay (Merck, Gillingham, UK).

279 **Enzyme assays.** Carboxyl esterase activity of purified proteins against ***p*-nitrophenyl (*p*NP)**
280 **or α-naphthyl (αN) esters** was determined by measuring the amount of *p*-nitrophenol released
281 by esterase-catalysed hydrolysis essentially as described previously (27,45). Under standard
282 assay conditions the reaction mixture contained 50 mM potassium phosphate buffer (pH 7.0),
283 1 mM *p*-nitrophenyl butyrate as substrate, and 0.2-1.8 µg of enzyme in a final volume of 200
284 µl. Reactions were incubated at 30°C for 3-5 min and monitored at 410 nm (for *p*NP esters) or

310 nm (for αN esters). Non enzymatic hydrolysis of ester substrates was subtracted using a blank reaction with denatured enzyme. The effect of pH on esterase activity was evaluated using the following buffers: sodium citrate (pH 4.0 and 5.0), potassium phosphate (pH 6.0 and 7.0), Tris-HCl (pH 8.0 and 9.0). The activity was monitored at 348 nm (the pH-independent isosbestic wavelength of *p*-nitrophenol). The effect of temperature on esterase activity was studied using a range of temperatures (from 20°C to 95°C). In order to assess the thermal stability of purified esterases, the enzymes were dissolved in potassium phosphate buffer (pH 7.0) and preincubated at the indicated temperature for 20 min. The enzyme solutions were then cooled down on ice and the residual activity was measured under standard conditions (at 30 ºC). Substrate specificity of purified enzymes was analysed using model *p*NP- and αN-esters with different chain lengths: *p*NP-acetate (C2), αN-propionate (C3), *p*NP-butyrate (C4), αN-butyrate (C4), *p*NP-hexanoate (C6), *p*NP-dodecanoate (C12), and *p*NP-palmitate (C16), obtained from Sigma-Aldrich and Tokyo Chemical Industry TCI. Kinetic parameters for these substrates were determined over a range of substrate concentrations (0.012-4 mM; 30 ºC) and calculated by non-linear regression analysis of raw data fit to Michaelis-Menten function using GraphPad Prism software v.6. Hydrolysis of 44 **soluble non-chromogenic monoester substrates** (Table S2) and **T-2 mycotoxin** (Merck Life Science S.L.U., Madrid, Spain) was assayed at 37ºC using a pH indicator assay with Phenol Red and monitored at 550 nm (46). The reaction products of enzymatic degradation of T-2 mycotoxin were analysed using reversed phase chromatography on a Waters 600 HPLC system equipped with a Zorbax Eclipse Plus C18 column (Agilent, 4.6 x 100 mm, 3.5 µm, 40ºC) and a light scattering detector (ELSD). The reaction products were separated using gradient elution (1.0 ml/min) with acetonitrile (with 0.2% (vol/vol) formic acid) and water (5%: 1 min, 5%-95%: 9 min, 95%: 3 min, 5%: 7 min). Polyester depolymerization activity of purified proteins against 3PET (bis(benzoyloxyethyl) terephthalate) was measured using 1.5% agarose plates containing 0.2% of emulsified polyesters. 3PET was purchased from CanSyn Chem. Corp. (Toronto, Canada). Agarose plates with emulsified 3PET were prepared as described previously (47). After protein loading, the plates were sealed and incubated at 37 ºC for 1-5 days. The presence of polyesterase activity was indicated by the formation of a clear zone around the wells with proteins. Apart from plate assays, activity assays of IS10, IS11 and IS12 for **3PET suspension hydrolysis** were performed in 50 mM Tris-HCl buffer, pH 8.0, at 30 °C, in a shaker 600 at rpm, the final reaction volume for each experiment was 0.2 mL, and the final protein amount 50 µg. The reactions were terminated after 13 h by filtering reaction mixture on a 10 kDa spin filter. 10 µL of filtrate was analysed using the high-performance liquid chromatography system (HPLC), Schimadzu, Prominence-I (Milton Keynes, UK) equipped with a Schimadzu C18 Shim-pack column (4.6 × 150 mm, 5 µm). The mobile phase was 25 % (vol/vol) methanol with 0.1% (vol/vol) H_3PO_4 in HPLC-grade water at a flow rate of 0.7 mL min^{-1} for 2 min, following increase to 55 % of methanol to 118 min, followed by 25% methanol at 22 min; the effluent was monitored at the wavelength of 240 nm, the column was conditioned at 40 ºC. The hydrolytic products of mono(2-hydroxyethyl)terephthalic acid (MHET), bis(2-hydroxyethyl)terephthalate BHET and terephthalic acid (TPA) were identified by comparing the retention times with their standards, reactions without enzyme were served as negative controls. All samples of each experiment were analysed in triplicate. **Enzymatic activity against PLA** was assayed by measurement of lactic acid production as follows: 5 mg of each PLA (all, acid-terminated and purchased from

329 PolySciTech (W. Lafayette, USA)), P(D)LA 10-15,000 Da, P(D,L,)LA (Resomer R202H, 10-
330 18,000 Da) or P(L)LA 15-25,000 Da) suspended in 0.5 mL of 0.4 M Tris-HCl (pH 8.0) were
331 mixed with 50 µg of purified enzyme and incubated for 48 h at 37 ºC with shaking (1000 rpm).
332 Samples were then centrifuged at 12,000 g for 5 min at 4 ºC. 200 µl of supernatant were mixed
333 with 200 µl of mobile phase (0.005 N H_2SO_4). Sample was filtered through 13 mm Millipore
334 PES syringe membrane filter (0.02 µm pore diameter) and analysed by HPLC Shimadzu,
335 Prominence-I (Milton Keynes, UK) with an ion exchange column Hi PlexH (300 x 7.7 mm)
336 (Agilent, Cheadle, UK) and 0.6 mL min^{-1} flow rate at 55 ºC (oven temperature) with UV
337 detector set at 190-210 nm.

338 **Protein crystallization and structure determination.** Native metagenomic esterases were
339 purified using metal-chelate affinity chromatography, and crystallization was performed at
340 room temperature using the sitting-drop vapor diffusion method (protein concentration 25
341 mg/ml, reservoir solution 0.1 M citric acid, pH 3.5 and 19% PEG 3350). The crystal was
342 cryoprotected by transferring into paratone oil and flash frozen in liquid nitrogen. Diffraction
343 data for the IS11 crystal was collected at 100 K at a Rigaku home source Micromax-007 with
344 R-AXIS IV++ detector and processed using HKL3000 (48). The structure was solved by
345 molecular replacement using Phenix.phaser (49) and a model built by AlphaFold2 (50). Model
346 building and refinement were performed using Phenix.refine and Coot (51). TLS
347 parameterization was utilized for refinement, and *B*-factors were refined as isotropic. Structure
348 geometry and validation were performed using the Phenix Molprobity tools. Data collection
349 and refinement statistics for this structure are summarized in Table S3.

350 **Accession numbers.** DNA sequences of positive fosmids were deposited to GenBank under
351 accession numbers OL304252, OL304253, and OL304254. The atomic coordinates of IS11
352 have been deposited in the Protein Data Bank, with accession code 7SPN.

353

354 **RESULTS and DISCUSSION**

355 **Natural microbial communities of terrestrial hydrothermal vents of Ischia and effect of**
356 **polyester enrichments.** To provide insights into the composition of natural microbial
357 communities and thermophilic enzymes of hydrothermal vents of the island of Ischia, four
358 sediment samples were collected from the Cavascura hot spring (samples IS1 and IS2) and
359 from Maronti beach near Sant'Angelo (samples IS3 and IS4) (see Materials and Methods).
360 Both sites represent thermophilic habitats with slightly different environmental conditions: IS1
361 (pH 7.0, 45 ºC), IS2 (pH 8.5, 55 ºC), IS3 (pH 4.5, 75 ºC), and IS4 (pH 5.0, 85 ºC) (Table S1).
362 From each sample, total DNA was extracted and subjected to barcoded amplicon sequencing
363 of the V4 region of 16S rRNA gene. Sequence analysis revealed that the IS1 community
364 comprised mainly *Pseudomonas* (17.2 %), class Anaerolineae (Chloroflexi) (12.3%), class
365 Armatimonadota (10.0%), *Elizabethkingia* (phylum Bacteroidota) (9.5%), other Myxococcota
366 (9.1 %), *Sphingobacterium* (order Sphingobacteriales, class Bacteroidia, phylum
367 Bacteroidota) (6.7 %), and class Nitrospirota (6.4%), whereas the IS2 community was
368 dominated by *Caldimonas* (order Burkholderiales, class Gammaproteobacteria) (63.9 %),
369 *Cutibacterium* (order Propionibacteriales, class Actinobacteria) (17.2%), and *Thermus*
370 (phylum Deinococcota) (16 %) (Figure 1). In contrast, the IS3 community was mainly

371 represented by Bacillales (Firmicutes), namely *Brevibacillus* (48.3%) and *Geobacillus* (42 %),
372 and other Bacilli (4.4 %), whereas IS4 comprised *Sphingobacterium* (Sphingobacteriales,
373 Bacteroidetes) (31.9 %), *Thermobaculum* (Thermobaculales, Chloroflexi) (17.4 %) and
374 *Geobacillus* (10.7 %), followed by *Pseudomonas* (7%) and *Bacillus* (6.1%) (Figure 1). The
375 observed differences in the taxonomic composition of the Cavascura (IS1 and IS2) and Maronti
376 (IS3 and IS4) samples can be attributed to different environmental conditions (temperature and
377 pH) at the sampling sites.

