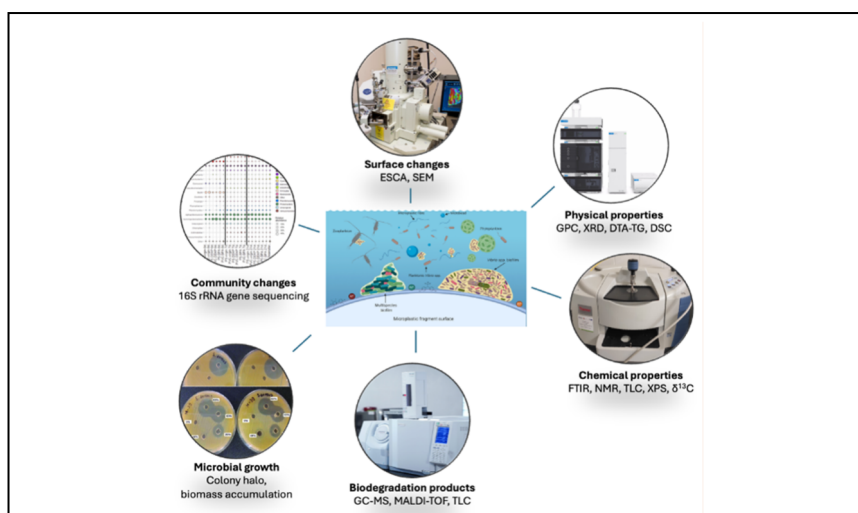


BIODEGRADATION OF PVC MICROPLASTICS OUTSIDE THE LABORATORY ENVIRONMENT



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Degree project for Bachelor of Science with a major in Biology

BIO603, Bachelor degree course in Biology, HT25, 30 hp

First cycle

Semester/year: Autumn 2025/Spring 2026

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Abstract

Polyvinyl chloride (PVC) is a major global plastic and the dominant anthropogenic sink for chlorine, yet its environmental fate as microplastic and the potential formation of chlorinated degradation products remain poorly understood. This thesis synthesizes current knowledge on PVC microplastic biodegradation, with a particular focus on the identity and environmental implications of chlorinated intermediates and end-products. A systematic literature review was conducted following PRISMA guidelines, complemented by quantitative analysis of reported biodegradation experiments, comparison of analytical methods, and compilation of organisms and enzymes implicated in PVC transformation.

Environmental monitoring reveals a pronounced “missing PVC” problem: despite large production volumes and high density, PVC rarely exceeds 5% of identified polymers in marine sediment datasets. Possible reasons are spectral changes, analytical bias, fragmentation, biodegradation. At the same time, field and laboratory studies indicate that soil and aquatic microbiomes can partially depolymerize and dechlorinate PVC, generating a range of chlorinated organic by-products. Bioinformatic searches in global ocean metagenomes reveal widespread homologs of recently characterized PVC-degrading enzymes, indicating a broad environmental potential for PVC transformation, though current data do not permit robust correlations with PVC pollution. Together, these findings challenge the traditional view of the PVC-backbone as environmentally inert and highlight the need to evaluate PVC biodegradation as a potentially significant source of chlorinated organic pollutants.

Sammanfattning

Polyvinylklorid (PVC) är en av världens mest producerade plaster och utgör den största enskilda sänkan för industriellt framställt klor. Trots detta är förekomsten av PVC som mikroplast i miljön, liksom bildningen av klorerade nedbrytningsprodukter, fortfarande bristfälligt kartlagd. Denna uppsats sammanställer kunskapsläget kring biologisk nedbrytning av PVC-mikroplaster utanför laboratoriemiljö, med särskilt fokus på att identifiera och påvisa miljömässiga konsekvenser av klororganiska mellan- och slutprodukter. Arbetet bygger på en systematisk litteraturöversikt enligt PRISMA-riktlinjerna, kvantitativ analys av rapporterade biodegraderingsförsök, jämförelse av analytiska metoder samt sammanställning av organismer och enzymer som kopplats till PVC-nedbrytning.

Mätningar i miljön visar på ett uttalat ”missing PVC”-problem: trots stora produktionsvolymerna och hög densitet utgör PVC sällan mer än 5% av identifierade polymerer i marina sediment. Vilket kan vara orsakat av analytiska systematiska fel, spektrala förändringar, fragmentering eller biodegradering. Fält- och laboratoriestudier indikerar att mikrobiella samhällen i jord och vatten kan kolonisera PVC-ytor, initiera dehydroklorering och oxidation samt delvis depolymerisera och deklorinera polymerkedjan, med bildning av olika klorerade organiska biprodukter. Bioinformatiska sökningar i globala marina metagenom påvisar spridda homologer till nyligen beskrivna PVC-nedbrytande enzymer, vilket antyder en bred miljöpotential för PVC-omvandling, även om dagens data inte medger robusta korrelationer till observerad PVC-mikroplastförorening.

Sammantaget utmanar resultaten antagandet att PVC-polymerens kol-kol-kedja är miljömässigt inert och pekar på att biodegradering av PVC-mikroplaster kan utgöra en underskattad källa till klorerade organiska föroreningar.

Abbreviations

Polymers and materials

MP – Microplastic

PE – Polyethylene

PET – Polyethylene terephthalate

PP – Polypropylene

PS – Polystyrene

PVC – Polyvinyl chloride

Analytical and imaging methods

AFM – Atomic force microscopy

ATR-FTIR – Attenuated total reflectance Fourier-transform infrared spectroscopy

$\delta^{13}\text{C}$ /IRMS – Carbon-13 isotope ratio mass spectrometry

GC-MS – Gas chromatography–mass spectrometry

GPC – Gel permeation chromatography

IR – Infrared (spectroscopy)

MALDI-TOF – Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry

NMR – Nuclear magnetic resonance spectroscopy

Py-GC-MS – Pyrolysis gas chromatography–mass spectrometry

SEM – Scanning electron microscopy

TEM – Transmission electron microscopy

TGA/DTA-TG – Thermogravimetric analysis/differential thermal analysis–thermogravimetry

TLC – Thin-layer chromatography

WCA – Water contact angle

XPS (ESCA) – X-ray photoelectron spectroscopy (electron spectroscopy for chemical analysis)

XRD – X-ray diffraction

Environmental and pollutant terms

CFC – Chlorofluorocarbon

DOC – Dissolved organic carbon

PCDD/Fs – Polychlorinated dibenzo-p-dioxins and dibenzofurans

PFAS – Per- and polyfluoroalkyl substances

PFOS – Perfluorooctane sulfonate

POSF – Perfluorooctane sulfonyl fluoride

WWTP – Wastewater treatment plant

1. Introduction

Polyvinyl chloride (PVC) is one of the world's most widely produced synthetic polymers and is often described as the most environmentally problematic major plastic, owing to its chlorine intensive chemistry and persistent toxic impacts from production to end of life (Kudzin et al., 2023). Global PVC production capacity was around 60 million tonnes in 2022, making it the third largest bulk plastic after polyethylene and polypropylene (Plastics Europe, 2025). PVC accounts for a substantial fraction of total chlorine consumption worldwide, around 35-40% of global chlorine output, linking the PVC sector closely to the broader chlorine industry and its environmental burdens (Figure 1).

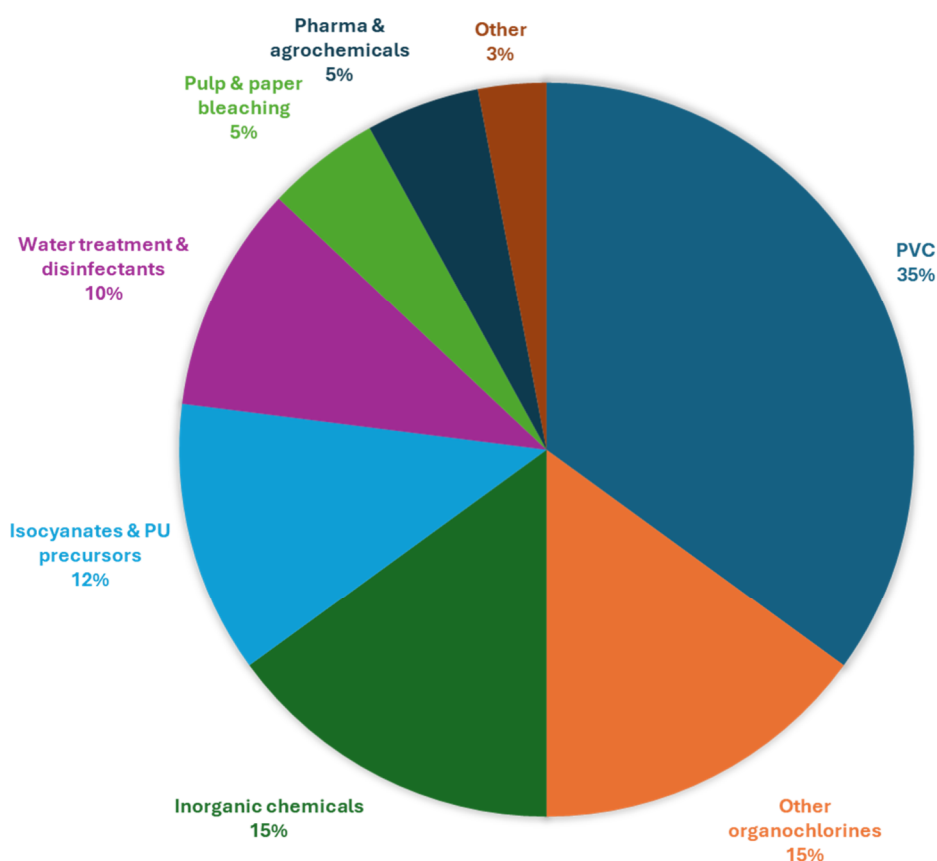


Figure 1. PVC dominates global chlorine consumption (percentage of produced tonnes) (Euro Chlor, 2010)

PVC has been produced on a vastly larger scale than most other halogenated organics. Global PVC production capacity is on the order of 60 million tonnes per year today and simple reconstruction of historical production suggests that cumulative PVC production since commercialization is likely to lie around 1 billion tonnes (Market Reports World, 2025).

By contrast, the key legacy groups of halogenated chemicals that dominate regulatory debates, CFCs, organochlorine pesticides, per- and polyfluoroalkyl substances (PFAS) and brominated flame retardants, have been produced at much lower absolute tonnages (Figure 2). Chlorofluorocarbon (CFC) production peaked at just over 1 million tonnes per year in the late 1980s, with cumulative production since the 1930s estimated above 25 million tonnes, still far below PVC by mass (Montzka et al., 2021). Global production of brominated flame retardants reached about 150–250 thousand tonnes per year around the 1990s–2000s, with cumulative production probably exceeding 10 million tonnes by 2020 (Lassen et al., 2014). The best quantified case for PFAS is perfluorooctane sulfonyl fluoride (POSF, the main perfluorooctane sulfonate (PFOS) precursor), for which total production from 1970–2002 was about 96,000 tonnes, illustrating how

even widely dispersed PFAS have been manufactured in volumes that are orders of magnitude below PVC (Lassen *et al.*, 2013). DDT and related organochlorine pesticides were also produced in the low million tonne range globally over several decades, again minor compared with PVC's cumulative output (van den Berg, 2008).

