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Preliminary Assessment of Microbial Enzyme Potential for Plastic Degradation: An *In-Silico* to *In-Vitro* Investigation

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Abstract

Plastic pollution remains a global issue due to the increasing production of plastics, which has more than doubled in the last two decades, raising both environmental and health concerns. This preliminary study explored the potential of microbial enzymes in plastic degradation using both in-silico and in-vitro approaches. Molecular docking was employed to evaluate the binding affinities of three enzymes: esterase hydrolase (PDB ID: 3KVN), dehydrogenase oxidoreductase (PDB ID: 4JZ6), and laccase oxidoreductase (PDB ID: 5LM8) with 23 plastic compounds from four major plastic types: polyester, polyolefins, polystyrene, and polyvinyl chloride. Fourteen of the plastic compounds exhibited strong binding affinities (≤ -5.0 kcal/mol) with the three enzymes. Notably, 2,6-naphthalene dicarboxylic acid (PubChem ID: 14357), a polyester precursor, showed the highest binding affinity with all the enzymes (-7.1 , -7.9 , and -7.2 kcal/mol, respectively). Microbial isolates (bacteria and fungi) from a local multi-waste dumpsite were screened for their ability to produce laccase and lipase (enzymes relevant to plastic degradation) employing both qualitative and quantitative assays. Positive enzyme activity was indicated by distinct reddish-brown and yellow colorations. Isolates with the highest enzyme activity were identified through molecular characterization as *Bacillus pumilus*, *Staphylococcus cohnii*, and *Penicillium citrinum*. These initial findings suggest that soil microorganisms may harbor enzymes with potential plastic-degrading capabilities. However, further in-vitro studies are required to validate the actual degradation of plastic compounds by these enzymes. This work lays the foundation for future development of enzyme-based biotechnological solutions for plastic waste management.

Keywords: Biodegradation; Microbial enzymes; Molecular docking; Plastic compounds; Plastic pollution



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1.0 Introduction

Synthetic plastics have become an essential part of modern society due to their versatility, particularly in packaging applications (Nikolaivits *et al.*, 2020). Unlike conventional packaging materials, synthetic plastics have unique properties such as mechanical strength, affordability, durability, and superior barrier qualities (AlMaadeed *et al.*, 2020; Desideriy & Lanotte, 2022). An estimated 350-400 million metric tons of plastics are produced globally each year (Danso *et al.*, 2019), with Polyethylene Terephthalate (PET), polyethylene (PE), polyvinyl chloride (PVC), polystyrene (PS), polypropylene (PP), polyamide (PA) and polyurethane (PUR) among the most commercially significant types.

Despite their usefulness, plastics are notoriously resistant to degradation and can persist in the environment for several decades or centuries. This contributes to severe waste disposal challenges and associated health risks (Duddu *et al.*, 2015). Equally worrisome is that treatment processes such as photolysis or natural weathering can degrade these plastics to potentially more hazardous secondary pollutants such as micro and nano- plastics which enter the food chain (Hantani *et al.*, 2018). Plastics may also contain toxic additives such as plasticizers, flame retardants, xylenes, zinc acetate (Folarin *et al.*, 2024; Lahimer *et al.*, 2017) as well as solvents, initiators and catalysts employed during preparation (Mendiburu-Valor *et al.*, 2021). These pollutants and their by-products are released during conventional waste management practices such as informal recycling, incineration, and landfilling, thus making these methods ineffective and potentially harmful (Rajmohan *et al.*, 2019). Developing countries are the most affected, accounting for about 92% of reported deaths linked to plastic pollution (Bartrem *et al.*, 2014; Landrigan *et al.*, 2018). It is thus imperative to devise novel technologies and eco-friendly remediation strategies (Almeida *et al.*, 2019; Ru *et al.*, 2020).

Remediation techniques may be chemical, thermal, biological or even excavation and dredging of polluted sites, possibly achieved *in situ* or *ex situ*. However, biological remediation remains the most sustainable technique employed for degradation and detoxification of pollutants in plastic waste management (Kumar *et al.*, 2018). A wide range of chemical pollutants like pesticides, nitroaromatic compounds, metals, polyaromatic hydrocarbons and halogenated petroleum hydrocarbons have been successfully biodegraded (Chen *et al.*, 2015). Microorganisms used for bioremediation are eco-friendly and are promising agents in reducing environmental

threats. The use of microorganisms in bioremediation is an attractive alternative because of its lower cost and high efficiency when compared with other physicochemical methodologies (Abatenh *et al.*, 2017). Microbial enzymes are superior biological substances derived from various microorganisms (bacteria, mold and yeast), particularly for application in industries on commercial scales. Oxidoreductase and hydrolase are two major classes of enzymes used in plastic degradation (Bhandari *et al.*, 2021). Hydrolase includes esterases, proteases, and cutinases while oxidoreductase includes dehydrogenases, laccases, and peroxidases. The degradation of plastics by hydrolases, specifically esterases, proceeds by ester bond cleavage and are active mainly on aliphatic polyesters while oxidoreductases catalyse bond cleavage in plastics via oxidation-reduction reactions (Chamas *et al.*, 2020).

In silico methods have emerged as efficient, cost-effective tools for screening microorganisms capable of plastic degradation. Studies on plastic degradation using *in silico* techniques are limited. A study by Almeida and co-researchers is one of the few available reports. They reported an *in silico* – *in vitro* approach for screening bacterial PET hydrolase enzymes from *Streptomyces* for PET degradation (Almeida *et al.*, 2019). Another study employed an *in vitro* to *in silico* approach to determine the biodegradation potentials of newly isolated *Pseudomonas* species from municipal landfill soils (Bhatia *et al.*, 2014). These microorganisms were used for low density polyethylene biodegradation (LDPE). A pure *in silico* study assessed the binding affinity of some plastic compounds on *Ideonella sakaiensis*, a hydrolase enzyme (Duru *et al.*, 2021).