378 Using the four sediment samples from two Ischia sites, twelve enrichment cultures were
379 established with different polyester plastics as carbon substrate including polyhydroxybutyrate
380 (PHB), polylactic acid (PLA) and commercial polyester blend (Table S1). After two weeks of
381 incubation with polyesters, the IS1 enrichment culture showed a drastic increase in the relative
382 abundance of members of the order Burkholderiales within the families Comamonadaceae and
383 Rhodocyclaceae (relative abundance 15.2-35.1 % across the three plastic enrichments),
384 *Fontimonas* (Solimonadaceae, 16.9-27.5%), and *Schleiferia* (order Flavobacteriales, 15.6-
385 34.4%) (Figure 1). Likewise, IS2 enrichment showed an increase in *Fontimonas* (11-26%),
386 *Schleiferia* (21% in PLA enrichment), whereas the relative content of the *Caldimonas*
387 decreased from 63 % to 5.7 %, in favour of members of other families of the order
388 Burkholderiales, namely Rhodocyclaceae, Hydrogenophilaceae and Comamonadaceae (18-
389 43%) Kapabacteriales (phylum Bacteroidota) 2.9-8% and Rehaibacterium (order
390 Xanthomonadales) 0.3-9.3% (Figure 1). The enrichment culture with the compostable P3 blend
391 stimulated the growth of Rhodocyclales, as both IS1 and IS2 showed a strong increase in
392 *Thauera* compared to experiments with PHB and PLA (Figure 1). In the enrichment cultures
393 IS3 and IS4, higher incubation temperature (75°C) selected for thermophilic bacteria, and the
394 nature of polyester used for enrichments influenced the microbial composition (Figure 1). The
395 PHB enrichment stimulated growth of *Thermus* (Deinococcota), which accounted for 66.7 %
396 (92-fold increase) and 90.9% (1,280-fold increase) of the total reads in IS3 and IS4,
397 respectively, followed by *Geobacillus* and other members of Firmicutes. In contrast, the PLA
398 culture favoured growth of *Geobacillus*, which reached a relative abundance of 95.8% in IS3
399 (2.3-fold increase) and 91.8% in IS4 (8.6-fold increase), followed by *Thermus* and
400 *Brevibacillus*. Finally, the commercial polyester blend promoted growth of both *Geobacillus*
401 (accounted for 68 % or 1.6-fold increase) and *Thermus* (accounted for 31.5% or 43.8-fold
402 increase) in the IS3 enrichment, whereas the IS4 culture was dominated by Firmicutes,
403 *Geobacillus* (81 %), *Paenibacillus* (11.9%), *Brevibacillus* (5.9 %), and *Thermus* (1.18%). As
404 expected, the Shannon index of microbial diversity (a measure of diversity of species in a
405 community) (Figure S1) revealed an overall tendency to decrease after incubation with
406 polyester plastics, with the exception of IS2, which also showed low diversity in the native
407 sample with the flattened rarefaction curve (Figure S1)

408

409 **Activity-based screening of the hydrothermal metagenome library from Ischia for**
410 **carboxylesterase activity.** After two weeks of incubation with polyesters, total DNA was
411 extracted from the enrichment cultures and combined for the construction of the metagenomic
412 fosmid library IS_Libr2. In order to identify carboxylesterases with high-temperature profiles,
413 this library was screened for esterase activity with tributyrin as substrate (for carboxylesterases
414 and lipases) at three temperatures: 37, 50 and 70 °C. Emulsified tributyrin gives a turbid
415 appearance to the plates, and the presence of active metagenomic esterases or lipases is seen as

416 a clear zone around the colony. After screening 3,456 clones from the IS_Libr2 library on
417 tributyrin agar plates, 64 positive hits were identified with 19 positive clones observed at 37
418 °C, 27 clones at 50 °C, and 18 clones at 70 °C. Furthermore, eight esterase positive clones
419 detected at 50 °C were found to be unique for this temperature, whereas one unique clone was
420 found at 70 °C suggesting that these esterases are mostly active only at elevated temperatures.
421 Following endonuclease digestion profiling and Sanger sequencing analysis, 14 non-redundant
422 fosmids were selected for insert sequencing using the Illumina platform, and fosmid inserts
423 were assembled with an average size of 39 kbp. Sequence analysis revealed 12 putative ORFs
424 encoding predicted hydrolases (including peptidases, carboxylesterases, β-lactamases, serine
425 proteases) homologous to proteins from Chloroflexi and metagenome assembled genome
426 (MAG) affiliated to thermophilic Chloroflexi. From candidate proteins cloned in *E. coli*, three
427 putative carboxylesterases (IS10, IS11, and IS12) were soluble, when expressed in *E. coli* cells,
428 and the presence of carboxylesterase activity in purified proteins was confirmed using
429 tributyrine agarose plates assay (Table 1) and were further selected for detailed biochemical
430 characterisation. Amino acid sequences of IS10 (314 amino acids), IS11 (455 aa), and IS12
431 (318 aa) showed no presence of recognizable signal peptides suggesting that they are
432 intracellular proteins. Both IS10 and IS12 belonged to the α/β hydrolase superfamily and had
433 56.8% sequence identity one to another, whereas IS11 showed no significant sequence
434 similarity to IS10 and IS12 as was a member of the large family of β-lactamases and penicillin-
435 binding proteins (Table 1). A blastP search of the nrNCBI database revealed that amino acid
436 sequences of IS10 and IS12 were identical to two putative α/β hydrolases HEG24678 from
437 uncultured Chloroflexi bacteria (GenBank accession numbers HEG24678.1 and HHR50377.1,
438 respectively), whereas the IS11 sequence exhibited the highest identity (99.1%) to the putative
439 "class A β-lactamase-related serine hydrolase" HDX58025.1 from uncultured
440 Dehalococcoidia. Interestingly, the top homologous proteins of Ischia esterases were the
441 proteins identified in metagenome from a deep-sea hydrothermal vent (black smoker) in the
442 Mid-Atlantic Ridge (South Atlantic Ocean) (52). The comparison with previously
443 characterised proteins showed the thermostable arylesterase, Are, from *Saccharolobus*
444 *solfataricus* (UniProt ID B5BLW5, 306 aa) being the top homologue for IS10 (42 % sequence
445 identity), whereas the metagenome-derived esterase Est8 (KP699699, PDB 4YPV, 348 aa) was
446 the top characterised homologue for IS12 (56 % sequence identity) (53,54) (Fig. S2). The IS11
447 sequence was homologous to penicillin-binding proteins and β-lactamases with low sequence
448 similarity to the CmcPBP from Actinobacteria *Amycolatopsis lactamdurans* (Q06317, 36 %
449 identity) and esterase EstB from *Burkholderia gladioli* (Q9KX40, 32 % identity) (55,56).
450 Domain and multiple sequence alignment confirmed the presence of conserved regions and
451 motifs linked to esterase activity in lipolytic families previously described (Fig. S2 and S3).
452 IS10 and IS12 contained an α/β hydrolase fold (PF07859), displaying the characteristic
453 catalytic triad composed of Ser^{155}, Asp^{250} and His^{281} and the conserved consensus motif G-x-
454 S-x-G around the active site serine (22), clustering together with representatives of family IV
455 (Fig. S2 and S3).

456 The protein IS11 contained a β-lactamase domain (PF00144) and the consensus tetrapeptide S-
457 x-x-K, perfectly conserved among all penicillin-binding enzymes and β-lactamases,
458 surrounding the active serine Ser68. In addition, Lys71 and Tyr160 were also conserved as part
459 of the catalytic triad of family VIII esterases, which groups enzymes with homology to class C
460 β-lactamases and penicillin-binding proteins (Fig. S2 and S3).