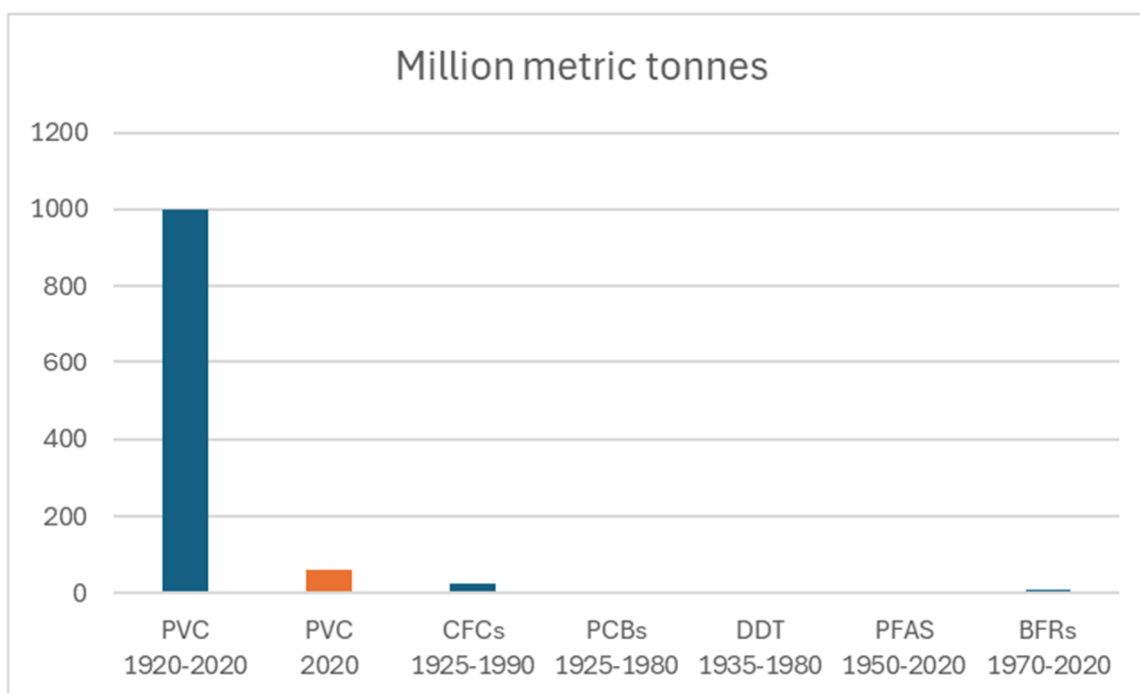


Figure 2. Cumulative production of halogenated chemicals (blue) and yearly production of PVC (orange)

During production of PVC hazardous waste is created (EDC tars). Highly chlorinated, viscous “heavy-end” residues generated during PVC production, comprising of a mixture of chlorinated ethanes and ethenes together with concentrated dioxins and furans. These tars act as a major sink for process-generated dioxins and thus represent a critical node in chlorine flows, since mismanagement (e.g. storage losses, leaking infrastructure or poorly controlled high-temperature treatment) can transfer persistent organohalogens into the environment. Historically, EDC-tar from PVC manufacture was dumped or incinerated at sea (Oslo and Paris Commissions 1996, 1996, Kudzin *et al.*, 2023).

End-of-life management of PVC remains particularly challenging. The polymer’s high chlorine content and complex additive package make it difficult to recycle mechanically and prone to contaminating recycling streams for other plastics, contributing to its very low recycling rate globally. Incineration and uncontrolled open burning of PVC-containing waste are major sources of polychlorinated dibenzo-p-dioxins and dibenzofurans (PCDD/Fs) and other chlorinated by-products, which are highly persistent, bioaccumulative and toxic at extremely low concentrations. These emissions contribute to human and ecological exposure via air, soil and food chains and PVC has been identified as a leading contributor to global dioxin formation among plastics (Kudzin *et al.*, 2023).

However, during both the use phase of PVC products and their eventual release into the environment, concern has primarily focused on the presence of additives rather than the polymer’s chlorine content. Plasticizers, stabilizers and other functional additives incorporated into PVC formulations can leach or volatilize over time, posing ecological and toxicological risks. In contrast, the chlorine bound within the PVC polymer matrix is generally considered not to biodegrade under environmental conditions and has not been identified as an environmental risk during use or when entering the environment. Consequently, environmental scrutiny of PVC plastics has largely centered on its additive composition rather than its inherent chlorine content.

As with other plastics, PVC products fragment over time into microplastics, but the environmental implications are shaped by the polymer's composition and persistence. Weathering, mechanical abrasion and aging of PVC materials (e.g. pipes, cables, flooring and coated textiles) generate PVC microplastics that enter wastewater, surface waters, soils and sediments through diffuse pathways such as stormwater runoff, wastewater discharges and the wear of construction and household materials. These PVC particles are long-lived, with half-lives estimated to exceed centuries. Once in the environment, PVC microplastics can be ingested by a wide range of organisms, from plankton to fish and invertebrates, with reported effects on development, reproduction and survival, partly due to both particle stress and associated chemical exposure (Salih *et al.*, 2026).

Given the persistence of PVC in the environment and the difficulty of managing its waste safely, substantial research efforts have been directed toward the biodegradation and bioremediation of PVC microplastics. Recent studies have investigated bacteria, fungi and microbial consortia capable of colonizing PVC surfaces, altering polymer chemistry and potentially facilitating fragmentation or dechlorination, with the aim of developing biological treatment strategies for contaminated soils and waters (Hatwar & Qureshi, 2025). However, PVC degradation is a complex process often initiated by dehydrochlorination, leading to release of hydrogen chloride, with subsequent oxidative steps producing carbonyl and hydroxyl functionalities. Critically, these transformations can generate a variety of chlorinated organic intermediates and by-products, including chlorinated hydrocarbons and, under certain conditions, dioxin-like compounds, whose environmental fates are poorly understood (Kudzin *et al.*, 2023).

Historical experience with CFCs, PFAS, DDT and brominated flame retardants shows that halogenated organic compounds produced in comparatively modest quantities can cause planetary scale problems when they are persistent, mobile and bioaccumulative. Against this backdrop, the prospect that biodegradation of a billion tonne scale chlorinated polymer such as PVC could generate smaller, more mobile chlorinated compounds underscores the need to interrogate not only whether PVC can be biologically degraded, but also what kinds of chlorinated transformation products are formed, how they behave in the environment and whether microplastic focused bioremediation strategies might inadvertently substitute one form of chlorinated pollution for another.

1.1. Aim

To date, most PVC biodegradation research has emphasized the potential of microbes and enzymes to reduce the burden of persistent microplastics in the environment. The possible formation and accumulation of chlorinated degradation products, by contrast, has received comparatively limited attention. The aim of this thesis is to address this gap by critically examining the biodegradation of PVC with a specific focus on the generation, identity and environmental implications of chlorinated compounds formed as intermediates or end products.

Specific aims

To provide an overview of the current state of PVC microplastic biodegradation research

In order to fulfil this aim, the thesis will (i) examine methodological approaches for assessing degradation, (ii) examine reported concentrations and distributions of PVC microplastics in the marine environment, (iii) compile PVC backbone-derived chlorinated organics reported from PVC microplastic biodegradation and (iv) compare chlorinated organics of environmental concern with those reported from PVC microplastic biodegradation.

To evaluate potential environmental risks associated with highly efficient PVC-degrading enzymes

In order to fulfil this aim, the thesis will (i) compile enzymes implicated in PVC microplastic biodegradation based on experimental studies, (ii) examine the global distribution of reported PVC-degrading enzymes in

marine datasets, and (iii) investigate correlations between reported PVC-degrading enzymes and global marine PVC microplastic pollution.

2. Methods

2.1. Preferred reporting items for systematic reviews and meta-analyses: the PRISMA statement

A systematic literature review was conducted following the PRISMA Statement (Moher *et al.*, 2009).

2.2. Statistical Analysis of experimental studies

To quantify methodological robustness in PVC biodegradation research, a dataset of 32 experimental studies was compiled from the systematic literature review (the quantitative synthesis). For each study, the following characteristics were recorded: (1) publication year, (2) PVC composition type (pure, plasticized or unclear), and (3) evidence methods employed (categorized as mass loss, structural change, mineralization, chloride balance, metabolite detection, isotopic labeling and chlorinated organic compound detection).

Studies were classified by evidence robustness based on the number of complementary methods used. The relationship between type of PVC composition and methodological robustness was evaluated by calculating the average number of evidence categories per composition type.

2.3. Data for enzymes from literature search

From the quantitative synthesis, enzymes that have been tested directly for PVC degradation were picked.

2.4. Mapping the global oceanic distribution of PVC-degrading enzymes

Ocean Gene Atlas query and OM-RGC v2 data

To investigate the global oceanic distribution of putative PVC-degrading enzymes, we queried the Ocean Gene Atlas web service (version 2.0; <https://tara-oceans.mio.osupytheas.fr/ocean-gene-atlas/>) using the Ocean Microbial Reference Gene Catalogue v2 (OM-RGC.v2) as reference gene set. OM-RGC.v2 compiles non-redundant protein-coding genes from Tara Oceans prokaryotic metagenomes and associated environmental metadata and captures the majority of gene-encoding diversity in these samples. For each target enzyme, we used the experimentally characterized PVC-degrading protein sequence as a BLASTP query against OM-RGC.v2 with an expectation value threshold of 1×10^{-50} , retaining only hits below this cut-off as high-confidence homologs. BLASTP searches and downstream visualizations (geographic maps,) were carried out through the Ocean Gene Atlas graphical interface following the procedures described by Villar *et al.* (2018) and in the OGA user manual.

Gene abundances in Tara Oceans samples were used as provided by Ocean Gene Atlas. For each enzyme, we exported the per-sample abundance matrix and associated station metadata (geographical coordinates, depth layer, size fraction, and basic physicochemical variables) via the Ocean Gene Atlas download function. Abundances of all homologous OM-RGC.v2 genes matching a given query enzyme were summed per sample to obtain a composite abundance per station and depth layer, which was then used for map visualizations. Environmental context and overall system description follow the Tara Oceans expedition sampling design as detailed in Villar *et al.* (2018) and Salazar *et al.* (2019).

BLASTP search against GenBank was performed using the NCBI web interface. The expectation value (E-value) threshold for reporting hits was set to 1×10^{-50} .

3. Overview of the current state of PVC microplastic biodegradation research

3.1. Literature review

Web of Science was searched using the terms: TS = ("PVC" OR "polyvinyl chloride" OR "poly?vinyl chloride" OR "polyvinylchloride") AND TS = ("Biological degrad*" OR "Biodegrad*" OR "Bio-degrad*" OR "Bioconversion*"), yielding 781 records. An additional 97 records were identified from references and review articles.

Records identified (n=881, no duplicates), and titles/abstracts were screened, excluding 712 records. Full-text eligibility assessment of 169 articles excluded 75 studies. Criteria for exclusion: pretreated or mixed with chemicals, composite/modified (e.g. PVC/cellulose), studies mainly on additives, biodegradation combined with chemical or thermal degradation (NB: UV degradation combined with biodegradation sometimes included). This resulted in 87 studies included in the qualitative synthesis (PRISMA flow diagram in Figure 3). 32 studies that reported results from experimental biodegradation tests on PVC from the qualitative synthesis, were included in the quantitative synthesis.