In this preliminary study, we aimed to assess the degradation potential of 3 enzymes: esterase (PDB ID: 3KVN), laccase (PDB ID: 5LM8), and dehydrogenase (PDB ID: 4JZ6) on 23 plastic compounds of 4 plastic types (polyester, polyolefins, polystyrene and polyvinyl chloride) employing *in silico* methods. We also examined the capacity of two types of microorganisms isolated from a dumpsite, to produce two of these enzymes, specifically lipase (an esterase) and laccase *in vitro*. This two-tiered approach offers preliminary insights into the feasibility of microbial enzyme application for plastic degradation and lays the groundwork for more robust experimental validation and optimization in future studies.

2.0 Experimental

2.1 Molecular docking

The crystal three-dimensional (3D) structures of three microbial enzymes: Esterase from *Pseudomonas aeruginosa* (3KVN), Salicylaldehyde dehydrogenase NahF, from *Pseudomonas putida* (4JZ6) and -laccase-like oxidoreductase from *Aspergillus niger* (5LM8) were selected as the protein target for molecular docking. These structures were retrieved from the Protein Data Bank (PDB) with resolutions of 2.50 Å, 2.42 Å and 1.70 Å respectively. Selected enzymes were screened based on absence of mutation, possessing resolution not lower than 1.60 Å, and belonging to the hydrolase or oxidoreductase family. The hydrolase and oxidoreductase enzymes have the potential to degrade plastics through reactions like oxidation, reduction, and ester bond cleavage. Enzyme preparation was performed using UCSF Chimera (Pettersen et al., 2004), during which non-amino acid residues and water molecules were removed, and polar hydrogens were added to the protein structures. This was necessary to enhance the intermolecular interactions between ligands and protein residues.

A total of twenty-three (23) chemical constituents of different plastic types were used as ligands for docking in this study. The 3D structures of these compounds were retrieved from the PubChem database and energy-minimized using the PyRx software package (Dallakyan & Olson, 2015). Molecular docking was done using AutoDock Vina (Trott & Olson, 2009) in order to understand the mode of binding interaction between target plastic compounds and enzymes (Rakesh et al., 2019). As a predictive tool, it allows for the calculation of the binding energies of compounds when they interact with enzymes. A lower binding energy indicates a better ability of the compound to bind within the active site of the enzyme or protein target. To ensure accurate docking, grid boxes were set to cover the active site of each enzyme. The grid box centers and dimensions were set as follows:

- Esterase (3KVN):
Center: x = -4.45, y = 40.89, z = 48.34
Size: x = 57, y = 51, z = 93
- Salicylaldehyde dehydrogenase (4JZ6):
Center: x = 63.57, y = -8.75, z = 14.34
Size: x = 53, y = 59, z = 50
- Laccase-like oxidoreductase (5LM8):
Center: x = -23.57, y = 0.71, z = -26.47
Size: x = 47, y = 56, z = 44

These grid parameters allowed for accurate targeting of the active sites, enabling reliable estimation of binding energies and

molecular interactions between the enzymes and the plastic compounds.

2.2 Isolation and characterisation of microorganisms

Soil was collected from a compost pile at a depth of 6 inches from a multi-waste dumpsite in Abeokuta, Ogun State, Nigeria. For bacteria and mold isolation, the sample was serially diluted and plated at 10^{-3} and 10^{-5} dilutions on Nutrient Agar (NA) and Potato Dextrose Agar (PDA), respectively. The NA plates were incubated at 37 °C for twenty-four hours while the PDA plates were incubated at 25 °C for five days (Thabet et al., 2023). After incubation, bacterial colonies were identified based on their morphological and biochemical properties, while molds were identified based on their morphological appearance on PDA plates and micro-morphological features using x10 and x40 objective lenses (Akinyemi et al., 2022). Pure cultures obtained by subculturing on fresh NA and PDA using the same incubation conditions were preserved on agar slants for further identification and characterisation.

2.2.1 Qualitative screening of mold and bacteria for laccase and lipase production

Qualitative screening was carried out to assess the ability of bacterial and mold isolates to produce laccase and lipase enzymes. For laccase screening, pure cultures were inoculated on NA and PDA plates containing 0.04% Guaiacol as an indicator. The plates were incubated at 37 °C for 5 days (bacteria) and 25 °C for 6 days (mold) as described by Salami et al. (2022). The development of a reddish-brown halo in the Guaiacol supplemented plates indicated a positive laccase secretion.

Lipase production was assessed using phenol red-based NA and PDA media. The media were prepared by dissolving PDA (39.5 g) or NA (14 g), peptone (6.67 g), phenol red dye (0.5 g) and substrate olive oil (5 mL) in 500 mL of distilled water. The mixtures were heated, agitated, and left to cool before adjusting the pH to 7.0 (PDA) and 6.7 (NA). Plates were autoclaved, inoculated with mold or bacterial cultures, and incubated at 25 °C for 3 days (molds) and 37 °C for 2 days (bacteria) (Ilesanmi et al., 2020; Tsui et al., 2019). A colour change from red to yellow indicated the release of fatty acids as a result of lipolysis.

2.2.2 Quantitative screening of mold and bacteria for laccase and lipase production

Isolates that tested positive for laccase and lipase production in qualitative screening were subjected to quantitative screening adapting the methods of Ilesanmi et al. (2020) and Tsui et al.

(2019). For laccase, 500 mL Erlenmeyer flask was filled with a nutrient medium containing 3.0 g peptone, 0.6 g KH_2PO_4 , 0.4 g K_2HPO_4 , 0.001 g ZnSO_4 , 0.05 g MnSO_4 , 0.0005 g FeSO_4 , 0.5 g MgSO_4 , 0.01 g CuSO_4 , and 2 g rice bran was added as substrate for molds. The pH was adjusted to 6.7 for bacterial cultures and 7.0 for molds. Flasks were autoclaved and inoculated after cooling and incubated in triplicates at 25 °C under static conditions for 15 days (molds), and at 37 °C on a gyratory shaker (125 rpm) for 6 days (bacteria).