461 **Biochemical characterisation of purified metagenomic carboxylesterases using model**
462 **esterase substrates.** The esterase activity of purified proteins (IS10, IS11, IS12) was initially
463 evaluated using model esterase substrates with different chain lengths (C2-C16) at 30ºC (to
464 diminish spontaneous substrate degradation at high temperatures). The proteins were found to
465 be active against several short acyl chain substrates with IS10 and IS11 showing a preference
466 to *p*-nitrophenyl butyrate (*p*NP-butyrate), α-naphthyl butyrate (αN-butyrate), and *p*NP-
467 hexanoate, whereas IS12 was most active with *p*-NP-acetate and αN-propionate (Figure 2). All
468 enzymes were active within a broad pH range (pH 6.0-10.0) with maximal activities at pH 9
469 (data not shown). The purified metagenomic carboxylesterases exhibited saturation kinetics
470 with model esterase substrates at optimal pH (9.0) and 30 ºC (Table 2). IS10 appeared to be the
471 most efficient esterase compared to IS11 and IS12, with the highest substrate affinity (lowest
472 K_M) and catalytic efficiency (k_{cat}/K_M) towards the tested model substrates. IS12 showed higher
473 substrate affinity to *p*NP-butyrate and higher activity with *p*NP-acetate than IS11, whereas the
474 latter was more active against *p*NP-butyrate (Table 2). Overall, both IS10 and IS12 appeared
475 to be more active against the tested model substrates compared to IS11.

476 Since the selected carboxylesterases originated from thermophilic environments, we
477 investigated the effect of temperature on the activity (temperature profiles) and thermostability
478 of purified carboxylesterases using *p*-NP-butyrate as substrate (Fig. 3). All enzymes showed
479 significant activity at 20ºC, but reaction rates increased 5-10 times at higher temperatures with
480 IS10 showing the highest activity at 60-70 ºC, whereas IS12 was most active at 70ºC-80ºC and
481 IS11 at 80-90 ºC (Fig. 3). The thermostability of purified enzymes was analysed using 20 min
482 preincubation at different temperatures (from 30 to 95ºC) followed by esterase assays with
483 *p*NP-butyrate at 30 ºC. IS10 retained 60% activity after preincubation at 50 ºC and showed a
484 complete loss of activity at 80ºC (Fig. 3). In contrast, both IS11 and IS12 revealed a significant
485 decrease of activity only after 20 min preincubation at 90 ºC and 70 ºC, respectively. After two
486 hours of incubation at 70 ºC, IS12 retained 50% of initial activity, but was completely
487 inactivated at 80 ºC (Fig. 4). However, IS11 showed no loss or a small reduction of activity at
488 70 ºC and 80 ºC, respectively, and required over three hours of incubation at 90ºC for
489 inactivation (Fig. 4). Thus, the metagenomic carboxylesterases from the Ischia hydrothermal
490 vents are the thermophilic enzymes highly active at 70-80 ºC with IS11 and IS12 also showing
491 significant thermostability at temperatures from 60 to 80 ºC. Furthermore, the thermostability
492 of IS11 and IS12 was comparable with, or exceeded the, thermostability of other metagenomic
493 esterases identified in high-temperature environments (40,57-60).

494 Esterase activity of purified metagenomic esterases was inhibited by high concentrations
495 of NaCl (50-67% of remaining activity in the presence of 0.5 M NaCl) with IS11 showing a
496 slightly higher resistance (Fig. S4). Similarly, IS11 retained higher activity in the presence of
497 non-ionic detergents (43% and 53% in the presence of 2% Triton X-100 and Tween 20) (Fig.
498 S4). With organic solvents, IS10 was inhibited by acetone, acetonitrile, ethanol, methanol, and
499 isopropanol (10 %, v/v) (Fig. S5). In contrast, IS11 was more tolerant to these solvents (10-50
500 %) and was stimulated by 10% ethanol (60% increase) and 30% methanol (84% increase).
501 Furthermore, low concentrations of these solvents (10%, v/v) stimulated esterase activity of
502 IS12 (26-34 % increase), whereas higher concentrations of acetone and isopropanol (30%)
503 were inhibiting. Finally, DMSO (10-30 %) stimulated esterase activity of all purified enzymes
504 (20-46 % increase) (Fig. S5).

505 **Substrate range of purified carboxylesterases.** To analyse the substrate range and preference
506 of metagenomic carboxylesterases from the Ischia hydrothermal vents, the purified proteins
507 were examined for the presence of hydrolytic activity against chemically and structurally
508 diverse esters, including alkyl and aryl esters (Materials and Methods). Both IS10 and IS12
509 revealed a broad substrate range with significant activity against all 51 esters tested ester
510 substrates and the highest activity with phenyl acetate, phenyl propionate, glyceryl
511 tripropionate, tributyrin, and naphthyl acetate (Table S2). IS12 was also highly active toward
512 pentane-1,5-diyl diacrylate, tri(propylene glycol) diacrylate, and vinyl propionate. The broad
513 substrate range of IS10 and IS12 correlates with relatively large effective volumes of their
514 active sites, 650.23 $Å^3$ and 780.5 $Å^3$, respectively (calculated as cavity volume/solvent
515 accessible surface area) (23). These volumes are the largest calculated for prokaryotic esterases
516 experimentally characterised so far, with only CalA lipase (Novozym 735) from the yeast *C.*
517 *antarctica* having a larger value (23). IS11 had a more restricted substrate range, showing
518 detectable activity against 22 ester substrates of 51 tested with a preference for benzyl (*R*)-(+)-
519 2-hydroxy-3-phenylpropionate (Suppl. Table S2). The three metagenomic esterases revealed
520 no apparent enantio-preference and hydrolysed both enantiomers of several tested
521 commercially available chiral substrates.

522 The purified metagenomic esterases were also tested for hydrolytic activity against the T-
523 2 mycotoxin, which contains three ester groups on its side chains. The T-2 and deacetylated
524 HT-2 toxins are members of the large group of trichothecene mycotoxins (over 190 derivatives)
525 containing a tetracyclic ring system (61). Mycotoxins are highly toxic fungal metabolites
526 frequently contaminating food and feed and causing negative effects on human health, animals,
527 and economy (62,63). While physical and chemical methods have been used to detoxify
528 mycotoxins, biological detoxification using enzymes or microbes is more attractive due to
529 specificity, safety, and costs. With T-2 as substrate, both IS10 and IS12 showed high esterase
530 activity based on a pH-shift assay with phenol red (2.3 U/mg and 4.4 U/mg, respectively, at
531 37ºC and pH 8.0), whereas IS11 was found to be inactive. Hydrolytic activity of IS10 and IS12
532 against T-2 was confirmed using HPLC, which also revealed the formation of different reaction
533 products (Fig. 5). IS10 produced HT-2 as the main product, whereas HT-2 was present as the
534 minor product in the reaction mixture with IS12, which produced mostly the T-2 triol as the
535 main product (Fig. 5). Since the T-2 triol is known to be less toxic than T-2 and HT-2 (64),
536 IS12 might represent a promising candidate for the biodetoxification of T-2 and HT-2.
537
538 Since our metagenomic libraries were prepared using enrichment cultures with synthetic
539 polyesters, the purified metagenomic esterases were also tested for the presence of polyesterase
540 activity. Although recent studies on biocatalytic depolymerization of synthetic polyesters
541 including PLA and polyethylene terephthalate (PET) have shown the potential of microbial
542 carboxylesterases, there is an urgent need to identify novel robust polyesterases for applications
543 in plastics recycling (35,47,65). The purified metagenomic esterases were screened for the
544 presence of polyesterase activity using an agarose plate assay with the emulsified PET model
545 substrate, 3PET. These screens revealed the presence of polyesterase activity against 3PET in
546 both IS10 and IS12, as indicated by the formation of a clear zone around the wells with loaded
547 enzymes after incubation at 37ºC (Fig. 6A). Purified IS11 did not show a visible clearance zone
548 on the 3PET plate, however the *in vitro* assay of hydrolysis of 3PET and HPLC analysis of
549 reaction products, showed an increase in MHET, which was the main hydrolysis product while

IS10 and IS12 produced BHET as the principal hydrolysis product. Thus, both IS10 and IS12 exhibit broad substrate profiles and were able to degrade both mycotoxins and polyesters.