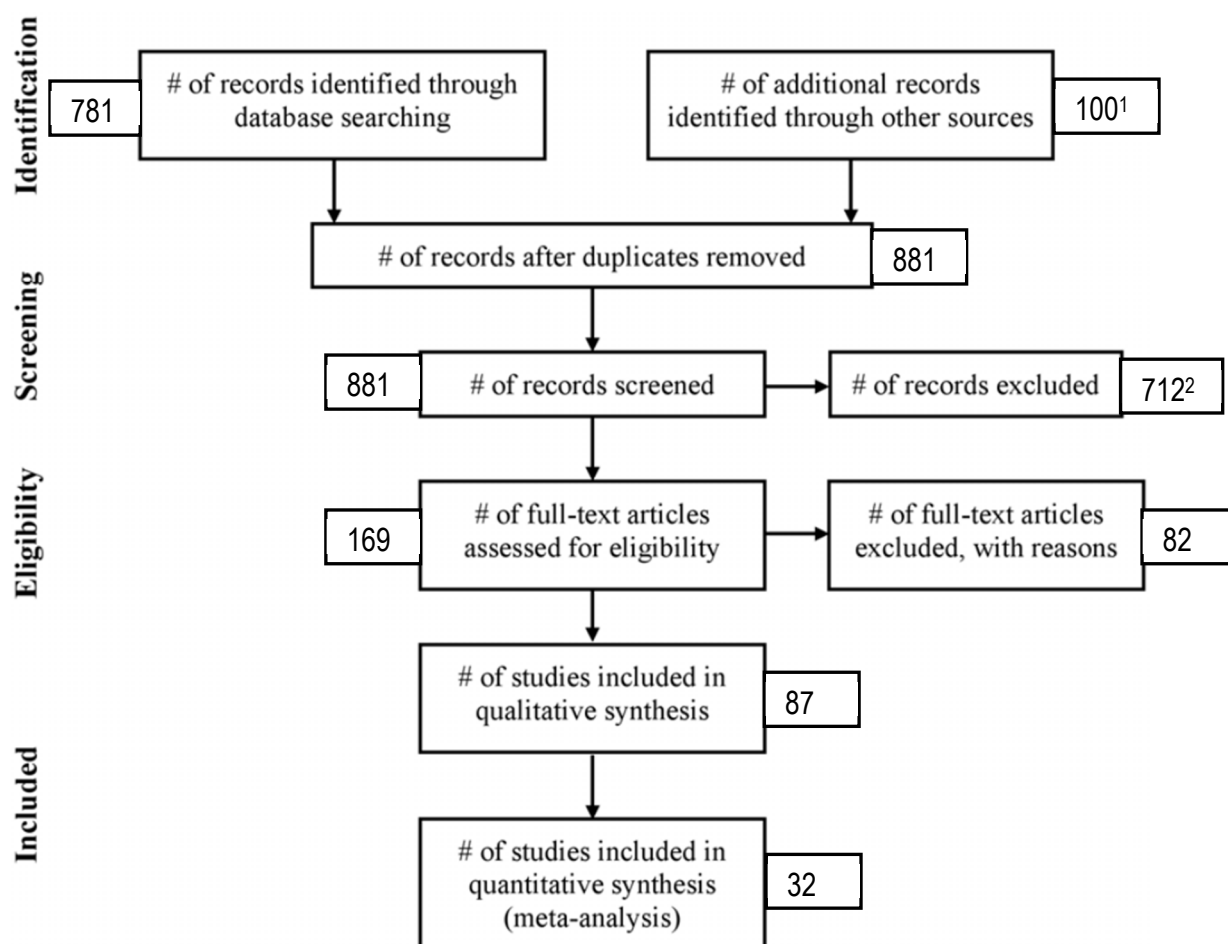


Figure 3. PRISMA flow diagram. ¹ found through review articles and references, ² excluded by title and abstract screening. Graphic adapted from Moher et al. (2009).

3.2. Biodegradation publications for the main plastics

Performing the same database search as above for the main plastics (polyethylene PE, polypropylene PP, polyvinyl chloride PVC, polyethylene terephthalate PET, polyurethane PUR, polystyrene PS) for each year since 1990, gives an estimate of the annual number of academic publications on biodegradation (Figure 4). Publications were negligible in the early 1990s, with sporadic counts under 10 per plastic annually, but exhibited steady growth after 2000, accelerating dramatically after 2017 amid rising environmental concerns over plastic pollution. By 2025, PE led with 558 publications, followed by PS (198), PET (175), PP (131), PUR (69), and PVC (44), reflecting an intensified research focus on biodegradable solutions for recalcitrant polymers.

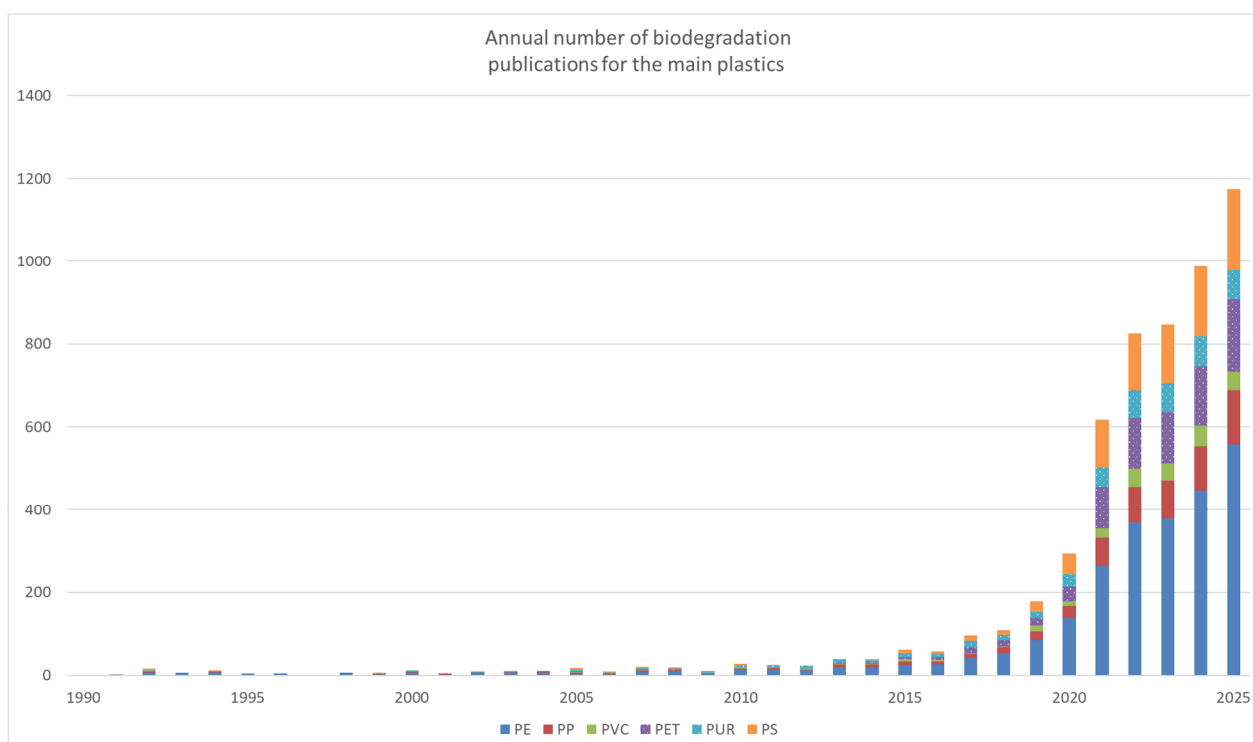


Figure 4. Annual number of biodegradation publications for the main plastics

3.3. Analytical methods for evaluating microplastic biodegradation

A wide range of analytical techniques has been used to evaluate microplastic biodegradation (Figure 5).

Surface Analysis Methods

Scanning electron microscopy (SEM), atomic force microscopy (AFM) and transmission electron microscopy (TEM) visualize surface changes like pits, cracks and biofilm, indicating microbial erosion. ESCA (XPS), energy-dispersive X-ray spectroscopy (EDS) and contact angle measure surface chemistry, oxidation and hydrophobicity shifts.

Structural and Thermal Methods

Gel permeation chromatography (GPC) tracks molecular weight reduction from chain scission, XRD assesses crystallinity changes, thermal techniques like DSC, TGA/DTA-TG reveal melting point shifts and mass loss. Tensile strength testing evaluates mechanical weakening, correlating with embrittlement in degrading polymers.

Spectroscopic Methods

FTIR (including ATR-FTIR) and Raman detect functional group oxidations (e.g., carbonyls), NMR identifies degradation products in solution, GC-MS and Py-GC-MS quantify volatiles and oligomers released. MALDI-TOF and TLC separate low-molecular-weight fragments.

Biological and Isotopic Methods

Colony halo assays screen enzymatic hydrolysis, biomass accumulation and 16S rRNA sequencing confirm microbial growth and degraders, respirometry measures CO_2/O_2 changes for mineralization. $\delta^{13}\text{C}/\text{IRMS}$ tracks fossil carbon assimilation into biomass, $^{13}\text{C}/^{14}\text{C}$ labelling provides unequivocal proof via labeled CO_2 or biomass incorporation.

Comprehensive Evaluation

These methods are not enough in isolation, robust studies need to combine surface/structural (SEM, GPC), spectroscopic (FTIR, NMR) and mineralization assays (respirometry, isotopes), with controls for abiotic

effects and biofilm interference. Weight loss is simple but insensitive for slow degradation, needs to be complemented with methods using isotopes for higher certainty to claim microplastic biodegradation (Lear *et al.*, 2021).

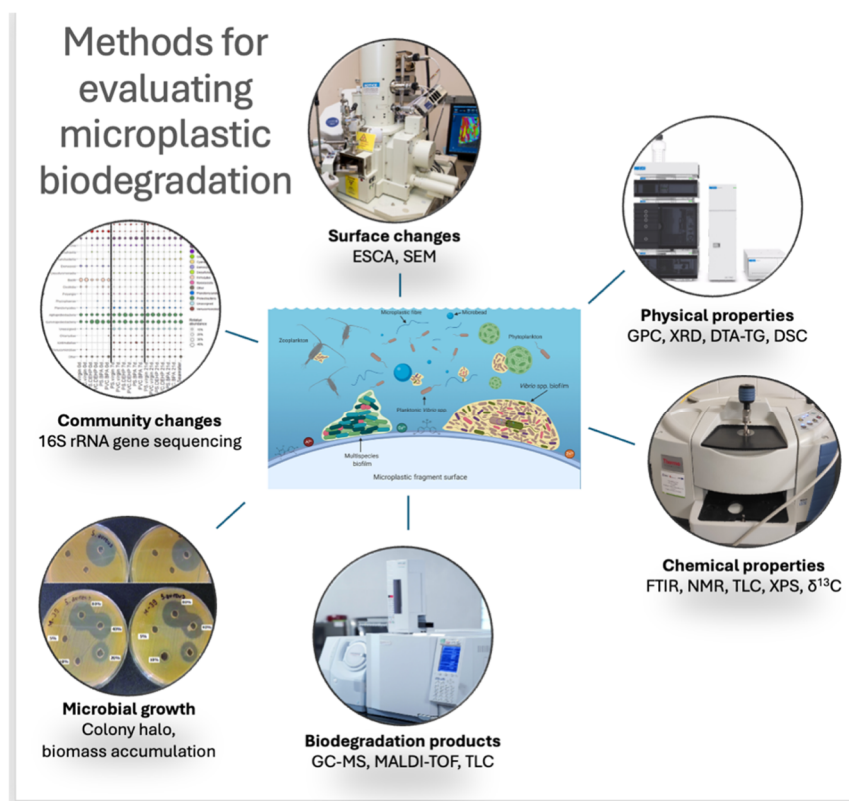


Figure 5. Methods for evaluating microplastic biodegradation

3.4. Methods in plastic biodegradation studies

A review of 408 studies shows that these studies seldom use all three categories for demonstrating biodegradation (Figure 6). Nearly half (48%) of reported plastic-degrading microorganisms were supported by evidence from only a single category, 39% combined methods from two categories and only ~10% used techniques spanning all three (structural change, mass loss and metabolite detection) (Lear *et al.*, 2021).

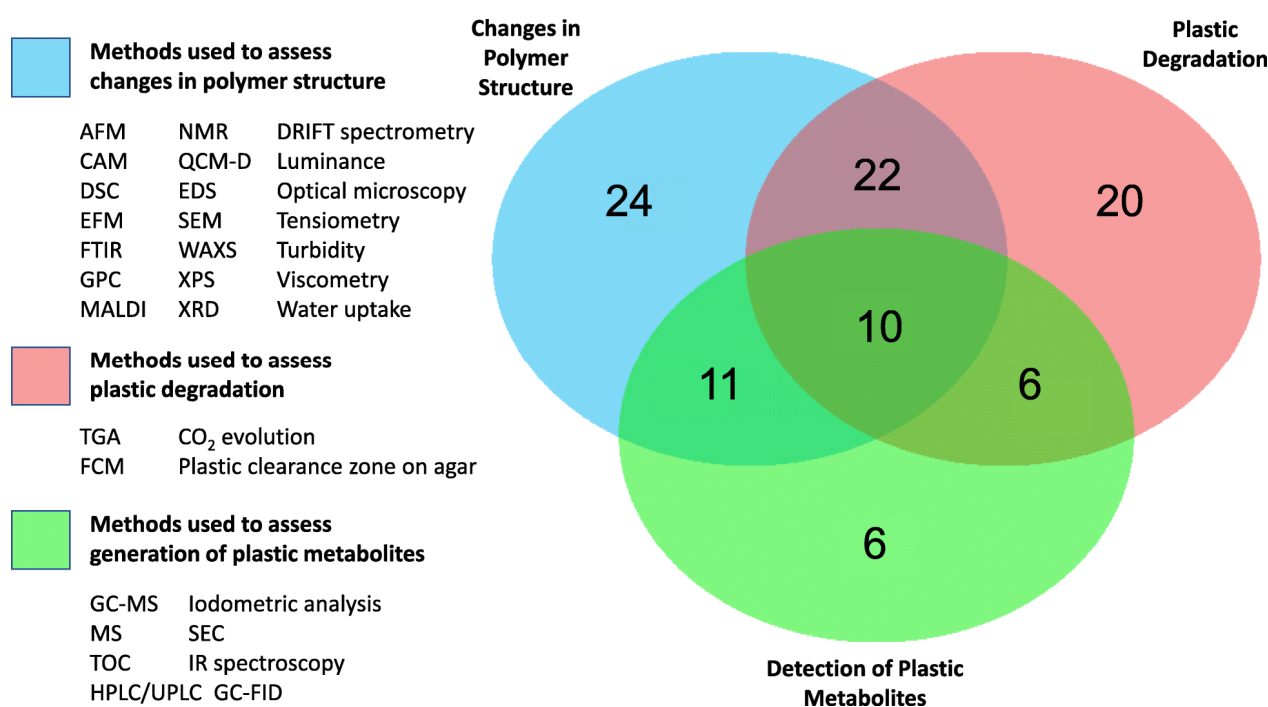


Figure 6. Percentage of studies using evidence for plastic degradation by microbial species based on: changes in polymer structure (blue), physical loss of plastic mass (red), detection of plastic metabolites (green) and these techniques in combination. Image taken from Lear *et al.* (2021).