For lipase, the isolates were inoculated on a medium containing 10 g peptone, 5 g yeast extract, 5 g NaCl, 2 g CaCl_2 , 0.3 g K_2HPO_4 , 1 g KH_2PO_4 , 2 g $(\text{NH}_4)_2\text{SO}_4$, 0.2 g $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, and 2% (v/v) olive oil, while rice bran 2 g was added as a substrate for mold. The media were incubated at 37° C for 3 days at pH 6.7 on a gyratory shaker (125 rpm) (bacteria), and at 25 °C for 7 days at pH 7 under static conditions (molds). After incubation, mold cultures were harvested by adding 50 mL of sterilized distilled water and shaking for one hour. The content was then filtered using 125 mm Whatman filter paper. Both bacterial and mold cultures were centrifuged at 10,000 rpm for 10 minutes at 4 °C using a high-speed tabletop centrifuge (HI850R, Clifton, Nickel, England). The supernatants were collected and labeled as crude enzyme extracts (Senthivelan et al., 2019).

2.2.3 Laccase enzyme assay

Laccase activity was determined by mixing 1 mL of 0.02% guaiacol, 3 mL of 10 mM sodium acetate buffer and 1 mL of the crude enzyme extract in test tubes. A blank solution consisted of 1 mL each of substrate, buffer distilled water. Reaction mixtures were incubated at 30 °C for 15 minutes in a water bath, and absorbance was measured at 470 nm using a UV spectrophotometer (Biobase 752N). One unit of enzyme activity was defined as the amount of enzyme required to oxidize 1 μmol of guaiacol per minute (Solanki et al., 2022). Laccase enzyme activity was calculated using the equation below.

$$E.A_{laccase} = \frac{A \times V}{t \times e \times v}$$

where $E.A_{laccase}$ is the laccase enzyme activity, A is absorbance, V is the total reaction mixture volume (mL), t is incubation time, e is extinction coefficient for guaiacol (0.6740 μM/ cm), and v is enzyme volume (mL).

2.2.4 Lipase enzyme assay

Lipase activity was measured using the titrimetric technique described by Edupuganti et al. (2017). Crude enzyme extract (2

mL) was added to 18 mL of a 100 mM phosphate buffer (pH 7.0) emulsion containing 5% acacia Arabic gum and 10% olive oil. The mixture was incubated at 37 °C for 15 minutes on a thermostatic orbital shaker. To terminate the reaction and extract fatty acids, 1 mL of a 1:1 (v/v) acetone and ethanol mixture were added. Using phenolphthalein indicator, the fatty acids released were titrated with 0.05M NaOH. One unit of lipase activity was defined as the amount of enzyme required to liberate 1 μmol of fatty acid per minute under the specified standard conditions. Experimentation was carried out in triplicates and lipase activity was calculated employing the equation below.

$$E.A_{lipase} = \frac{\Delta V \times C \times 1000}{v \times t}$$

Where $E.A_{lipase}$ is the lipase enzyme activity ΔV represents NaOH consumption expressed in ml/min, C is the concentration of NaOH in mM, 1000 is a coefficient that converts the concentration into g/mL, v is the volume (ml) of enzyme used, and t is the incubation time.

2.3 Molecular identification of isolates

The identities of the two bacterial isolates and one mold isolate with the best laccase and lipase activity were confirmed using molecular techniques. Genomic DNA was extracted using the Quick-DNA™ Fungal/Bacteria Miniprep Kit (Zymo Research, Cat. No. D6005). Evaluation of the DNA concentration and purity was done with the use of Nanodrop Spectrophotometer (ND-1000, Thermo Scientific, USA). PCR amplification was carried out using the following primers: 16S-27F (5'-AGAGTTTGATCMTGGCTCAG) and 16S-1492R (CGGTTACCTTGTACGACTT) for bacteria, and ITS-1 (5'-TCCGTAGGTGAACCTGCGG) and ITS-4 (5'-TCCTCCGCTTATTGATATGC) for mold. Amplification was done using OneTaq® Quick-Load® 2X Master Mix (NEB, Cat. No. M0486). PCR products were subjected to gel electrophoresis and purified using the EXOSAP method. Sequencing and alignment were followed by BLAST analysis (NCBI) for species identification (Tamura et al., 2011).

2.4 Statistical Analysis

All enzyme data were analyzed using SPSS version 25 for Windows (SPSS, Chicago IL, U.S.A.). Results were obtained from triplicate measurements, and significant differences between means were separated using Duncan's Multiple Range Test (DMRT) at a significance level of $\alpha \leq 0.05$ (Adelabu & Kareem, 2022).

3.0 Results and discussion

3.1 Binding affinities and molecular interactions of target enzymes with investigated plastic compounds (*In Silico* Analysis)

Microbial enzymes represent one of the most sustainable approaches to plastic degradation (Mohan et al., 2020). In this study, twenty-three chemical constituents of different types of plastics were used as ligands for docking against three microbial enzymes: esterase (3KVN), a dehydrogenase (4JZ6), and a laccase (5LM8). The results of these docking simulations are summarized in Table 1, with selected 2D and 3D interaction visualizations for the two compounds with the highest binding affinity shown in Figs. 1 and 2 respectively.

Binding energies of the plastic ligands with 3KVN (esterase), 4JZ6 (dehydrogenase), and 5LM8 (laccase) ranged from -2 to -7.1 kcal/mol, -2 to -7.9 kcal/mol and -2.4 to -7.2 kcal/mol respectively (Table 1). The ligand 2,6-naphthalene dicarboxylic acid (NDA) showed the lowest binding energy across all the three enzymes (-7.1, -7 and -7.2 kcal/mol respectively), indicating the strongest binding affinity. In contrast, ethylene showed the highest binding energy (-2, -2, -2.4 kcal/mol respectively), suggesting the weakest interaction. Overall, fourteen of the ligands showed strong binding affinity, with energies ≤ -5 kcal/mol across the three enzymes (Table 1).