Structural studies of metagenomic carboxylesterases. To provide structural insights into the active site and activity of metagenomic carboxylesterases, purified proteins (IS10, IS11, and IS12) were subjected to crystallization trials. IS11 produced diffracting crystals, and its crystal structure was determined by molecular replacement (Table S3, Materials and Methods). The overall structure of IS11 revealed a protein dimer with protomers composed of two structural domains, an N-terminal β-lactamase-like serine hydrolase domain (1-345 aa) connected via a flexible linker (346-358 aa) to a C-terminal lipocalin domain (Fig. 7). Protein oligomerization has been suggested to contribute to thermostability of several thermophilic carboxylesterases (e.g. AFEst, PestE, EstE1) (33,60,66). Accordingly, the results of size-exclusion chromatography of purified IS11, as well as IS10 and IS12, suggest that these proteins exist as dimers in solution (Figure S7).

The serine β-lactamases (classes A, C, and D) are structurally and evolutionary related to penicillin-binding proteins (the targets of β-lactam antibiotics), which also include hydrolytic DD-peptidases (67,68). The overall structure of the IS11 β-lactamase domain is composed of a mostly α-helical (all-α) sub-domain inserted into an α/β/α sandwich (or an α/β sub-domain) (Fig. 7 and 8 and Fig. S6). The α/β/α sandwich sub-domain includes a nine-stranded antiparallel β-sheet flanked by two helices on each side, whereas the mostly helical sub-domain comprises nine α-helices (Fig. 8). The two sub-domains form a groove accommodating the catalytic residues including Ser68 and Lys71 (1st motif S-x-x-K), Tyr160 and Asn162 (2nd motif Y-x-N/S), and His299 (3rd motif H/R/K-T/S/G-G). Accordingly, the IS11 structure revealed the presence of an additional electron density positioned near the side chains of Ser68, Tyr160, and His299, which can represent a small molecule ligand tightly bound in the active site (Fig. 9). The positioning of these catalytic residues was also conserved in the active sites of the biochemically characterised carboxylesterases with a β-lactamase fold (family VIII): EstB from *Burkholderia gladioli* and Pab87 from *Pyrococcus abyssi* (69,70), suggesting a common catalytic mechanism with acylation-deacylation. The catalytic cleft of IS11 also contains several hydrophobic and polar residues potentially involved in substrate binding (Asp126, Phe128, Trp158, Asn304, Ile307, Leu309) (Fig. 9).

The C-terminal domain of IS11 represents a typical lipocalin fold with one α-helix and an eight-stranded antiparallel β-barrel containing a hydrophobic core (Fig. 10). Lipocalins are a diverse family of small individual proteins or domains (160-180 aa), which bind various hydrophobic molecules (e.g. fatty acids) in a binding pocket located inside the barrel (71). Although lipocalins are very divergent in their sequences and functions, their structures exhibit remarkable similarity. The lipocalin α-helix of IS11 closes off the top of the β-barrel, whose interior represents a ligand-binding site coated mostly with hydrophobic residues (Fig. 10). In the IS11 protomer, the lipocalin domain covers the β-lactamase domain shielding the catalytic cleft with the extended proline-rich strand (Pro391-Ser409) containing eight Pro residues (Pro391, Pro396, Pro401, Pro402, Pro404, Pro406, Pro407, and Pro408) (Fig. 10). In the thermophilic carboxylesterase Est2 from *Alicyclobacillus acidocaldarius*, the increased number of Pro residues has been suggested to be important for thermostability, because they reduce the flexibility of loops and other structural elements making them more resistant to denaturation (72). The side chains of several residues of the lipocalin domain and proline-rich strand are positioned close to the IS11 active site suggesting that they can be involved in

595 substrate binding (Phe395, Arg397, Arg398, Arg403, Arg449). Typically for all lipocalins, the
596 interior of the IS11 β-barrel is coated by mostly hydrophobic and polar residues (Leu373,
597 Ser374, Ile376, Leu387, Gln389, Leu426, Ser429, Phe444, Phe446, Phe451). Proline-rich
598 sequences are also known to be directly involved or facilitating protein-protein interactions or
599 oligomerization (73). However, the IS11 dimer structure revealed no obvious interactions
600 between the individual lipocalin domains suggesting that the lipocalin domain of IS11
601 participates in substrate binding, rather than in the oligomerization.

602 High-quality structural models of IS10 and IS12 proteins constructed using the Phyre2
603 server (Fig. S8) revealed the presence of a core domain with a classical α/β hydrolase fold and
604 an all-helical domain, as well as a serine hydrolase catalytic triad (Ser155, His280, and Asp250
605 in both proteins) (Fig. S9). The putative catalytic nucleophile Ser155 is located on the classical
606 nucleophilic elbow, a short sharp turn between a β-strand and α-helix. It is located at the bottom
607 of the active site, which is mostly covered by the all-helical lid domain (Fig. S9). Both acyl-
608 and alcohol-binding pockets of IS10 and IS12 include several hydrophobic and polar residues
609 potentially involved in substrate binding (IS10: His81, Trp85, His93, Asn159, Tyr183, Val185,
610 Leu252; IS12: Trp85, Ile87, His93, Asn159, Tyr183, Leu252, Ile279, Val283, Trp284,
611 Leu285) (Fig. S9). Furthermore, the lid domains of both enzymes contain additional
612 hydrophobic residues, which can contribute to substrate binding (IS10: Phe34, Met38, Phe203,
613 Leu204, Met208, Met209, Tyr211; IS12: Phe22, Met34, Tyr195, Leu203, Leu204, Met209,
614 Phe212, Trp213).

615

616 **CONCLUSION**

617 Present work has demonstrated a high value of high-temperature microbial habitats,
618 particularly of the volcanic island of Ischia (Italy), Terme di Cavascura and Maronti Beach
619 hydrotherms populated by taxonomically diverse microorganisms, as a resource for discovery
620 of high-temperature active enzymes. As revealed by an in-depth characterization of three
621 metagenomics-derived carboxylesterases (IS10, IS11 and IS12) they were active at
622 temperatures as high as 70-90 ºC and were capable to degradation of bio-based and synthetic
623 polyester plastics. The 3PET was hydrolysed by IS10 and IS12 to predominantly bis(2-
624 hydroxyethyl)terephthalate (BHET), while IS11 produced mono(2-hydroxyethyl)terephthalate
625 (MHET) as a main product. Interestingly, IS12 further degraded mycotoxin T-2, a common
626 agent causing poisoning the animal feed, to the less toxic T-2 triol. The three wild-type
627 enzymes may readily be applicable in pilot trials in industrial processes relevant to the circular
628 bioeconomy for plastics and/or in the production of toxin free foods and feeds. This study can
629 also serve as a starting point for deepening our knowledge on structural determinants for
630 substrate specificity in carboxylesterases and for rational engineering to further improve their
631 catalytic efficiencies to make them accepting PET oligomers larger than 3PET.