3.5. Methods in PVC biodegradation studies

Among the 32 studies included in the quantitative synthesis, 15 (46.9%) explicitly used pure, additive-free PVC, 9 studies (28.1%) used PVC formulations containing additives, and 13 studies (40.6%) did not clearly specify the PVC composition. This lack of clarity in material characterization is a major limitation, because plasticizers and other additives can be degraded by microorganisms, leading to misattribution of apparent biodegradation to the PVC backbone rather than to additives (Giacomucci *et al.*, 2019, Novotny *et al.*, 2022). Some studies working with plasticized PVC explicitly attempted to control for this issue, for example by characterizing additive loss separately or by combining structural analyses with measurements of released additives (Peng *et al.*, 2025, Gulizia *et al.*, 2025).

The most used evidence for biodegradation methods across the 32 studies were structural change (26 studies, 81.2%) and mass loss (25 studies, 78.1%) (Appendix I). These basic methods provide initial evidence of material transformation but are insufficient on their own to establish true biodegradation of the polymer backbone, as it can be hard to distinguish between additive loss, surface erosion and actual depolymerization. Metabolite detection was documented in 8 studies (25.0%). Dechlorination tracking, which is particularly critical for PVC given its high chlorine content, was assessed in only half of the studies. Chloride balance measurements were reported in 11 studies (34.4%) and detection of chlorinated organic intermediates was documented in 6 studies (18.8%). When combined, 16 studies (50.0%) included at least one form of dechlorination evidence, while the remaining 16 studies (50.0%) provided no information on the fate of chlorine released during degradation (Table 1, Figure 7). Only 3 studies (9.4%) used either mineralization or isotopic methods. These methods provide the most rigorous proof of biodegradation by directly tracing the fate of polymer carbon.

Table 1. Methods and combination of methods used in the 32 articles. A denotes mass loss and/or structural change, B Metabolite detection, C Chloride balance and/or mineralization and/or isotopic methods

Category	Number of studies	Percentage (%)
A	15	46.9
A + B	4	12.5
A + C	8	25.0
A + B + C	4	12.5
B	1	3.1

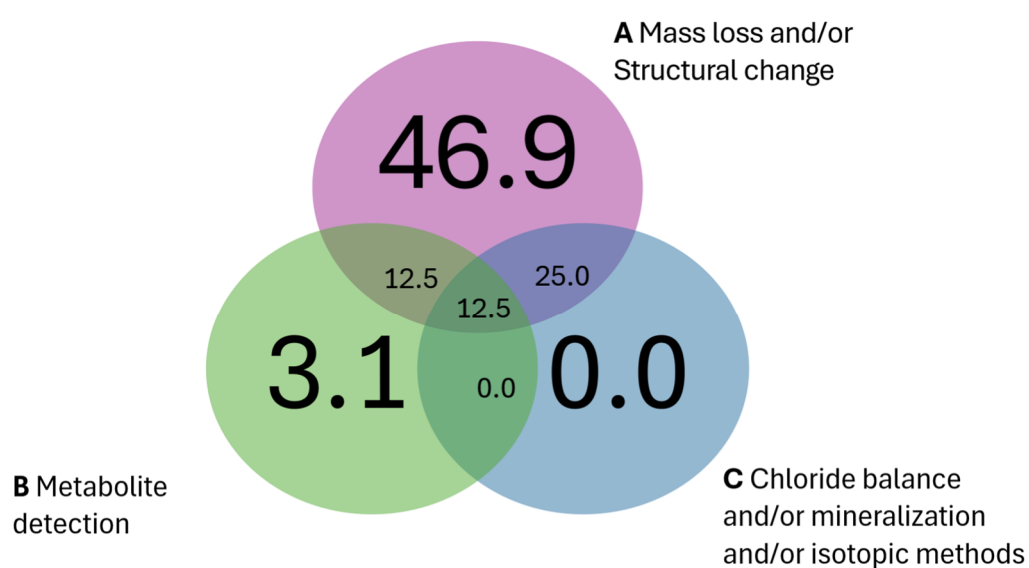


Figure 7. Percentage of studies using evidence for PVC biodegradation based on: **A** Mass loss and/or structural change (purple) **B** Metabolite detection (green), **C** Chloride balance and/or mineralization and/or isotopic methods (blue) and these techniques in combination.

4. PVC microplastics in the environment

4.1. Microplastics vertical distribution in the marine environment

Microplastics are present from sea surface to deep-sea sediments (Figure 8). Their vertical distribution is controlled by polymer density, size, shape and biofouling. Low-density plastics such as PE and PP dominate surface and near-surface waters, while denser polymers like PVC and PET are expected to be found at deeper depths and in benthic sediments (Fernández-González *et al.*, 2022).

Studies on vertical distribution that include individual polymer types generally do not include PVC and when they do, it appears only in low amounts (Quintana *et al.*, 2025). PVC microplastics should, in theory, be relatively enriched in deeper compartments because their density favors sinking and weathering or biofouling further increases effective density. However, monitoring studies report PVC in only about half of sediment datasets, usually at <5% by count.

Fragmentation below detection limits have been proposed as part of the explanation of the low levels (Pfohl *et al.*, 2022, Fernández-González *et al.*, 2022). Other reasons could be weathering-induced spectral changes that make PVC look like oxidized PE in IR libraries, use of NaCl for density separation, harsh oxidative, acidic or alkaline digestions and extrapolation from small, spectroscopically analyzed subsets that already under-represent PVC (Fernández-González *et al.*, 2022).

4.2. Microplastics geographical distribution in the marine environment

Microplastics are today a near-ubiquitous contaminant. At the surface, elevated concentrations consistently occur in the subtropical gyres of the North and South Pacific, North and South Atlantic and Indian Ocean, where convergent circulation with relatively low vertical mixing, favor the retention of buoyant polymers (Figure 9).

Higher concentration of microplastics is generally found more in coastal waters than in offshore regions. Concentrations typically decrease with distance from land, although processes such as upwelling, fronts and eddies can generate local "hotspots". Semi-enclosed seas (for example the Mediterranean and Baltic) often show particularly elevated levels due to restricted flushing combined with intense coastal loading.

Microplastic abundances are increasingly reported at high northern and southern latitudes. Nevertheless, the geographical distribution of microplastics is uncertain due to lack of data in general, and specifically from the Southern Hemisphere, deep ocean and coastal regions in the Global South.

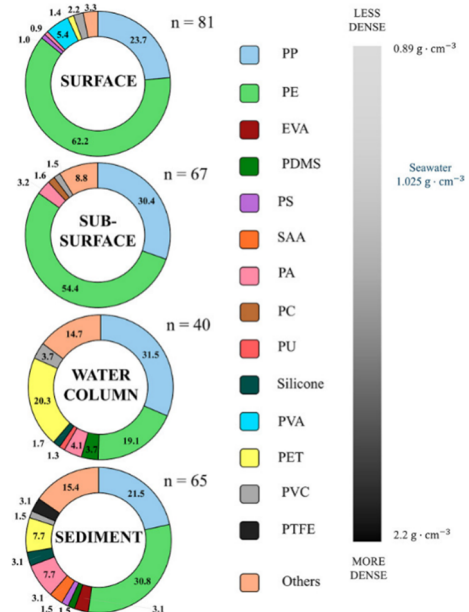


Figure 8. Plastic composition in surface, subsurface, water column, and sediments. Polymers are ordered from lowest to highest density: polyethylene (PE), polypropylene (PP), ethyl vinyl acetate (EVA), polydimethylsiloxane (PDMS), polystyrene (PS), styrene allyl alcohol (SAA), polyamide (PA), polycarbonate (PC), polyurethane (PU), silicone, polyvinyl acetate (PVA), polyethylene terephthalate (PET), polyvinyl chloride (PVC), and polytetrafluoroethylene (PTFE). Others include poly(ethyl acrylate) (PEA), copolymer, poly(vinyl stearate) (PVS), melamine urea formaldehyde (MUF), rubber, styrene butadiene copolymer (SBC), and acrylonitrile butadiene styrene-polyvinyl chloride (ABS-PVC). Numbers show percentage. Taken from Quintana *et al.*, 2025

Data for the geographical distribution of PVC microplastic, is even more scarce than for other plastics (Fernández-González *et al.*, 2022).

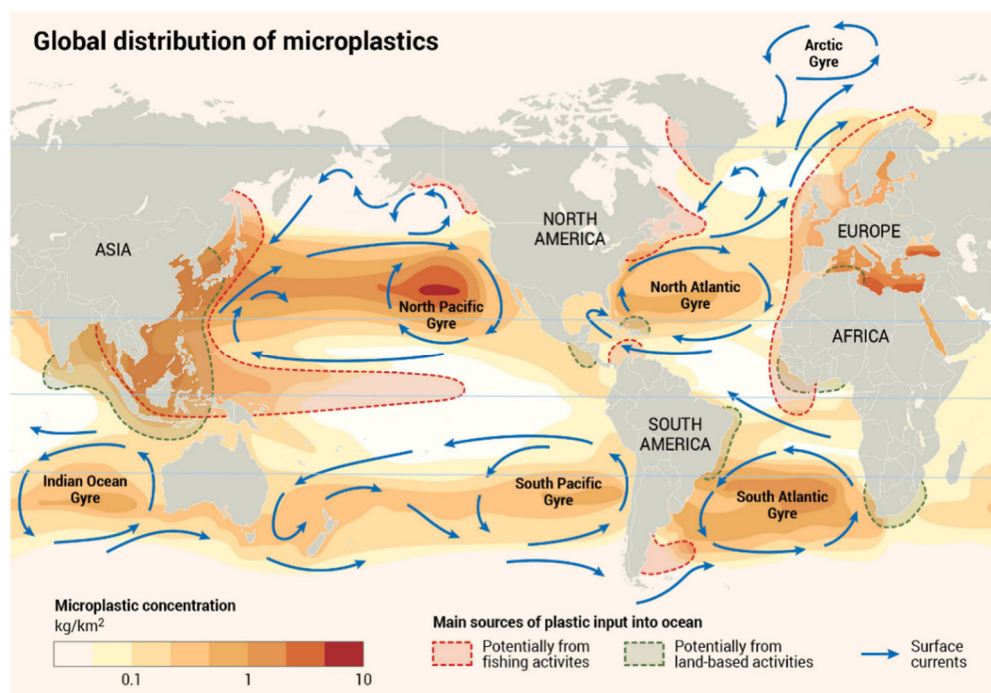


Figure 9. Global distribution of microplastics Sources: E. van Sebille *et al.*, 2015; K. Lavender Law, 2016; H. Ritchie & M. Roser, 2018; J. R. Jambeck *et al.*, 2015; R. Geyer *et al.*, 2017; L. Lebreton, 2017; K. Martini, 2016. Based on two maps from R. Pravettoni, 2016 (<https://www.grida.no/resources/13339>).