Table 1: Studied plastic chemical constituents and their binding energies (kcal/mol) with three target microbial enzymes

s/n	Compounds	PubChem ID	Canonical Smiles	3KVN	4JZ6	5LM8
1	2,6-naphthalene dicarboxylic acid	14357	<chem>C1=CC2=C(C=CC(=C2)C(=O)O)C=C1C(=O)O</chem>	-7.1	-7.9	-7.2
2	Diisononylphthalate	590836	<chem>CC(C)CCCCCOC(=O)C1=CC=CC=C1C(=O)O</chem>	-5	-7.5	-6.7
3	Bis(2-ethylhexyl) terephthalate	22932	<chem>CCCC(C)COC(=O)C1=CC=C(C=C1)C(=O)OCC(C)CCCC</chem>	-5.1	-7.3	-6.5
4	Bis (2-hydroxyethyl) terephthalate	13739	<chem>C1=CC(=CC=C1C(=O)OCCO)C(=O)OCCO</chem>	-6.6	-6.4	-5.7
5	Mono-Methyl Terephthalate	15513	<chem>COC(=O)C1=CC=C(C=C1)C(=O)O</chem>	-6.1	-6.3	-6
6	Dimethyl Terephthalate	8441	<chem>COC(=O)C1=CC=C(C=C1)C(=O)OC</chem>	-6.5	-6.3	-5.6
7	Diethyl phthalate	6781	<chem>CCOC(=O)C1=CC=CC=C1C(=O)OCC</chem>	-5.1	-6.2	-5.6
8	Dimethyl phthalate	8554	<chem>COC(=O)C1=CC=CC=C1C(=O)OC</chem>	-5	-6.2	-6.3
9	Terephthalic acid	7489	<chem>C1=CC(=CC=C1C(=O)O)C(=O)O</chem>	-6.4	-6.1	-6
10	phenyl acetic acid	999	<chem>C1=CC=C(C=C1)CC(=O)O</chem>	-6.2	-5.8	-6
11	Phenylacetaldehyde	998	<chem>C1=CC=C(C=C1)CC=O</chem>	-5.6	-5.6	-5.3
12	Styrene maleic anhydride	62707	<chem>C=CC1=CC=CC=C1.C1=CC(=O)OC1=O</chem>	-5.8	-5.4	-5.4
13	styrene oxide	7276	<chem>C1C(O1)C2=CC=CC=C2</chem>	-5.6	-5.4	-5.4
14	Styrene	7501	<chem>C=CC1=CC=CC=C1</chem>	-5.7	-5.4	-5.4
15	1,3 propanediol	10442	<chem>C(CO)CO</chem>	-3.7	-3.9	-3.9
16	Ethylene glycol	174	<chem>C(CO)O</chem>	-3.7	-3.1	-3.4
17	Styrene butadiene	62697	<chem>C=CC=C.C=CC1=CC=CC=C1</chem>	-3.7	-3.1	-3.6
18	Butadiene	7845	<chem>C=CC=C</chem>	-3.7	-3.1	-3.7
19	Isobutylene	8255	<chem>CC(=C)C</chem>	-3.6	-3.1	-3.5
20	Acrylonitrile	7855	<chem>C=CC#N</chem>	-3.7	-3	-3.6
21	Propene	8252	<chem>CC=C</chem>	-2.9	-2.5	-3.2
22	Vinyl chloride	6338	<chem>C=CCl</chem>	-2.6	-2.2	-2.8
23	Ethylene	6325	<chem>C=C</chem>	-2	-2	-2.4

The binding energy (B.E) values were categorized using a 3-level colour scale and icon sets, viz., (I) B.E ≥ -4 (red diamond, low affinity/high energy); (II) $-4 > \text{B.E} > -6$ (brown triangle, intermediate affinity); (III) $\text{B.E} \leq -6$ (green circle, high affinity/ low energy)

The order of ligand affinity for esterase was: 2,6-naphthalene dicarboxylic acid > terephthalic acid > styrene > bis(2-ethylhexyl) terephthalate > diisononyl phthalate. For dehydrogenase, the order was: 2,6 naphthalene dicarboxylic acid > diisononyl phthalate > bis(2-ethylhexyl) terephthalate > terephthalic acid > styrene. The same pattern as that in dehydrogenase was observed for laccase, although overall interactions were weaker, as reflected in generally higher binding energies. The exceptional binding affinity of NDA for all the three enzymes may be due to its structural complexity and polyaromatic nature which allows for multiple types of interactions- especially hydrogen bonding and pi interactions with enzyme active sites (El-Haj & Ahmed, 2020; Lu et al., 2020). NDA contains functional groups such as hydroxyl and carboxyl groups, which increase reactivity, and two benzene rings that enhance hydrophobic interactions with enzyme residues (Shi et al., 2023). This plastic compound is a precursor to the high-performance polyethylene naphthalate (PEN), a polyester introduced more recently to replace polyethylene terephthalate (PET) where a high tensile strength and higher modulus are of utmost importance (Menczel, 2020). Similarly, diisononyl phthalate (DINP) exhibited high binding affinity with the three enzymes. DINP is a widely used plasticizer in polyvinyl chloride (PVC) to soften the plastic (Folarin et al., 2024; Wang & Qian, 2021) and is known for its potential health hazards, including endocrine disruptions causing irreversible reproductive dysfunctions and other chronic health effects in humans and other animals (Verma et al., 2016). Another plastic compound with notable interactions with the enzymes was bis (2-hydroxyethyl) terephthalate (BHET), a PET hydrolysis product used in PET recycling. PET is one of the commonly used compounds in the packaging and textile industries- ranking fifth in the list of major polymers produced globally, and contributing to the enormous amount of wastes generated annually (Westover & Long, 2023). The ability of these enzymes to bind BHET suggests potential application in downstream plastic degradation.