632

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645

FIGURES

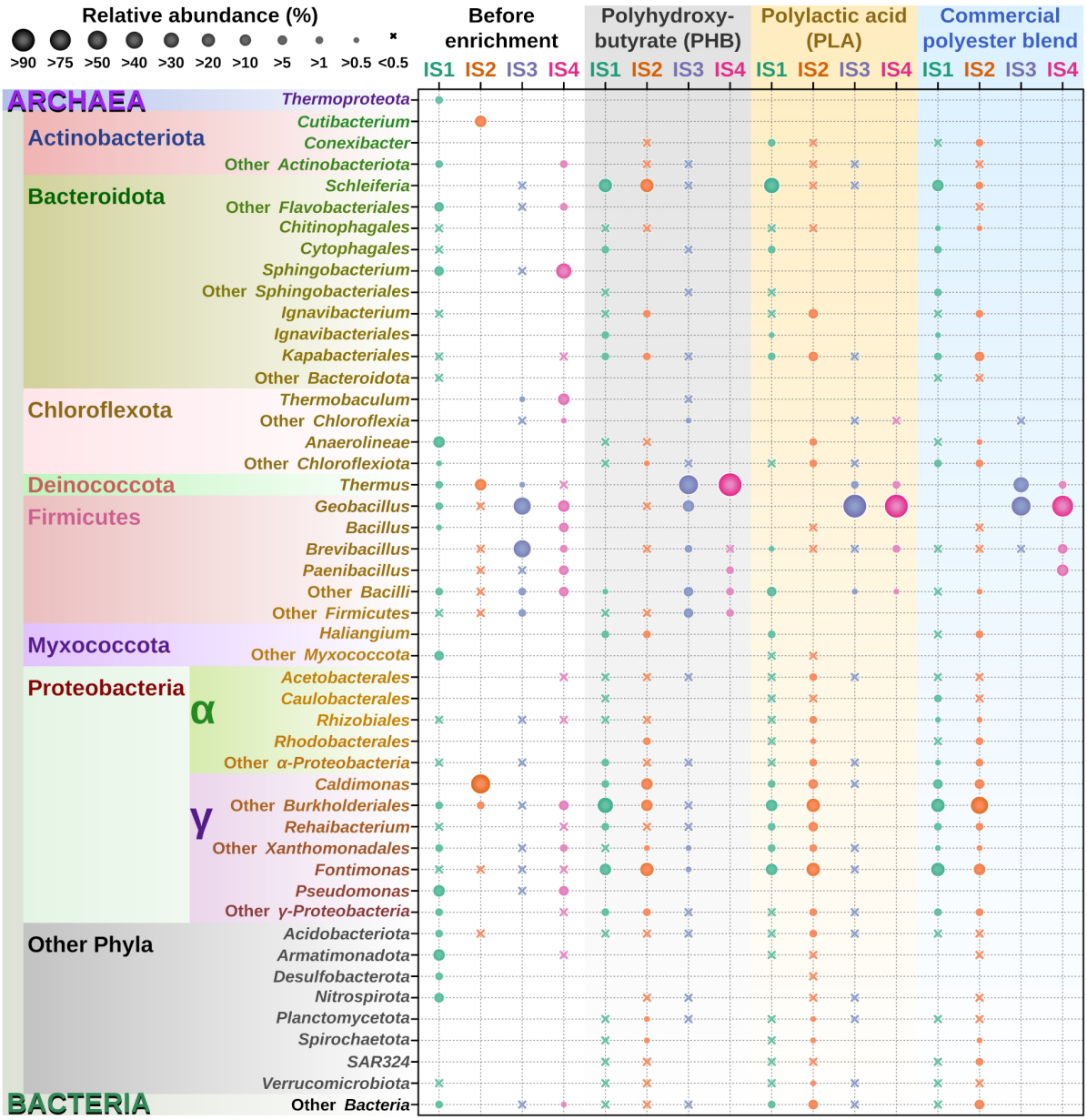


Figure 1. The composition of microbial communities of native samples (IS1-IS4) and polyester enrichment cultures from the Ischia hydrothermal vents. as revealed using barcoded amplicon sequencing of the V4 region of 16S rRNA gene.

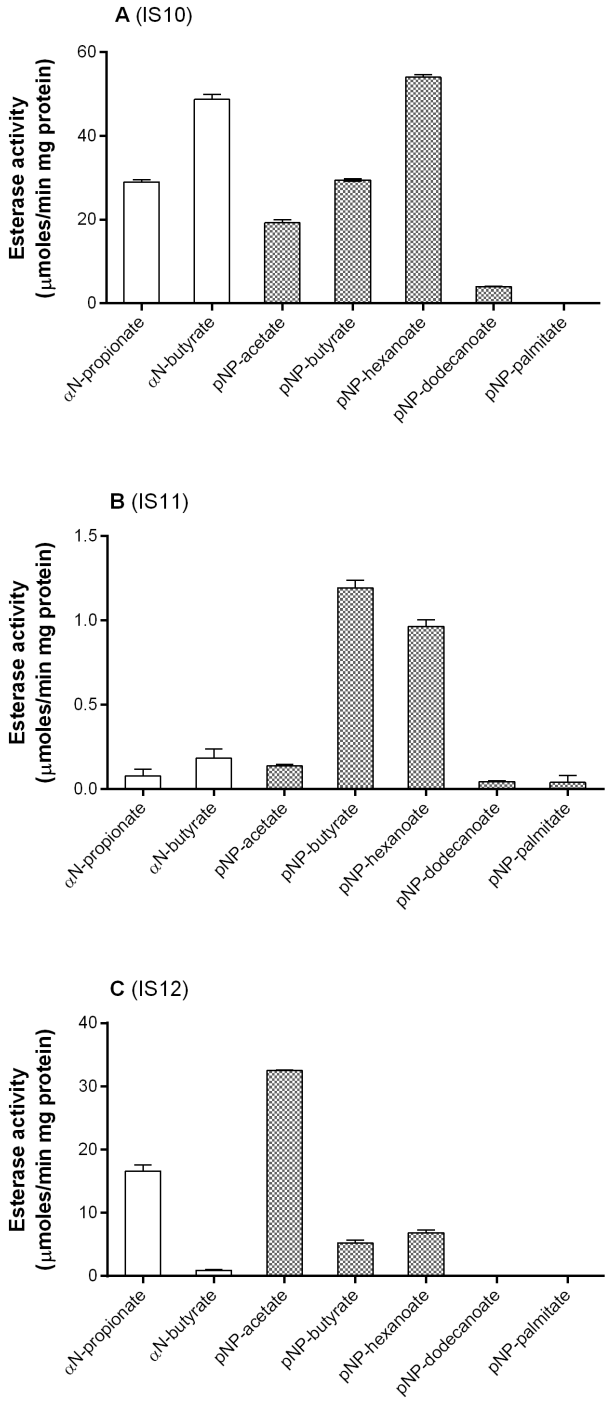


Figure 2. Hydrolytic activity of purified IS10 (A), IS11 (B) and IS12 (C) against model esterase substrates. The reaction mixtures contained the indicated *p*-nitrophenyl esters (*p*NP, white bars) and α-naphthyl esters (αN, grey bars) with different acyl chain lengths (reaction temperature 30ºC, see Materials and Methods for details).

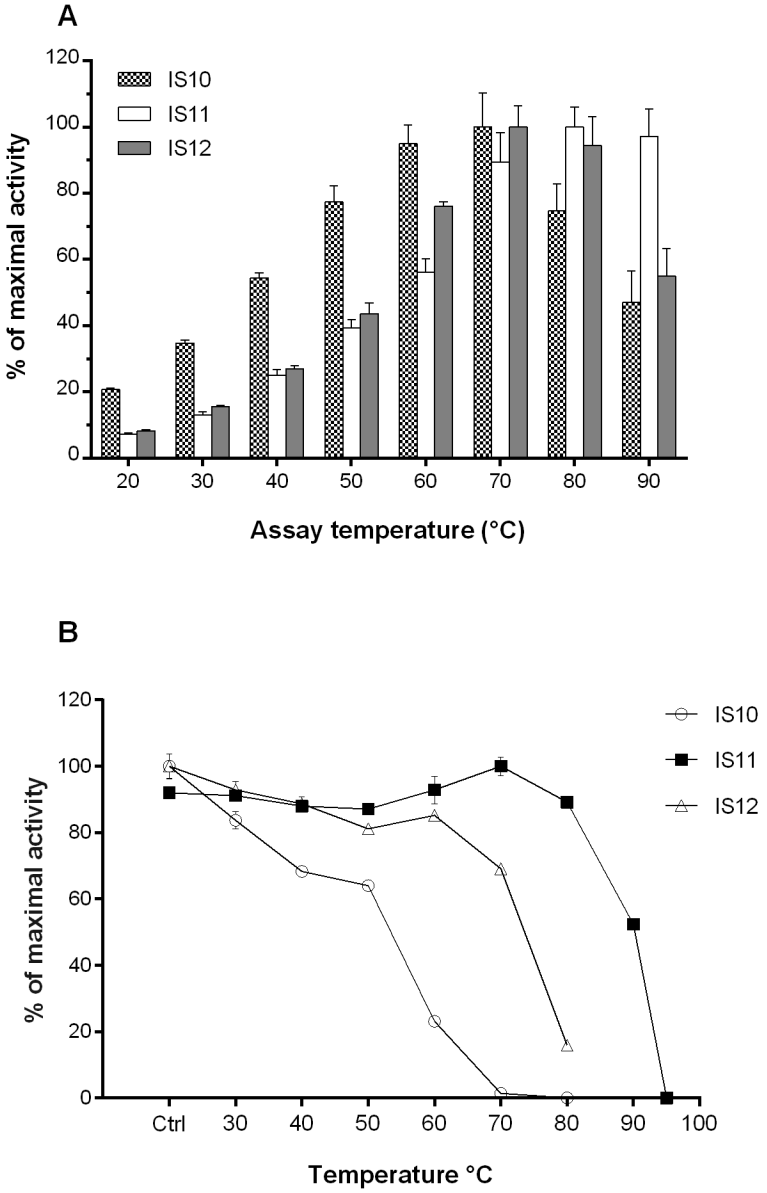


Figure 3. Activity temperature profiles and thermostability of purified metagenomic carboxylesterases from Ischia. (A) Esterase activity of purified enzymes with *p*NP-butyrate at different temperatures. **(B)** Thermostability of purified enzymes measured as residual activity after 20 min preincubation at different temperatures. Esterase activity was determined with *p*NP-butyrate as substrate at 30ºC.