4.3. PVC microplastics in soil

In an agricultural soil seeded with PVC powder at realistic pollution levels, optical microscopy revealed a marked reduction in PVC microplastics over one year, with particle numbers and surface area decreasing by about 50–65%. Because experimental handling and extraction procedures were the same for PVC-amended and control soils, the authors interpret this decline as evidence that soil processes, including biological activity, contribute to PVC degradation (Barili *et al.*, 2023).

5. PVC biodegradation

5.1. PVC degrading organism

PVC-degrading organisms reported in the literature span insect gut consortia, environmental isolates and enrichment cultures, but the strength of evidence for true PVC backbone degradation varies widely. Many of the strains listed in Appendix 1 probably mainly act on additives (Jendrossek, 2024, Scott *et al.*, 2025). Without direct measurements of chloride release or identification of metabolites it remains uncertain whether the PVC backbone is affected. In several cases (e.g. *Pseudomonas citronellolis*, *Bacillus flexus*, *Bacillus amyloliquefaciens*) data suggest degradation or removal of additives and other low-molecular-weight components, implying biodeterioration of PVC materials rather than biodegradation of the backbone.

A recent group of studies (e.g. on *Klebsiella* sp. EMBL-1, *Citrobacter koseri*, gut consortia from *Tenebrio molitor* larvae and the EF1 consortium) provide more convincing indications of PVC depolymerization and partial dechlorination. These studies combine evidence of chain shortening, loss of C–Cl signatures, chloride release and/or detection of degradation products (Appendix II).

5.2. Intermediates and byproducts in PVC biodegradation studies

Only a small subset of the 32 PVC biodegradation studies reported intermediates or byproducts at compound level. Most described broad classes such as "chlorinated organics," "aromatic compounds" or "oxidized PVC fragments" without full structural identification.

In the *Klebsiella* sp. EMBL-1 system, GC–MS suggested formation of long-chain aliphatic esters as putative dechlorinated PVC fragments (Zhang, Z. et al., 2022). A soil consortium from the Tibetan Plateau produced long-chain alkanes and released chloride, indicating coupled depolymerization and dechlorination (Jiang et al., 2025). Freshwater *Streptomyces* isolates and marine bacteria generated mixtures of aromatic compounds and PVC degradation products that were not fully resolved to individual structures (Rodriguez-Fonseca et al., 2022). Several insect-gut and consortia studies similarly reported chlorinated intermediates, oxidized PVC oligomers and inorganic chloride as evidence for ongoing dechlorination (Peng, B. et al., 2020, Xu et al., 2023, Peng, H. et al., 2025, Jiang et al., 2025).

Even though few studies included metabolite detection, some specific organochlorines were reported. These were dichloroethane, hexachloroethane, 1,2-dichlorobenzene, [trichloroacetic acid, hexadecyl ester], [3-chloropropionic acid, heptadecyl ester], 5-chloro-(2,4-dichlorophenoxy) phenol, 2,3-Chlorobicyclo-oct-2-en-6-methyl-1,3-dioxolane, dioxins, furans and 1-chlorohexadecane (see Appendix III).

In a study on two PVC degrading strains (*Acinetobacter* sp. strain PVC-6A and *Bacillus* sp. strain PVC-6B) by Zhang, H. et al., (2026) it is shown that organochlorines can be produced during PVC biodegradation both as intermediate and end products. Strain PVC-6A produces 1-chlorehexadecane as an intermediate whereas strain PVC-6B produces it as a dead-end product.

None of the studies reported metabolite detection for their controls. As an example of why this is critical, chlorobenzene (one of the reported compounds) is also a PVC-specific confirmation peak in Py-GC-MS. Without applying the same analytical protocol to all controls, it is impossible to exclude the possibility that chlorobenzene arises as an analytical artefact rather than from PVC biodegradation.

5.3. PVC degrading enzymes

Although many enzymes have been proposed for PVC degradation based on transcriptomics/proteomics (e.g. laccases, alcohol dehydrogenase, glutathione dehydrogenase, aldehyde dehydrogenase, haloacid dehalogenase, acetaldehyde dehydrogenase, catechol 2,3-dioxygenase, etc. (e.g. Sumathi et al., 2016, Wang et al., 2024)) only a few have been tested directly for PVC degradation (Table 2).

Table 2. Enzymes tested for PVC degradation

Enzyme	Notes	Reference
NAD-dependent oxidoreductase (NDO) from <i>Enterococcus casseliflavus</i> strain EMBL-3	NDO treatment significantly reduced the molecular weight of PVC (Mn from 79.34 to 69.81 kDa; Mw from 164.04 to 140.97 kDa), consistent with polymer chain depolymerization. It also caused significant dechlorination, releasing 0.74 mg/L chloride relative to untreated controls.	Peng et al., 2025
Dehalogenase (SerB) from <i>Rhodococcus</i> p. strain P14	GC–MS analysis revealed PVC degradation products, including alkane, ester, and chlorinated compounds (e.g. trichloroacetic acid, hexadecyl ester). SerB-treated PVC powder showed a chloride ion release of 9.7 mg/L and increases in Mn, Mw, and Mz (6.7%, 6.3%, and 4.4%, respectively), indicating enzymatic dechlorination and depolymerization of the polymer.	Jiang et al., 2025

Enzyme	Notes	Reference
Catalase-peroxidase (CAT) from <i>Acinetobacter</i> sp. strain PVC-6A	Exhibited dechlorination and depolymerization activity, achieving reductions of xx %, xx %, xx % in CHCl-, 35Cl-, 37Cl-, and 5.1 %, 6.0 %, 7.2 % in Mz, Mw, Mn compared to the control group, respectively	Zhang, H. <i>et al.</i> , 2026
Laccase (LAC1) from <i>Acinetobacter</i> sp. strain PVC-6A	Exhibited dechlorination and depolymerization activity, achieving reductions of 56 %, 77 %, 75 % in CHCl-, 35Cl-, 37Cl-, and 8.1 %, 10.4 %, 13.1 % in Mz, Mw, Mn compared to the control group, respectively	Zhang, H. <i>et al.</i> , 2026
Laccase (LAC2) from <i>Bacillus</i> sp. strain PVC-6B	Exhibited dechlorination and depolymerization activity, achieving reductions of xx %, xx %, xx % in CHCl-, 35Cl-, 37Cl-, and 7.6 %, 5.2 %, .6 % in Mz, Mw, Mn compared to the control group, respectively	Zhang, H. <i>et al.</i> , 2026

5.4. Mapping of global distribution of PVC biodegrading enzymes in the marine environment

Peng *et al.* (2025) investigated the gut microbiota of *Spodoptera frugiperda* larvae and isolated *Enterococcus casseliflavus* strain EMBL-3 encoding a NAD-dependent oxidoreductase (NDO) that directly dechlorinates additive-free PVC polymer. Purified NDO reduced the molecular weight of PVC powder (Mn by 12.02%, Mw by 14.07%) and released 6.48 mg/L chloride in the presence of NADH, providing enzymatic evidence for PVC backbone dechlorination.

Jiang *et al.* (2025) enriched a PVC-degrading microbial consortium from soil microbes in the Tibetan Plateau's alpine grasslands, confirming PVC degradation through mass loss (3.1%), chloride ion release, long-chain alkane formation and surface changes observed via FTIR, XPS, SEM and GC-MS. Metaproteomics identified 298 proteins with high expression in the PVC-degrading consortia across six key categories (dehalogenase, peroxidase, monooxygenase, dioxygenase, esterase, dehydrogenase), highlighting an upregulated dehalogenase SerB from *Rhodococcus* that dechlorinates chloroacetic acid and PVC films.

Zhang, H. *et al.*, (2026) isolated two bacterial strains, *Acinetobacter* sp. PVC-6A and *Bacillus* sp. PVC-6B, from the gut microbiome of *Tenebrio molitor* larvae. These strains did utilize additive-free PVC films as the sole carbon source, achieving weight loss, with degradation confirmed via SEM, AFM, ATR-FTIR, GPC and WCA showing surface roughening, oxidation and increased hydrophilicity. GC-MS identified chlorinated product 1-chlorohexadecane. Genomics/transcriptomics identified key oxidases. A catalase-peroxidase (CAT) from PVC-6A and two laccases (LAC1 from PVC-6A, LAC2 from PVC-6B)

For four enzymes (NAD-dependent oxidoreductase from *Enterococcus casseliflavus* strain EMBL-3, dehalogenase SerB from *Rhodococcus* sp., catalase-peroxidase CAT from strain *Acinetobacter* sp. PVC-6A and laccase LAC2 from *Bacillus* sp. PVC-6B) FASTA sequences were available. These enzymes were run individually against the Ocean Gene catalogue (Figure 10).

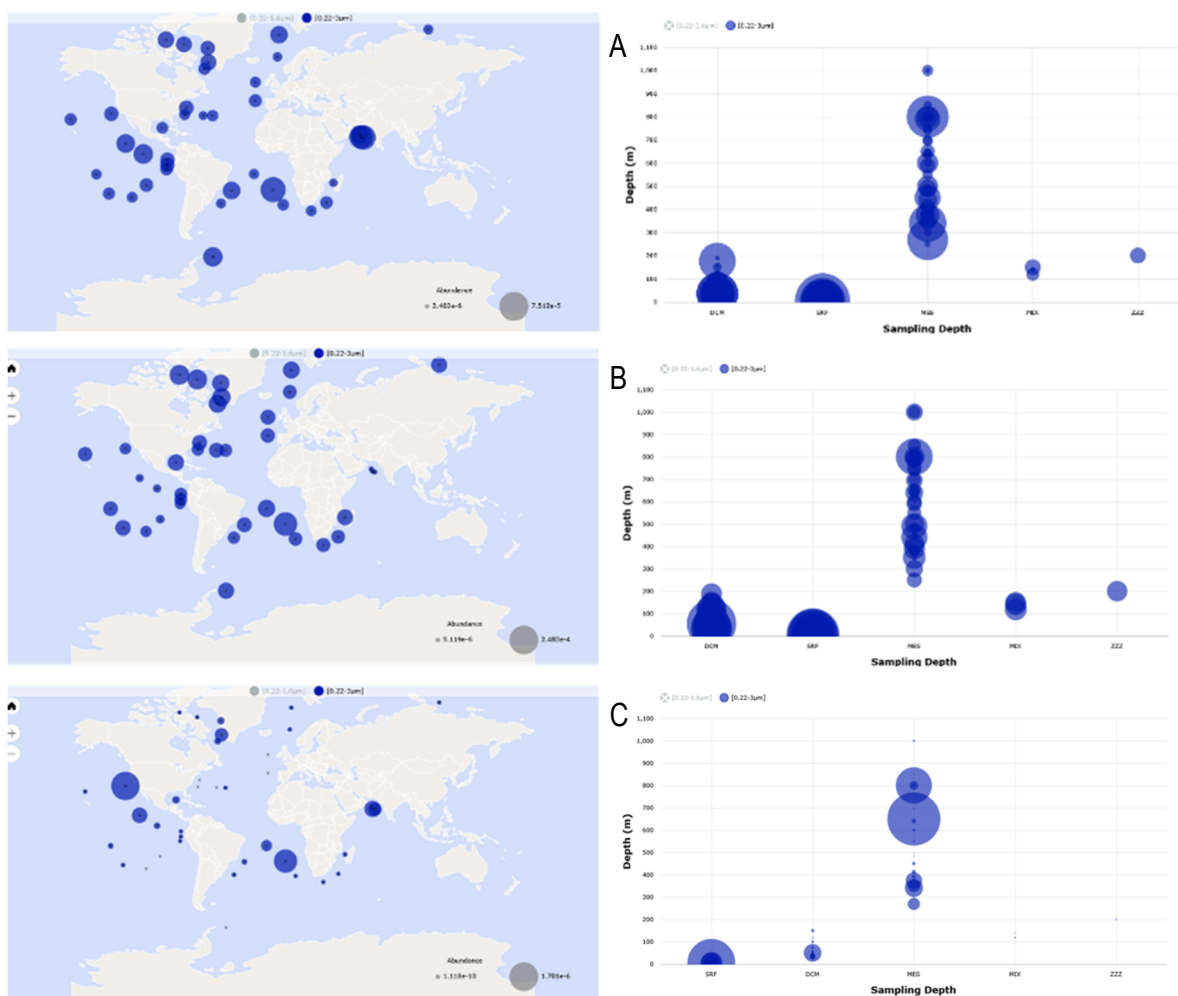


Figure 10. Homolog abundance in the mesopelagic zone (200-1000m) and homologs abundance versus depth (m) for e -values $\leq 1.0E-50$. **A** Dehalogenase SerB from *Rhodococcus* sp. **B** Catalase-peroxidase CAT from strain *Acinetobacter* sp. PVC-6A. **C** Laccase LAC2 from *Bacillus* sp. PVC-6B (Villar et al., 2018)

NDO from *Enterococcus casseliflavus* did not yield any high-confidence homologs in the Ocean Gene Catalogue, and independent BLASTP searches in GeneBank likewise only recovered close matches within *E. casseliflavus*, indicating that this NAD-dependent oxidoreductase is not detectably represented in open-ocean Tara metagenomes. In contrast, the dehalogenase SerB from the Tibetan Plateau PVC-degrading consortium produced numerous, high-confidence hits across almost all Tara Oceans stations and depth layers, with SerB-like genes forming a ubiquitous and abundant component of the marine gene catalog. The catalase-peroxidase CAT from *Acinetobacter* sp. PVC-6A showed a similar pattern, with CAT-like homologs widely distributed throughout the Tara Oceans dataset, consistent with the widespread occurrence of catalase-peroxidases in marine microbial communities. By comparison, the laccase LAC2 from *Bacillus* sp. PVC-6B returned relatively few high-confidence homologs, but these were concentrated in a small subset of samples where summed abundances were comparatively high, suggesting a more spatially restricted but locally enriched distribution of LAC2-type multicopper oxidases (Figure 10).