On the other hand, ethylene and vinyl chloride, important monomers in the production of polythene and PVC- two of the most widely used plastics, showed the lowest affinities, indicating that these enzymes may not target monomers effectively. However, high binding affinities with complex compounds, such as polyester and plasticizers suggest that these enzymes may find application in post-consumer plastic degradation. Notably, interactions with TRP148 and TRP403 amino acid residues in laccase and dehydrogenase were

observed to be consistently associated with higher binding affinity. These residues may play a key role in forming stable enzyme-substrate complexes with plastic compounds.

3.2 Isolation, characterization and assay of potential plastic degrading microorganisms

A total of eighteen (18) mold and twenty-one (21) bacterial isolates were obtained using standard microbiological techniques. Qualitative screening for laccase production carried out on bacterial isolates revealed varying intensities of dark brown colouration on guaiacol supplemented agar plates. Eight (8) of the twenty-one (21) bacterial isolates produced reddish-brown coloration, with three (3) isolates showing most reddish-brown coloration (Plate 1). *B. cereus* showed the deepest colouration followed by *Staphylococcus* sp while *E. aerogenes* had the faintest colouration. Lipase production was screened using phenol-red olive oil agar. A red-to-yellow color shift indicated the secretion of extracellular lipase (Plate 2). Five (5) bacterial isolates were confirmed as lipase producing organisms (Table 2), with *Bacillus cereus* showing the deepest yellow colouration, followed by *Staphylococcus* sp while *E. coli* showed the least colouration. Among the mold isolates, *Penicillium* sp produced the most intense reddish-brown (laccase) and yellow (lipase) colorations, followed by *Aspergillus* sp while *Mucor* sp. showed the faintest color development in both assays.

3.2.1 Quantitative assay of enzyme activity in Bacterial isolates.

To confirm enzyme production, laccase and lipase activities in bacterial isolates were quantified using standard enzyme assays (Table 2). *Bacillus cereus* had the highest laccase activity (1.122 ± 0.01 U/mL), followed by *Staphylococcus* sp (0.983 ± 0.09 U/mL) while *Enterobacter aerogenes* and *E. coli* had the lowest laccase activity (0.124 ± 0.00 U/mL). Similarly, *Bacillus* sp exhibited the highest lipase activity (1.49 ± 0.01 U/mL) followed by *Staphylococcus* sp (1.26 ± 0.10 U/mL) while the least lipase activity was observed in *E. coli* (0.07 ± 0.11 U/mL) (Table 2). Duncan's Multiple Range Test revealed that laccase by *Bacillus cereus* showed statistically distinguishable activity at $\alpha \leq 0.05$, implying that this bacterium is a potential laccase producing microorganism.

Our study agrees with the report of Narayanan et al. (2015) where *Bacillus subtilis*, *Enterobacter aerogenes* and *E. coli* were isolated from agricultural residue dumpsite. Comparably, Jyothi et al. (2021) reported *Bacillus* and *Enterobacter* sp isolated from contaminated sites as laccase producing bacteria. Another study