646

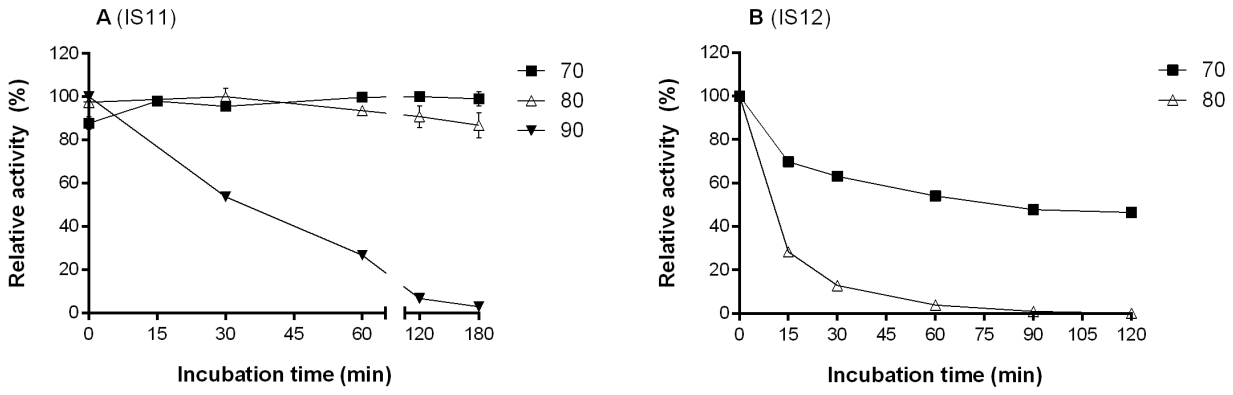


Figure 4. Thermoinactivation of purified IS11 (A) and IS12 (B) at different temperatures. Activity data are presented as relative activity from triplicate measurements ± SD. Residual activity was determined with *p*NP-butyrate at 30 ºC.

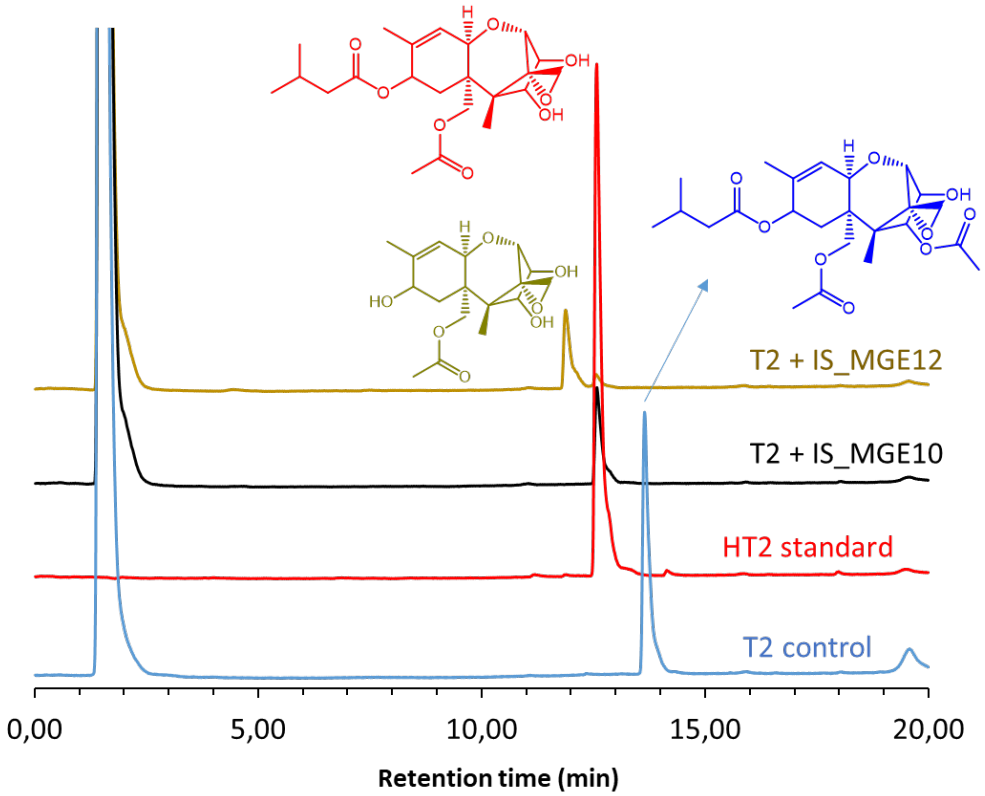
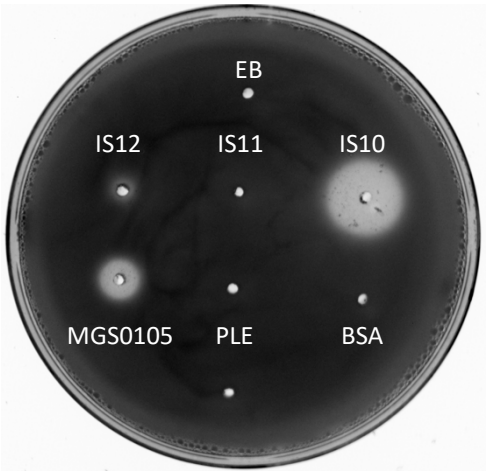


Figure 5. Hydrolytic activity of purified IS10 and IS12 against the mycotoxin T-2: HPLC analysis of reaction products. Purified IS10 and IS12 were incubated with T-2 (at 37 ºC and pH 8.0), and reaction products were analysed using HPLC (see Materials and Methods for experimental details).

A



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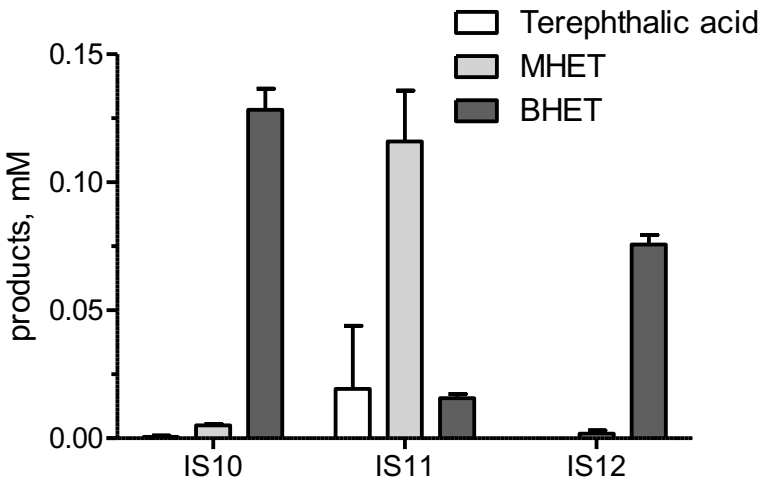

C

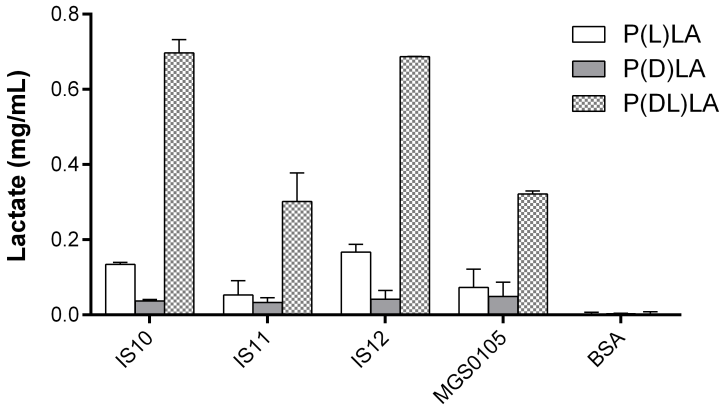

Figure 6. Polyesterase activity of metagenomic esterases against PLA and 3PET. **(A)** plate assay with emulsified 3PET as substrate. The formation of a clear zone around the wells with loaded enzyme indicates the presence of polyesterase activity. Agarose plates (1.5%) containing 0.2% emulsified 3PET and loaded proteins (50 µg/well) were incubated at 37ºC and monitored for three days. Porcine liver esterase (PLE), bovine serum albumin (BSA) and elution buffer (EB) were used as a negative, MGS0105 (45) as a positive control. **(B)** HPLC assay of 3PET hydrolysis products after 16 h of incubation at 30 ºC, elution buffer was used as a negative control (not shown). **(C)** HPLC analysis of hydrolysis of PLA incubated with metagenomic esterases for 48 hrs at 30 ºC