Zhang, Z. et al. (2022) claimed that a purified catalase-peroxidase from *Klebsiella* sp. EMBL-1 could depolymerize PVC. An independent study failed to replicate the results (Stepnov et al., 2024), the original authors then repeated their enzymatic and FTIR analyses and likewise found no significant reduction in PVC molecular weight or clear degradation products. They now acknowledge that previously reported FTIR signals may have arisen from residual enzyme proteins rather than true PVC oxidation and that GC-MS products could be attributable to components in their self-prepared PVC powder instead of enzymatic activity. Consequently, the proposed role of this catalase-peroxidase in PVC degradation is considered

unproven, although the remainder of the original study's findings are stated to remain valid (Zhang, Z. *et al.*, 2025).

5.5. Global correlation between plastic pollution and plastic-degrading enzymes

Zrimec *et al.* (2021) use screened global ocean and soil metagenomes to show that the abundance of putative plastic-degrading enzyme genes covaries positively with plastic pollution.

A study by Gambarini *et al.* (2024) finds no significant global correlation between plastic pollution levels and expression of putative plastic-degrading genes, nor strong regional or depth-specific links.

5.6. PVC degrading systems for bioremediation

A bacterial consortium enriched from the gut of *Tenebrio molitor* has been described as “capable of efficiently degrading PVC polymer” and suggested as a feasible option for PVC waste removal. Enriched marine consortia able to deteriorate PVC films have likewise been proposed as potential tools for managing PVC contamination in marine or waste-handling environments. Individual isolates such as *Klebsiella* sp. EMBL-1, recovered from lepidopteran larvae and shown to depolymerize PVC, are explicitly framed as promising PVC-degrading bacteria that could underpin future eco-friendly PVC mitigation strategies. Soil consortia from remote environments, including the Tibetan Plateau, have also been enriched on PVC and put forward as candidates for PVC waste bioremediation in terrestrial settings. Beyond these naturally enriched systems, conceptual reviews on microplastic bioremediation argue that isolates like EMBL-1 could be genetically optimized and expressed in robust hosts for applied bioremediation.

6. Discussion

6.1. Overview of the current state of PVC microplastic biodegradation research

The analysis of biodegradation publications demonstrates that PVC is substantially underrepresented in biodegradation research compared to other major plastics. This underrepresentation is probably mainly due to its chemistry making it one of the hardest plastics to attack biologically and because additives and toxicity complicate experiments (Bansal *et al.*, 2025, Rodriguez-Fonseca *et al.*, 2022, Novotny *et al.*, 2022, Zhang, Z. *et al.*, 2022). Most PVC biodegradation studies have focused on bioremediation and therefore mainly been interested in complete mineralization to CO₂ or mass loss as primary indicators of “successful” PVC degradation. This framing tends to treat intermediate steps, such as partial dechlorination or backbone scission, as transient steps on the way to benign end products rather than as outcomes that may themselves carry environmental significance.

The quantitative analysis of 32 experimental studies revealed that evidence for PVC biodegradation is often fragmentary. Only a small fraction of studies combined structural or mass-loss data with information on chlorine fate and metabolite profiles. Nearly half of the studies relied exclusively on structural change and/or weight loss, which can reflect removal of additives, biofilm formation or physical abrasion rather than true backbone degradation. Recently, biodegradation research on non-hydrolysable polymers has undergone a clear methodological shift and new research stresses the need for well-characterized substrates, explicit separation of additive loss from backbone degradation, and multi-method approaches that couple GPC, surface analyses, mineralization assays, dechlorination measurements and metabolite detection (Scott *et al.*, 2025).

In many of the studies there was also a lack of clarity in PVC composition. This is a major limitation because plasticizers and other additives can be degraded by microorganisms, leading to misattribution of apparent biodegradation to the PVC backbone rather than to leachable components (Giacomucci *et al.*, 2019; Novotny *et al.*, 2022). However, most PVC microplastics in the environment contain additives, so understanding how these influences the onset and extent of backbone degradation is relevant, even though it complicates experimental interpretation.

6.2. Distribution of PVC microplastics and the "Missing PVC" problem

Most research on distribution of PVC microplastics in the marine environment reasons from theoretical assumptions that PVC mainly ends up in deeper water columns, shelves and estuaries due to its high density. Actual measurements data do not support this assumption, monitoring studies report PVC in only about half of sediment datasets, usually at less than 5% by count (Quintana et al., 2025). These low levels are particularly puzzling given that PVC accounts for substantial global plastic production (60 million tonnes annually) and cumulative production likely exceeds 1 billion tonnes comprising of about 13% of total plastic production.

Reasons for the low levels has been proposed by Fernández-González *et al.* (2022): weathering-induced spectral changes can make PVC appear similar to oxidized PE in IR libraries, use of NaCl for density separation may exclude denser PVC particles, harsh oxidative or alkaline digestions may alter PVC structure and extrapolation from small spectroscopically analyzed subsets may already under-represent PVC. Fragmentation below detection limits has also been proposed as part of the explanation (Pfohl *et al.*, 2022; Fernández-González *et al.*, 2022). However, fragmentation to smaller PVC microplastics and nanoplastics would lead to a much higher specific surface area. They then present more oxidized, more fractured and more colonized surfaces per unit mass, which would favor continued biodegradation.

If substantial fractions of environmental PVC are either misclassified, lost during sample processing or fragmented beyond current detection thresholds, then present monitoring data are unlikely to capture where and how strongly biological transformation is occurring. The "missing PVC" problem therefore makes it hard to correlate PVC-degrading enzymes with actual PVC pollution in the environment. At the same time, the apparent capacity of soil and gut-derived consortia to substantially reduce PVC particle numbers under experimental conditions (Barili *et al.*, 2023) suggests that efficient PVC-transforming communities could contribute to this discrepancy in ways that current monitoring cannot yet resolve.

6.3. Chlorinated organics from PVC biodegradation

The evidence assembled here demonstrates that PVC biodegradation generates a spectrum of chlorinated organic products, including dichloroethane, hexachloroethane, 1,2-dichlorobenzene, chlorinated esters, cyclic chlorinated acetals, dioxins, furans and long-chain chloroalkanes such as 1-chlorohexadecane. Many of these compounds exhibit toxicity profiles equal to or exceeding those of the parent polymer, including carcinogenicity, aquatic toxicity, bioaccumulation potential and environmental persistence (Appendix III). In several experimental systems, incomplete dechlorination was observed, with a substantial part of the polymer-bound chlorine ending up in organic intermediates rather than being mineralized to chloride. This indicates that PVC biodegradation can act as a source of diverse organochlorines, rather than a simple sink that irreversibly detoxifies the polymer.

The same transformation product can play very different roles in different systems. For example, 1-chlorohexadecane is produced during PVC degradation by one bacterial strain as an intermediate that can be further metabolized but accumulates as a dead-end product in another strain. If PVC-transforming communities channel degrades PVC-backbone into mobile, bioavailable organochlorines that persist or accumulate, the net effect could be a shift from relatively immobile particles to more widely distributed molecular pollutants. Yet, because most studies were designed to assess "successful" degradation, many of these compounds are reported, if at all, as transient intermediates rather than as potential endpoints of concern.

To rule out artefacts generated during metabolite detection (e.g. during pyrolysis), substances should also be analyzed in appropriate control samples. However, none of the studies reviewed reported substance analyses for their controls.

6.4. PVC-degrading enzymes in the environment

Only a few enzymes have been directly tested on PVC, but those that have shown that single proteins can catalyze both depolymerization and dechlorination of the polymer. For example, dehalogenase (SerB) from a soil consortium and oxidoreductases and laccases from insect gut derived strains produce measurable changes in molar-mass distribution, release chloride, and generate chlorinated and dechlorinated products. These results demonstrate that specific enzyme activities can target PVC's backbone and chlorine-bearing sites, at least under laboratory conditions.

Investigations of correlations between reported plastic-degrading enzymes and global marine microplastics pollution have given contradictory results. While Zrimec *et al.* (2021) finds correlation between plastic degrading enzymes in the marine environment and plastic pollution, a later study by Gambarini *et al.* (2024) finds no such correlation. The question is whether it is at all feasible to draw any scientific correlation conclusions with the methods applied in these studies and with currently available data. As most global pollution datasets do not differentiate among types of microplastics, the authors have been constrained to try to correlate between plastic pollution in general and all known plastic degrading enzymes, regardless of which plastic they have been shown to degrade. Several factors limit the feasibility of such an approach. First, plastic-degrading enzymes act on distinct functional groups that vary between polymer classes. Second, enzymes described as "plastic-degrading" have likely evolved for other biological functions unrelated to plastic metabolism, meaning their presence may not necessarily indicate plastic degradation. Finally, and maybe most important, it is not unlikely that plastic pollution and other organic matters aggregate in the same areas and, considering the previous point, it will be hard to distinguish between enzymes operating on "natural" organic matter and plastics.

In this study, instead of bunching all PVC-degrading enzymes together, individual searches in the Ocean Gene Atlas were made. This reveal pronounced contrasts in how different experimentally validated PVC-degrading enzymes are represented in the Tara Oceans metagenomes. NDO, a NAD-dependent oxidoreductase from *Enterococcus casseliflavus* strain EMBL-3, shows no detectable homologs in the Ocean Microbial Reference Gene Catalogue v2 at the stringent BLASTP cut-off used here, and GenBank BLASTP searches similarly only recover close matches within *E. casseliflavus*. This pattern suggests that while *E. casseliflavus* may very well be present in marine systems as a gut-associated microbe from vertebrates and invertebrates, it has not diversified into a free-living organism in marine systems.

By contrast, dehalogenase SerB, identified from a Tibetan Plateau soil consortium that degrades PVC and releases chloride and long-chain alkanes, shows abundant and widespread homologs across Tara Oceans stations when queried against OM-RGC.v2. High-confidence SerB-like sequences occur in surface waters, the deep chlorophyll maximum and mesopelagic samples at virtually all sampled regions, indicating that SerB-type dehalogenases belong to a broadly distributed set of functions in marine microbial communities rather than being restricted to specialized PVC-degrading consortia. Given that SerB catalyzes dechlorination of chloroacetic acid and participates in PVC dechlorination in the Tibetan consortium, its pervasive oceanic distribution likely reflects a more general role in halogenated metabolite turnover, with PVC transformation representing one possible substrate niche rather than its primary ecological function.