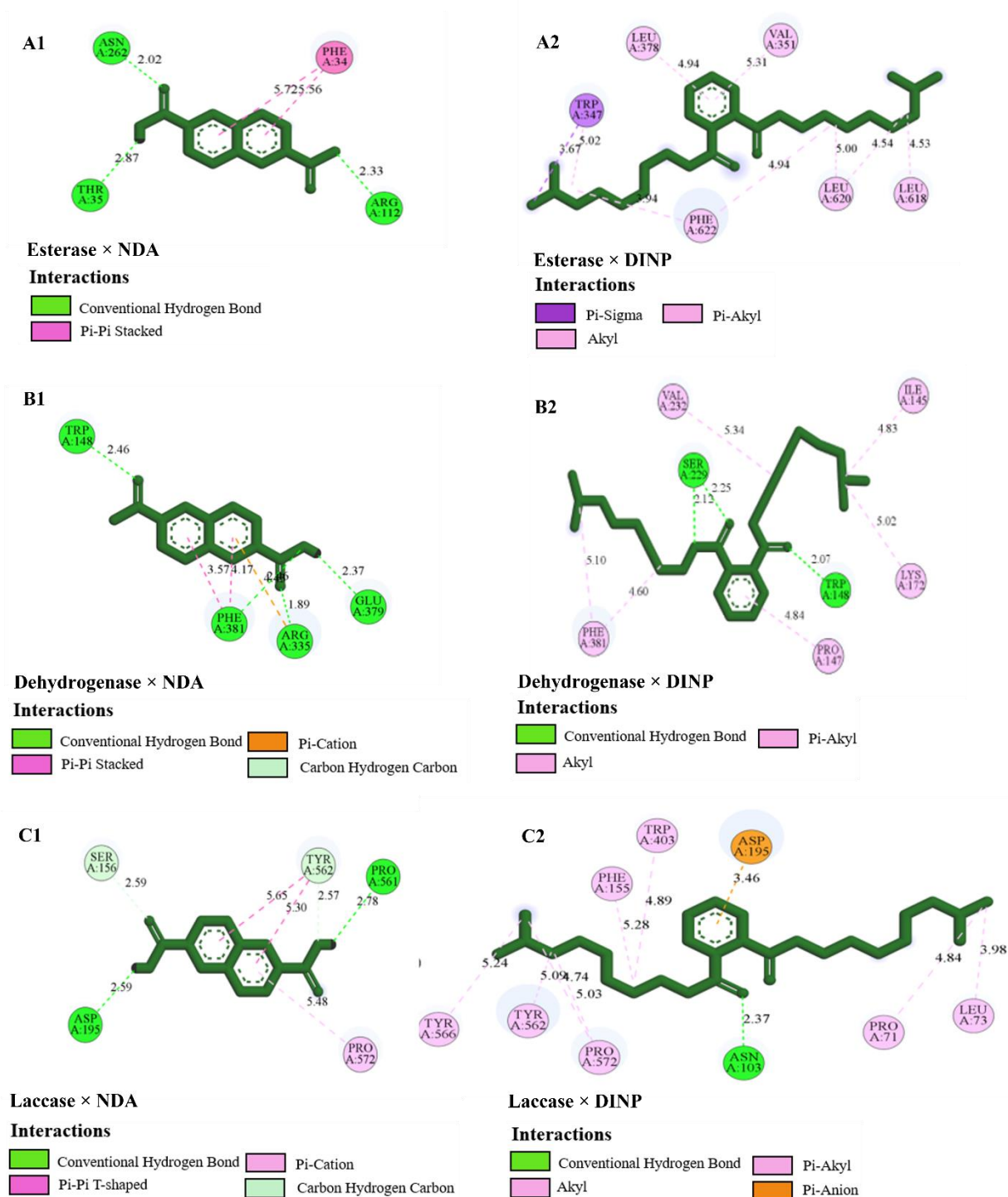


Fig. 1: 2D interactions of 2,6-naphthalene dicarboxylic acid (NDA) and Diisononylphthalate (DINP) with esterase (3KVN), dehydrogenase (4JZ6) and laccase (5LM8). The interactions of the plastic compound with the highest binding affinity (NDA) with target enzymes are on the left and labelled A1, B1, and C1 for 3KVN, 4JZ6, and 5LM8 respectively. Likewise, the interactions of the plastic compound with the second highest binding affinity with target enzymes are on the right, and labelled as A2, B2, and C2 respectively.

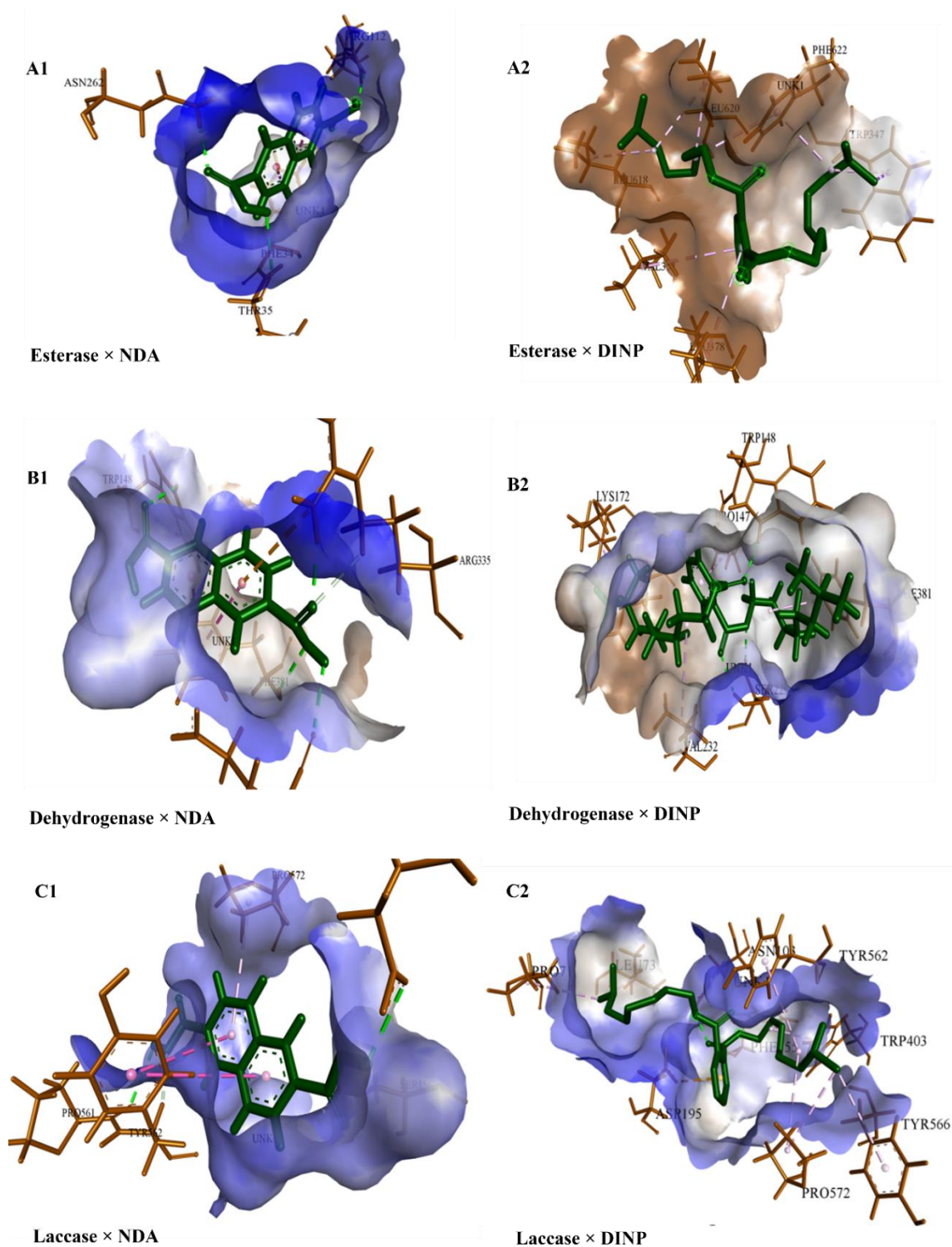


Fig. 2: 3D interactions of 2,6-naphthalene dicarboxylic acid (NDA) and Diisononylphthalate (DINP) with esterase (3KVN), dehydrogenase (4JZ6) and laccase (5LM8). The interactions of the plastic compound with the highest binding affinity (NDA) with target enzymes are on the left and labelled A1, B1, and C1 for 3KVN, 4JZ6, and 5LM8 respectively. Likewise, the interactions of the plastic compound with the second highest binding affinity with target enzymes are on the right, and labelled as A2, B2, and C2 respectively.