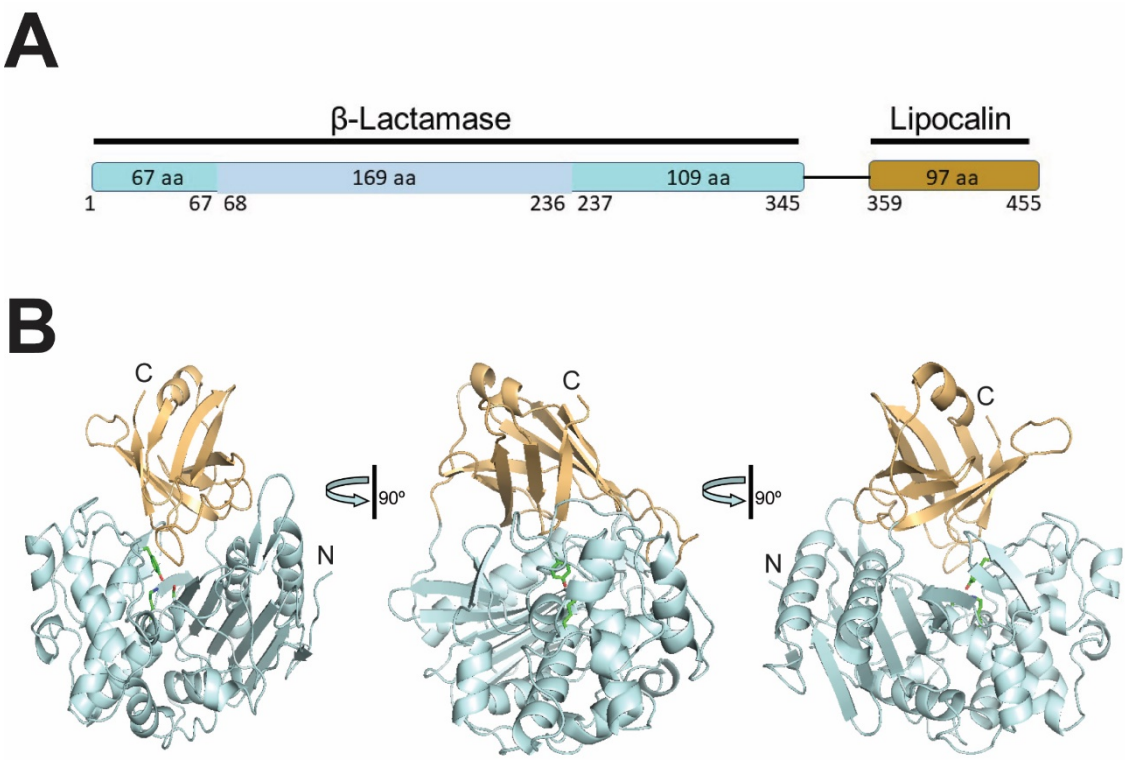

Figure 7. Crystal structure of IS11. (**A**), Schematic representation of the IS11 domains: the N-terminal β-lactamase related Ser hydrolase domain is colored cyan with all-helical sub-domain shown in light blue, whereas the C-terminal lipocalin domain in orange. (**B**), overall fold of the IS11 protomer shown in three views related by 90º rotations. The protein domains are shown as ribbon diagrams with the core domain (β-lactamase) colored pale cyan, whereas the C-terminal lipocalin domain is colored light orange. The position of the active site is indicated by the side chains of catalytic Ser68, Lys71, and Tyr160, whereas the protein N- and C-terminal ends are labelled (N and C).

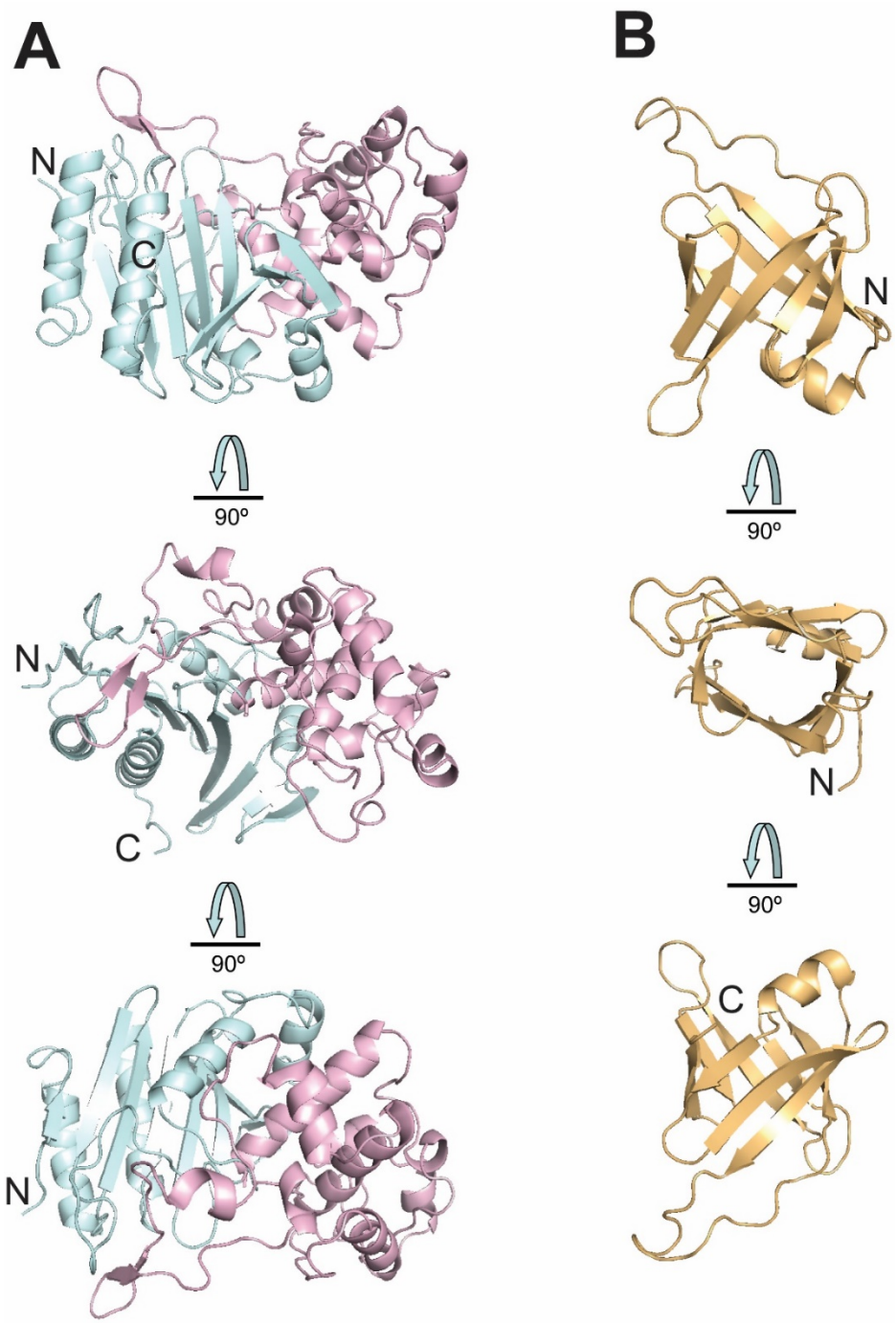

Figure 8. Crystal structure of the IS11 β-lactamase and lipocalin domains. (A), The N-terminal β-lactamase-like domain with two sub-domains colored pale cyan (α/β) and light pink (all-helical). (B), The lipocalin domain. The domains are shown in three views related by 90º rotations with the N- and C-termini labelled (N and C).