A similar picture emerges for the catalase-peroxidase CAT from *Acinetobacter* sp. strain PVC-6A, which was shown to mediate both depolymerization and dechlorination of additive-free PVC films under laboratory conditions. CAT homologs are detected throughout the Tara Oceans dataset with a broad geographic and vertical distribution, consistent with catalase-peroxidases being core components of oxidative stress responses and redox metabolism across many marine taxa. Their wide occurrence underscores that enzymes capable of oxidizing PVC under experimental conditions are often embedded in ubiquitous metabolic pathways, complicating efforts to infer PVC degradation potential from gene presence alone.

In contrast to SerB and CAT, the laccase LAC2 from *Bacillus* sp. strain PVC-6B exhibits a more restricted but locally abundant pattern in the Ocean Gene Atlas output. Only a limited number of Tara samples contain

high-confidence LAC2-like homologs, yet where they do occur, summed abundances can be relatively high, suggesting that LAC2-type multicopper oxidases are concentrated in particular communities or environmental settings. Because LAC2 has been directly implicated in PVC depolymerization and dechlorination and the few apparent “hotspots” for LAC2-like genes may spatially overlap with regions of elevated plastic pollution, this distribution tentatively points to a small subset of taxa with enhanced capacity for oxidative attack on PVC.

Polymer types are increasingly added to plastic pollution datasets, which will make it easier to do more specific analysis with polymer types and corresponding enzymes, but this does not alleviate the other points. The “missing PVC” problem makes it even more unlikely to find correlations between PVC pollution and PVC-degrading enzymes and no such attempts were made in this study. Nevertheless, the global distribution of PVC biodegrading enzymes (Figure 10), and the distribution of general global plastic pollution (Figure 9), at least shows that they co-exist in the same regions. Which, of course, is a basic criterion for PVC biodegradation to occur.

6.5. Highly efficient PVC-degrading systems and their environmental implications

With the limited number of studies on PVC biodegradation and the lack of comprehensive data on PVC distribution, it is not probable that the most efficient PVC-degrading systems have been found (probably consortia working in concert). This, together with findings such as the 50-65% reduction observed in soil, suggests that more efficient microbiomes for degrading PVC could exist, at least partly explaining the missing PVC phenomenon.

Several studies have suggested that genetically modified or naturally enriched organisms with highly efficient PVC-degrading enzymes could form the basis of technological solutions to PVC microplastic pollution. Applications range from closed bioreactors treating PVC-rich industrial waste streams, through bioaugmentation of wastewater treatment systems, to more speculative ideas about environmental release or bioremediation in polluted sediments and soils. These applications need to be evaluated not only in terms of their ability to reduce visible microplastic loads, but also with respect to the nature, persistence and mobility of the chlorinated products they generate. From a precautionary perspective, if enzymes or consortia capable of degrading PVC at very high rates are discovered or engineered, a central question is whether they should be deployed for bioremediation at all, given the potentially vast risks that uncontrolled spread and subsequent formation of toxic, mobile organochlorines could pose to ecosystems and human health.

6.6. Future research

Future work should close the chlorine mass balance in PVC biodegradation experiments by tracking inorganic chloride, organochlorines and residual polymer-bound chlorine. Isotopically labeled PVC and targeted or non-targeted high-resolution analytics can help resolve the main transformation pathways. In parallel, realistic microcosm and field studies using natural sediments or soils and authentic PVC loads should test whether the mechanisms inferred from laboratory work occur in situ. Such studies need to co-measure PVC microplastics, candidate degradation genes or enzymes and chlorinated compounds, and distinguish PVC-derived products from natural occurring organochlorines or legacy organochlorine contamination.

7. Conclusion

In the environment PVC’s chlorine content has traditionally not been viewed as an environmental problem, because it was regarded as essentially inert and not amenable to biodegradation under realistic conditions, despite the vast quantities of chlorine bound in PVC produced over time. The evidence compiled in this thesis shows that this assumption is no longer tenable: multiple experimental systems now demonstrate partial depolymerization and dechlorination of PVC, it is probable that more efficient PVC-degrading consortia and enzymes exist in the environment than those captured in the current literature. Given the billion-tonne scale of cumulative PVC production and its roughly 57% chlorine content by mass, even

biodegradation of a small fraction would represent a vast, largely uncharacterized source of organochlorines.

Acknowledgements

I would like to thank my supervisor, Ingela Dahllöf, for her support and help, and for keeping me grounded.

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Appendix I

Analytical methods used in studies

Author	Methods							PVC Composition		
	Mass Loss	Structural Change	Mineralization	Chloride Balance	Metabolite Detection	Isotopic Method	Chlororganics	Not Clear	Plastizised	Pure
Ameen <i>et al.</i> , 2025	√	√						√		
Giacomucci <i>et al.</i> , 2019	√	√							√	
Saeed <i>et al.</i> , 2022	√	√						√		
Bansal <i>et al.</i> , 2025	√	√			√		√	√		
Giacomucci <i>et al.</i> , 2020	√								√	
Jin <i>et al.</i> , 2022	√								√	
Khandare <i>et al.</i> , 202 [√]	√	√	√	√						√
Khandare <i>et al.</i> , 2022					√		√			√
Nyamjav <i>et al.</i> , 2023	√	√	√	√						√
Peng <i>et al.</i> , 2020	√	√		√						√
Peng <i>et al.</i> , 2023a	√									√
Peng <i>et al.</i> , 2023b	√	√					√	√		
Peng <i>et al.</i> , 2025	√			√					√	√
Sumathi <i>et al.</i> , 20 [√] 6		√			√		√	√		
Wu <i>et al.</i> , 20 [√] 8.	√	√						√		

Methods							PVC Composition			
Author	Mass Loss	Structural Change	Mineralization	Chloride Balance	Metabolite Detection	Isotopic Method	Chlororganics	Not Clear	Plastizised	Pure
Xu <i>et al.</i> , 2024	√	√							√	
Xu <i>et al.</i> , 2023	√	√		√	√					√
Zhang, Z. <i>et al.</i> , 2022	√	√		√	√				√	√
Bule Možar <i>et al.</i> 2023		√						√		
Jiang <i>et al.</i> 2025	√	√		√	√		√		√	√
Ye <i>et al.</i> 2024		√						√		
Andleeb <i>et al.</i> 2025		√		√				√		
Xu <i>et al.</i> 2025	√	√				√				√
Gulizia <i>et al.</i> 2025	√	√							√	√
Ren <i>et al.</i> 2023	√							√		
Dudek <i>et al.</i> 2025		√						√		

Methods							PVC Composition			
Author	Mass Loss	Structural Change	Mineralization	Chloride Balance	Metabolite Detection	Isotopic Method	Chlororganics	Not Clear	Plastizised	Pure
Rodriguez-Fonseca <i>et al.</i> 2022	✓	✓		✓	✓					✓
Stepnov, A <i>et al.</i> 2024	✓	✓						✓		
Kumari <i>et al.</i> 20✓8	✓	✓								✓
Rajashree <i>et al.</i> 20✓2		✓		✓				✓		
Zhang, H. <i>et al.</i> 2026	✓	✓			✓		✓			✓
Hatwar <i>et al.</i> 2025	✓	✓		✓					✓	✓

Appendix II

Organism biodegradation evidence

Organism	Notes	Evidence for dechlorination	Citation
<i>Klebsiella</i> sp. EMBL-1	Able to depolymerize and utilize pure PVC as sole energy source	Inferred: Proposed pathway includes dechlorination of intermediates; supported by metabolite profiles and enzyme candidates, but no explicit Cl ⁻ release data	Zhang, Z. <i>et al.</i> , 2022
<i>Citrobacter koseri</i>	Can utilize pure PVC film as a carbon source	Inferred: Decreased chlorine atomic% and increased oxygen on film surface by EDS/XPS, plus structural degradation, but no explicit Cl ⁻ release data	Nyamjav <i>et al.</i> , 2023
<i>Streptomyces gobitricini</i>	Unclear but probably plasticized PVC. Unclear if degradation occurred	None	Ameen <i>et al.</i> , 2025
<i>Pseudomonas citronellolis</i>	Shown to act mainly against PVC additives, exhibiting a low biodegradation rate of PVC polymer.	None	Giacomucci <i>et al.</i> , 2019
<i>Bacillus flexus</i>	Shown to act mainly against PVC additives, exhibiting a low biodegradation rate of PVC polymer.	None	Giacomucci <i>et al.</i> , 2019
<i>Bacillus amyloliquefaciens</i>	Weight reductions probably represented degradation and removal of molecules of the additive rather than of the PVC polymer		Novotny <i>et al.</i> , 2022
<i>Bacillus toyonensis</i> Cbmb3	Unclear but probably plasticized PVC. Able to utilize PVC as the sole carbon source.		Wang <i>et al.</i> , 2024
<i>Acinetobacter baumannii</i>	Unclear but probably plasticized PVC	None	Bansal <i>et al.</i> , 2025

Organism	Notes	Evidence for dechlorination	Citation
Marine anaerobic microbial consortia	Able to degrade plasticized films apparently acting against both the additives and the polymer chains.	None High NaCl contents in the microcosm media did not allow dechlorination determination.	Giacomucci <i>et al.</i> , 2020
<i>Vibrio</i> , <i>Altermonas</i> and <i>Cobetia</i>	All three bacterial isolates showed biodeterioration of pure PVC film	Inferred: Loss of C–Cl FTIR bands and reduced Cl signal by EDS on PVC surfaces, but no explicit Cl [–] release data	Khandare <i>et al.</i> , 2021
<i>Tenebrio molitor</i> larvae gut microbiome	Capable of performing broad depolymerization/biodegradation but limited mineralization of pure PVC MPs.	Fraction of PVC chlorine mineralized to Cl [–] , combined with FTIR and GPC changes of PVC	Peng, B. <i>et al.</i> , 2020
<i>Tenebrio molitor</i> larvae gut microbiome	Data indicated that the polymer chains of the ingested PS and PVC were effectively shortened and reduced after passage through the gut of mealworms, demonstrating the biodegradation of the microplastics.		Peng, B. <i>et al.</i> , 2023
Consortium EF1 from the gut of <i>Tenebrio molitor</i> larvae; <i>Stenotrophomonas</i> (~78%) <i>Enterococcus</i> (~15%) <i>Acinetobacter</i> (~2%) <i>Xylella</i> , <i>Pseudochrobactrum</i> , <i>Ochrobactrum</i> , <i>Lactobacillus</i> , <i>Streptococcus</i> , <i>Bacillus</i> and others (~4%)	Able to degrade and mineralize pure PVC.	Increase in Cl [–] in medium plus loss of C–Cl signatures (FTIR/ToF-SIMS) and appearance of dechlorinated metabolites	Xu <i>et al.</i> , 2023

Organism	Notes	Evidence for dechlorination	Citation
<i>Tenebrio molitor</i> larvae gut microbiome	Effectively biodegrade four high-purity MPs (LDPE, PS, PVC and PLA)	the $\delta^{13}\text{C}$ stable isotope values of residual PE, PS, PVC, and PLA extracted from respective frass consistently increased after the MPs were degraded in the mealworms, confirming biodegradation	Xu <i>et al.</i> , 2025
<i>Stenotrophomonas maltophilia</i> PVC-SHT	Able to degrade PVC using plastic as the sole carbon source, the efficiency was confirmed by SEM analysis. Unclear if PVC were plasticized or pure.		Ye <i>et al.</i> , 2024
<i>Spodoptera frugiperda</i> larvae gut microbiome	Degrade PVC film through multiple pathways, including both plasticizers and polymer degradation	Enzyme directly dechlorinates additive-free PVC: lower M_n/M_w , structural changes, and Cl^- release dependent on NADH	Peng, H. <i>et al.</i> , 2025
Consortium DC from lignin enriched Tibetan grasslands. 16S rRNA gene sequencing demonstrated that the DC selectively recruit polymers-response bacteria <i>Burkholderia</i> , <i>Rhodococcus</i> and <i>Dyella</i> under the exposure of synthetic polymers (PVC) and natural polymers (lignin).	Physicochemical alterations and degrading intermediates of DC-treated PVC pure and plasticized plastics confirmed its degrading capability.	Cl^- release with substrate loss and detection of long-chain alkanes/dechlorinated products	Jiang <i>et al.</i> , 2025
Vermibacteria from the gut of <i>Eisenia fetida</i>	Unclear if PVC were plasticized or pure. Effectively degrade PVC plastic.		Andleeb <i>et al.</i> , 2025