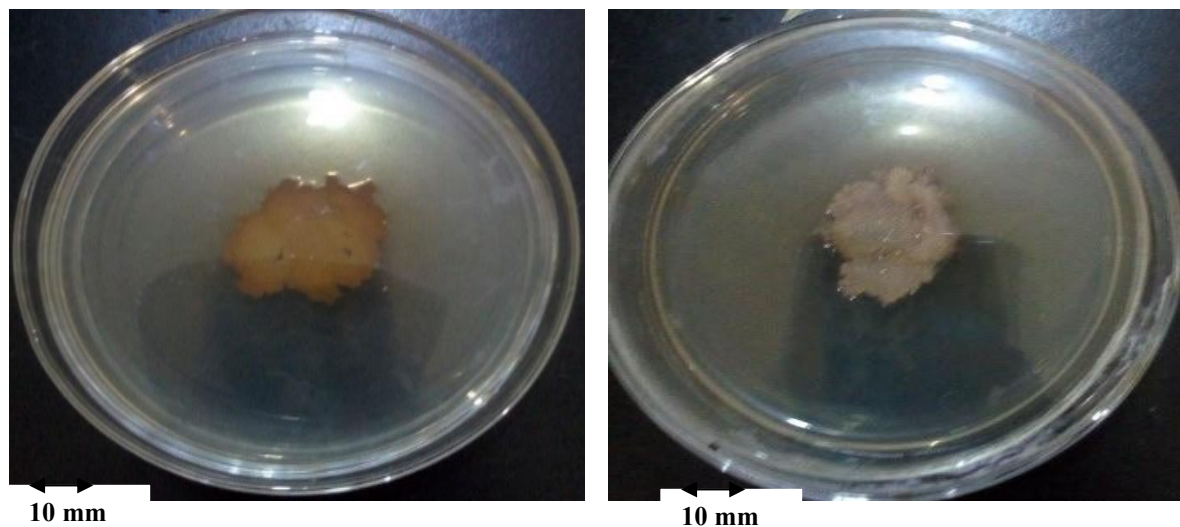


Plate 1: Plate assay for laccase activity. The **left plate**, supplemented with guaiacol shows reddish **brown coloration** indicating **positive guaiacol oxidation** by the isolate. The **right plate** serves as a control with no visible color change. **Scale bar = 10 mm.**

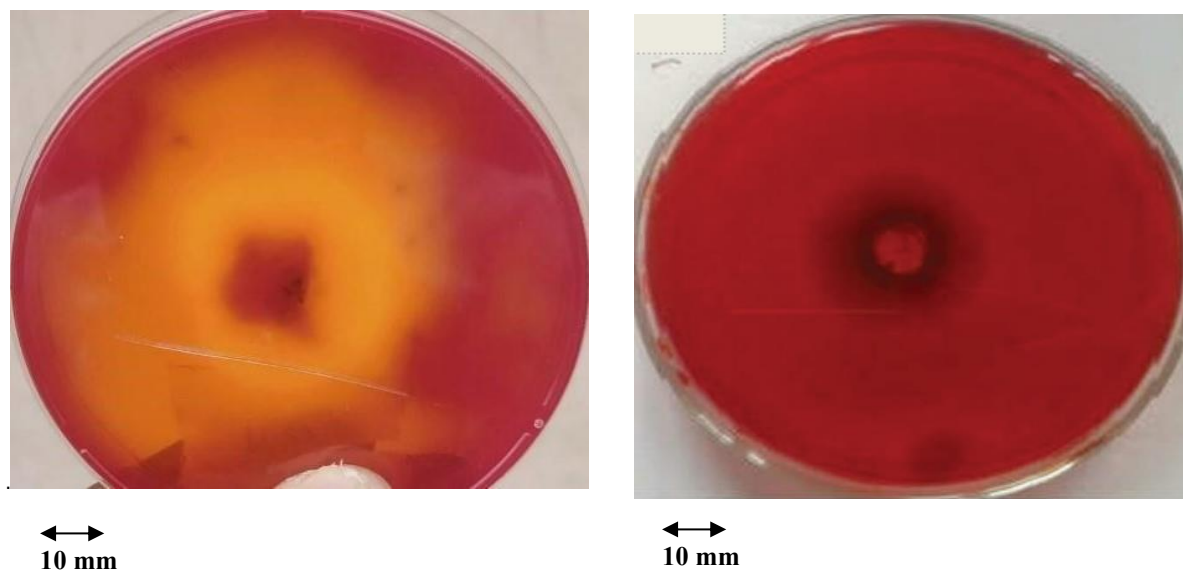


Plate 2: Plate assay for lipase activity. The phenol red-olive oil agar plate (left) shows yellow **coloration** indicating **positive** secretion of extracellular lipase by the isolate. The **right plate** serves as a control with no visible color change. **Scale bar = 10 mm.**

also produced and purified laccase enzyme secreted by *Bacillus* spp (Srinivasan et al., 2019). The ability of these organisms to oxidize guaiacol faster than others could be that they possess

genes that code for rapid laccase production (Janusz et al., 2020).

Bacillus sp has been reported to secrete lipase enzymes for growth on different substrates. This is attributed to its high reaction specificity, stereo specificity and less energy consumption (Lee et al., 2015). The presence of lipids at the

dumpsite may have enhanced lipase gene expression in *B. pumilus* and the other bacteria, consistent with earlier observations (Demirkan et al., 2021).