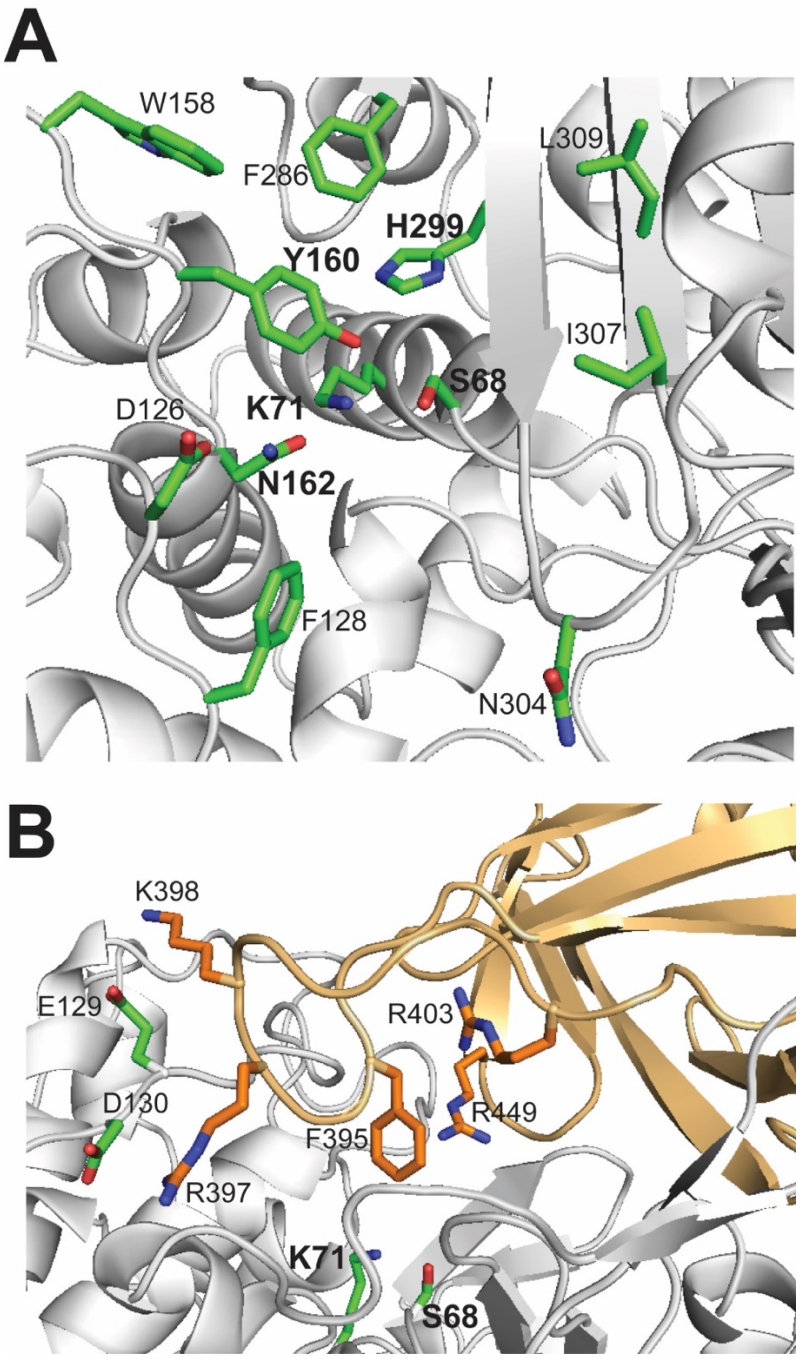

Figure 9. Close-up view of the IS11 active site. (A), The core domain showing the active site cleft with catalytic residues: motif-1 (Ser68 and Lys71), motif-2 (Tyr160 and Asn162), and motif-3 (His299). (B), The proline-rich loop of the lipocalin domain covering the active site and residues potentially contributing to substrate binding. Protein ribbon diagrams are coloured grey (the β-lactamase domain) and light orange (the lipocalin domain), whereas the side chains of residues are shown as sticks with green and orange carbons, respectively.

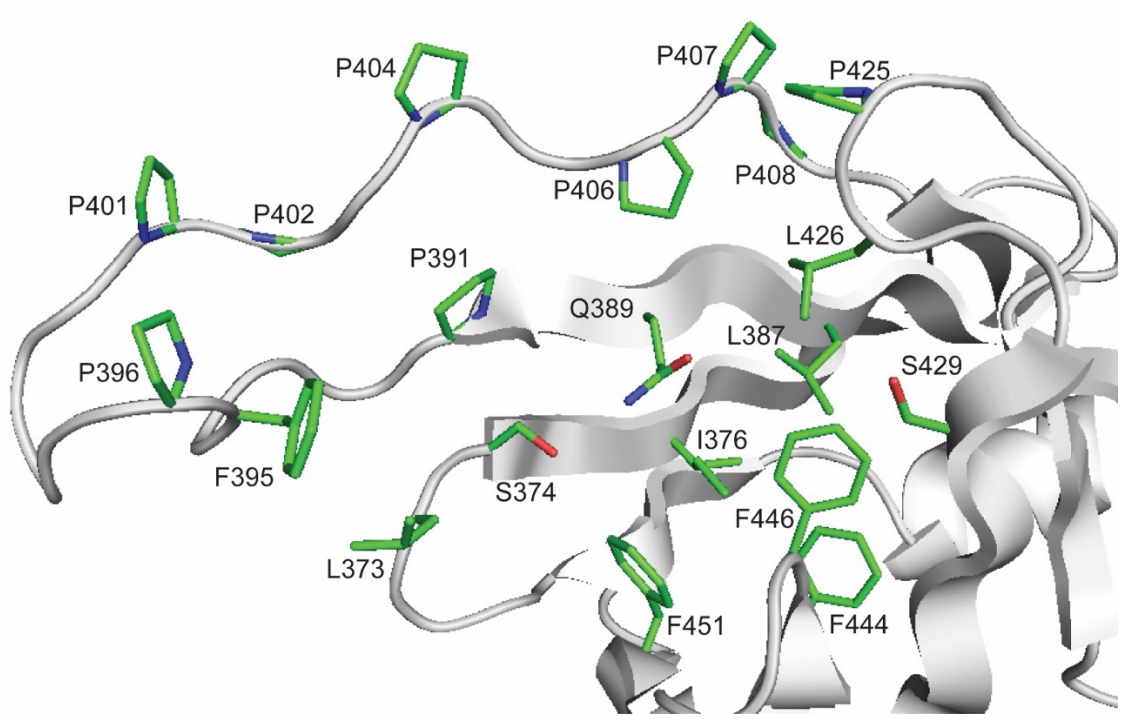

Figure 10. Crystal structure of the IS11 lipocalin domain: ligand binding site and proline-rich loop. The protein ribbon diagram is coloured in grey with the residues of ligand binding pocket shown as sticks with green carbons and labelled.

TABLES

Table 1. Novel carboxylesterases from the Ischia polyester enrichment metagenomes selected for biochemical and structural characterisation in this study.

Protein name	**Fosmid ID**	**Protein length**	**Predicted M.w.**	**Protein superfamily**	**Host organism** (phylum)
IS10	L2B6_15	314 aa	34.3 kDa	α/β hydrolase	Chloroflexi
IS11	L2F9_18	455 aa	49.4 kDa	β-lactamase	Chloroflexi
IS12	L3G23_11	318 aa	33.9 kDa	α/β hydrolase	Chloroflexi

Table 2. Kinetic parameters of purified metagenomic carboxylesterases from the Ischia hydrothermal vents with model esterase substrates[a].

Protein	**Substrate**	K_M **(mM)**	k_{cat} **(s^{-1})**	k_{cat}/K_M **(s^{-1} M^{-1})**
IS10	*p*NP-acetate	0.05 ± 0.01	41.97 ± 1.79	7.9 x 10^5
	*p*NP-butyrate	0.06 ± 0.01	66.21 ± 3.24	1.2 x 10^6
	*p*NP-hexanoate	0.04 ± 0.01	86.79 ± 3.06	2.0 x 10^6
	αN-propionate	0.06 ± 0.02	31.20 ± 1.93	5.0 x 10^5
	αN-butyrate	0.12 + 0.04	58.60 ± 5.89	4.9 x 10^5
IS11	*p*NP-acetate	0.53 ± 0.31	1.60 ± 0.30	3.0 x 10^3
	*p*NP-butyrate	0.20 ± 0.02	68.81 ± 1.37	3.5 x 10^5
	*p*NP-hexanoate	0.08 ± 0.02	40.28 ± 1.39	5.3 x 10^5
	αN-butyrate	0.09 ± 0.02	5.93 ± 0.49	6.9 x 10^4
IS12	*p*NP-acetate	0.22 ± 0.05	57.10 ± 3.78	2.6 x 10^5
	*p*NP-butyrate	0.08 ± 0.01	8.77 ± 0.29	1.1 x 10^5
	*p*NP-hexanoate	0.09 ± 0.01	19.05 ± 0.50	2.1 x 10^5
	αN-propionate	0.69 ± 0.19	39.45 ± 3.7	5.7 x 10^4

[a] Reaction conditions were as indicated in Materials and Methods (pH 9.0, 30ºC). Results are mean ± SD of three independent experiments. αN = α-naphthyl, *p*NP = *p*-nitrophenyl.

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