Organism	Notes	Evidence for dechlorination	Citation
Three freshwater-derived <i>Streptomyces</i> strains were identified with closest neighbours, <i>S. albospinus</i> (290), <i>S. chattanoogensis</i> (250) and <i>S. kasugaensis</i> (208).	High-yield PVC biodegradation was achieved. Pure PVC.	PVC weight loss + TGA/GC–MS intermediates + increase in supernatant Cl ⁻	Rodriguez-Fonseca <i>et al.</i> , 2022
<i>Micrococcus luteus</i>	Unclear but probably plasticized PVC. The growth of isolated strain on the surface of PVC film gives positive intimation that the isolate can be used as potent biodegrading agent	Inferred: "PVC degrading" strains reported, no analytical Cl ⁻ data, dechlorination mostly assumed in narrative	Rajashree, 2012
<i>Acinetobacter</i> sp. strain PVC-6A	Able to efficiently degrade pure PVC and utilize it as the sole carbon source for growth. Produced 1-chlorohexadecane.		Zhang, H. <i>et al.</i> , 2026
<i>Bacillus</i> sp. strain PVC-6B	Able to efficiently degrade pure PVC and utilize it as the sole carbon source for growth. Could utilize 1-chlorohexadecane.		Zhang, H. <i>et al.</i> , 2026

Appendix III

Chlorinated organic compounds

Name	Comment	Citation
Dichloroethane	Human carcinogen (IARC Group 2B), mobile and volatile, readily contaminates groundwater.	Sumathi <i>et al.</i> , 2016
Hexachloroethane	Highly persistent in air, water, and soil (half-lives up to months). Candidate for long-range atmospheric transport. Acute aquatic toxicity: Highly hazardous to aquatic organisms	Khandare <i>et al.</i> , 2022
1,2-Dichlorobenzene	Aquatic bioaccumulation: High bioconcentration factors in fish lipid. Toxic to invertebrates and fish at mg/L levels. Sediments: Strong adsorption to organic matter; can accumulate in benthic food webs.	Sumathi <i>et al.</i> , 2016
Trichloroacetic acid, hexadecyl ester (C ₁₈ H ₃₃ Cl ₃ O ₂)	Hydrolysis releases trichloroacetic acid (TCAA): TCAA is highly phytotoxic. Causing chlorosis, necrosis, and growth inhibition in terrestrial and aquatic plants at µg/L–mg/L doses. Soil and sediment risk: Long-chain ester strongly sorbs to organic matter.	Jiang <i>et al.</i> , 2025
3-Chloropropionic acid, heptadecyl ester	Specific ecotoxicity unknown; generic chlorinated ester hazards apply.	Khandare <i>et al.</i> , 2022

Name	Comment	Citation
5-Chloro-(2,4-dichlorophenoxy) phenol	Structural analogy hazards: Chlorinated phenols and phenoxy compounds are typically persistent, strongly sorbing to soils/sediments, and toxic to aquatic organisms; potential for bioaccumulation and endocrine/developmental effects. Secondary chlorination: May form more highly chlorinated by-products (including dioxin precursors) via oxidation or further chlorination in environmental matrices.	Sumathi <i>et al.</i> , 2016
2,3-Chlorobicyclo-oct-2-en-6-methyl-1,3-dioxolane	Aquatic hazard: Likely harmful to aquatic life with long-lasting effects, based on generic chlorinated cyclic acetal behaviour. Transformation products: Oxidative or microbial cleavage may yield chlorinated alcohols, aldehydes, or carboxylic acids of uncertain but potentially higher toxicity and mobility.	Sumathi <i>et al.</i> , 2016

Name	Comment	Citation
Dioxins	Extreme persistence: Soil half-lives 25–100 years; highly lipophilic (log Kow >6); bioaccumulate and biomagnify through food chains to top predators and humans. Multiple toxicity endpoints: Carcinogenic (2,3,7,8-TCDD is IARC Group 1), immunotoxic, endocrine-disrupting, and developmentally toxic at pg–ng/kg doses. Long-term ecosystem risk: Even trace levels pose chronic risk; effects include reproductive impairment, immune suppression, and wasting syndrome in wildlife.	Bansal <i>et al.</i> , 2025
Furans	Co-toxicity with dioxins	Bansal <i>et al.</i> , 2025
1-chlorohexadecane	Aquatic toxicity: Classified as very toxic to aquatic organisms with potential for long-term adverse effects; marine pollutant designation. High persistence in water/soil, low in air: Expected to strongly partition into sediments and organic matter; low mobility but high local accumulation risk. Bioaccumulation potential: Long aliphatic chain (C₁₆) favours lipid partitioning and bioaccumulation in benthic invertebrates and fish	Zhang, H. <i>et al.</i> , 2026

Appendix IV

FASTA sequences for PVC-degrading enzymes

Nucleotide sequence of gene for NAD-dependent oxidoreductase (NDO) from *Enterococcus casseliflavus* strain EMBL-3

> NAD-dependent oxidoreductase (NDO)

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ATGAAAATCATTATCATAGGCGGGTCCTTTGGGGGTGTCAGCTGCGCCCGTGAAGCACGCCGATT
ATACCCTGACGCAGAGATTTTATTGATAGAAAAAAGTCCATCTTGGGTTTGTTCGAAGCGGTT
TGTTATTGCTGATCGAAGGCAGGATCGCATCGCTGGAAGAAGCATTCTTTTGTACGAAGGAGCAG
CTGGAGGCAGAAACGATCGACGTTGCCTTAGAAGAAACGCTTCTGGAGATTTTTCCTTCGGATCA
TCGGATTTCGAACGGATAAGCGAGAATAAGTTATGATCGACTCGTCTTGGCAGCAGGCTCCAGTC
AAGATTCCTACTGTTTTGCCACAACCAGAAGAAGCACTACTGACCTACAAGGAATATGAGGCAGCC
AAGCATTTCTTGCAGCAATTGCCCCAAGCAGAGTCGATTACCATCGTAGGTGCTGGTCAAGCGGG
GATGGAAGCGGCGAATACCTTGACTGCGATCGGAAAAAAGTCAGTGTGATCGAATCAATGTCAT
ATCCTTTATTCAAGTACTTTGATCACGATTTTTTGCAGCCCTTTTAAACGGAGATCGAAAAAATC
CCCAACTTGCAGATGCATTGGTCCAAGCCAACCTTGGCAGTCGTTAAAACGGAAACAGGCTTTCG
GATCGAAACCGCCGATCAAGGCTATGAAAGCGATCTGGTATTGACGACAGTCAACGTTTCATCCTC
GCTTGCCAGAGGCATTTGCGGTCTTTGAATTACACAGTGATCAAACCATCTGGACAGATGCCTAC
TTGGAAACTTCTGCCACGGATATTTTTGCGGTGCGCGATTTGATCCAAATTCCGAATGCTATTAC
GAAAGACACGGTCTATATGCCCTTAGTCAACAATGCTGTTCGCTCAGGAATCGCAGCAGCTCGTA
ATCTGGCAAGCAAAACCAACCCCGTTTCGTGGCGGATTGCGGACAGTCGGAACGCAACTGTTTGGG
TGGTACTTAGCAAGCACCGGCTTGACCGAGTCGGATCGGTTTTTCTTCGAATCTCCGATCGTCTG
TCATGCGTTTACTGCCGCCAGTTCCTTGTTTGATCCAACACAGGTTTCATGGAAAAGTGATGATCG
AACAAGCCAGCGGCCGAATCGTTGGTGCGCAGCTTTTATCAAAAGCCAATATTTTGGAAAAAATC
AATTTACTAGCGTTTGCGATCGAGCAGCAGGCAACGATGGAGGAGTTGACCCAAAAAGACTTTTT
CTTCCATCCACGGTTCCTAATGTAATCGACGAACTTTTCTATGGTCGGGAAGTGATGCCGATG
AGACTTGA
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Amino acid sequence of Dehalogenase (SerB) from *Rhodococcus* p. strain P14

>A0A098BUH4 (SerB)

```
MASDTAMLVTVTGPDPHGVTSVLFAALTRHDVDLLDVEQVVIRGRLLTGLVLVSCPADPDALQDEI
EAAMATIGMHAQVQTGVEPGIGSSVSTHALVVLGSPVSARALRSVGRELARQGANIDSIRGIADY
PVTGLELMVTAADPGSEADARLRAGLAELAAGLEV DIAVERAGLARRSKRLIVFDVDSTLVQGEV
IEMLAHAGVEDKVRVTEAAMRGEIDFTESLNQRVATLAGLPASVIDEVAENLELTPGARTTIR
TLRRLGFRCGVVS GGFRQVIDGLAHELELDFVRANTLEIVDGKLTGRVVGEVVDRAAKARALREF
AAEAGVPIEQTVAVGDGANDIDMLGAAGLGIAFNAKPALREVADTALSHPYLDAVL FVLGVTRDE
VEAADRV DGT LRRVPLDTGA
```

Amino acid sequence of Catalase-peroxidase (CAT) from *Acinetobacter* sp. strain PVC-6A

>CAT (katG)

```
MSNESKCPFSGHNSKPQVTVGGGTANLHWWPNQLRVDLLNQHSE
RSNPLGKDFNYRQEFKKLDYYALKADIKNVLTDSQDWWPADWGN YTG LFI RLAWHAAG
TYRMGDGRGGAGRGQQRFAPLNSWPDNASLDKARRLLWPVKQKYGQKISWADLFILAG
NIALESSGFRTFGFGAGREDVWEPDNDVNWGD EKEWLAHRNSEALAGSNLAATEMGLI
YVNPEGPQASGDPRSAAPFIRATFGNMAMDDEEIVALIAGGHTLGKTHGAASADHVQA
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DPEGAPIEQMGFGWANSYGTGVGKDAITSGLEVIWSQTPTQWSNYFFENLFKYEWVQE
RSPAGAIQWVAADAEAIIPDPFDPSIKRKPTMLTTDLTLRFDPEFEKISRRLNDPQA
FANAFARAWFKLTHRDMGPKARYLGPEVPAEDLIWQDPLPAASATPSSASIADAKAKI
VALGLSTGELVSLAWASASTFRGGDKRGGANGARIALSPQREWEVNKKAVETLTKIEE
LKASTQLSLADLIVLAGNVGVEQAAQAAGFNITVPFAPGRVDALQSQTDVESFQLLLG
LADGFRNWKKQGVNTPAEVLLIDKAQQLTLTAPELTALIGGLRVLGTNWDGSQHGVFT
QQVGVLSTDFFTNLLDMSNVWAPVDSTSEVFEGKDRKSGTVKFTATRNDLVFGSNSIL
RALAEVYAQADGKEKQVQDFVAAWTKVMNLDRFDLA

Amino acid sequence of Laccase LAC2 from strain *Acinetobacter* sp. PVC-6B

> LAC2 (multicopper oxidase)

MNLEKFVDELPIPEVAKPVKKNPRQTYEIAMEEVFLKVHRDLP
PTKLWTYNGSLPGPTIKANRNEKIKVKWMNKLPLKHFLPVDHTIHSGHHDEPEVKTVV
HLHGGVTPASSDGYPEAWFSRDFEATGPFFERETYVYPNHQQACTLWYHDHAMALTRL
NVYAGLAGFYLISDAFEKSLELPKDDYDIPLMIMDRTFQEDGSLFYPSRPNDTPEDSD
IPDPSIVPFFCGETILVNGKVWPYLEVEPRKYRFRILNASNTRTYELHLDNDATILQI
GSDGGFLPRPVRHQFSIAPAERFDVIIDFSAYENKTITLKNTAGCGQDVNPETDANI
MQFKVTRPLKGRVPKTLRPFIKPLPALRPSRADRERTLTLTGTQDKYGRPILLLDNQF
WNDPVTENPRLGSLEVWSIVNPTRGTHPIHLHLVQFRVLDRRPFDETEVYQSTGEIVYT
GPNEAPPLHEQGYKDTIQAHAGEVIRIVARFVPYSGRYVWHCHILEHEDYDMMRPMDI
IQ