Table 2: Screening for laccase and lipase production in bacterial and mold isolates

Bacterial isolates	Enzyme activity (U/mL)		Mold isolates	Enzyme activity (U/mL)	
	Laccase	Lipase		Laccase	Lipase
<i>Bacillus cereus</i>	1.12±0.01 ^f	1.49±0.01 ^e	<i>Aspergillus</i> sp	0.17±0.00 ^d	0.08±0.00 ^d
<i>Staphylococcus</i> sp	0.98±0.09 ^e	1.26±0.10 ^d	<i>Penicillium</i> sp	0.19±0.11 ^e	0.09±0.00 ^e
<i>Burkholderia cepacian</i>	0.71±0.11 ^d	0.15±0.00 ^b	<i>Mucor</i> sp	0.16±0.00 ^{bc}	0.07±0.00 ^c
<i>E.coli</i>	0.12±0.00 ^a	0.07±0.11 ^a	<i>Aspergillus</i> sp	0.11±0.11 ^b	0.05±0.00 ^b
<i>B. subtilis</i>	0.39±0.01 ^b	0.16±0.10 ^c	<i>Trichoderma</i> sp	0.09±0.10 ^a	0.04±0.00 ^a
<i>E. aerogenes</i>	0.12±0.10 ^a	Nil	<i>Fusarium</i> sp	0.15±0.01 ^c	0.05±0.00 ^b
<i>K. pneumonia</i>	0.41±0.12 ^b	Nil	<i>Aspergillus</i> sp	0.16±0.01 ^c	0.06±0.00 ^{bc}
<i>Serratia. Marcescens</i>	0.52±0.00 ^c	Nil	-	-	-

Results are values of mean ± standard deviation for three replicate determinations.

Values in a column that are followed by various letters (superscripts) indicate significant differences in enzyme activity of organisms according to Duncan's Multiple Range Test at $\alpha \leq 0.05$.

3.2.2 Screening for enzyme production in mold isolates

Five mold genera were identified: *Aspergillus*, *Penicillium*, *Mucor*, *Trichoderma* and *Fusarium*. Of these, *Aspergillus* and *Penicillium* were the most predominant. They are widely distributed and have the capacity to thrive on a wide variety of substrates (Kareem et al., 2017). Enzyme assay results showed *Penicillium* sp to have the highest laccase and lipase activity (Table 2). This is supported by Khan et al. (2023) who reported *Penicillium* sp from plastic-polluted dumpsite soils in India as a potent laccase and lipase producing mold. *Mucor* sp and *Aspergillus* sp also showed moderate enzyme activities, consistent with previous findings (Abdel-Razek et al., 2020; Alabdallal et al., 2020; Kareem et al., 2017). *Aspergillus* sp are known to withstand harsh environmental conditions, hence can secrete different enzymes for survival including lipase (Abdel-Razek et al., 2020).

3.2.3 Molecular Identification of high enzyme-producing isolates

The three isolates with the highest enzyme activity- two bacteria and one mold, were subjected to molecular identification via 16S rRNA and ITS sequencing. Biochemical characterization identified the predominant bacterium as *Bacillus cereus*. However, molecular characterization confirmed it as *Bacillus pumilus* (NCBI Accession No. PP140677.1, 99.47% identity). *Bacillus pumilus* and *B. cereus* are both members of the *Bacillus* genus, and biochemical tests may not be able to

distinguish between certain species. Hence, molecular confirmation is usually required (Parvathi et al., 2009). The second bacterium was identified as *Staphylococcus cohnii* (CP054807.1, 99.93%) while the mold isolate was confirmed as *Penicillium citrinum* (OP040154.1, 99.45%).

B. pumilus, like most other *Bacillus* species, can survive in extremely harsh environments, and also exhibits high protease and lipase activity (Parvathi et al., 2009); hence their ability to grow in multi-waste dumpsite. *B. pumilus* isolated from a municipal dumpsite in India showed in as little as 60 days, a significant biodegradative capacity of plastic beads containing low density polyethylene (LDPE) (Banerjee et al., 2024). A study in Owerri, Nigeria also confirms the biodegradative capacity of *B. pumilus* on LDPE using microbial growth in liquid medium (Uwakwe et al., 2025). *Staphylococcus cohnii* has been shown to enhance the biodegradability of LDPE/starch blended films (Samanta et al., 2024). *P. citrinum* has also been shown to have high capacity in the biodegradation of LDPE (Khan et al., 2023).

3.3 Limitations

Despite the promising findings from this preliminary study, a few limitations are hereby acknowledged. Firstly, while molecular docking provides predictive insights into enzyme-substrate interactions, it does not account for complex environmental factors that affect actual degradation, such as pH, temperature, and enzyme kinetics. Further in vitro and in vivo

tests are required to validate these binding interactions under simulated environmental conditions. In addition, this study did not directly measure the breakdown of plastic polymers into intermediate or final degradation products. Future studies should integrate analyses to confirm the actual degradation of plastics and characterize the resulting by-products. Notwithstanding, findings from this study provide a strong basis for further exploration into enzyme-based plastic bioremediation.

4.0 Conclusion

To the best of our knowledge, this is one of the first studies to investigate the degradation potentials of multiple enzymes on multiple plastic compounds. Our *in-silico* study revealed strong binding interactions between plastic compounds, most especially the polyester plastic compounds, with all the three enzymes tested. Additionally, our results from *in vitro* investigations validated high production of laccase and lipase enzymes in two bacteria and one mold (*Bacillus pumilus*, *Staphylococcus cohnii* and *Penicillium citrinum*) isolated from a multi-waste dumpsite soil sample. These findings suggest that these microorganisms and their enzymes hold significant promise for the biodegradation of plastic pollutants. Further studies are needed to validate their performance under real world environmental conditions and to scale up enzyme production for applied plastic waste bioremediation.

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Conflict of interest

The authors declare no conflict of interest.

Authors' contributions

Conception: BTF

Design: BTF, BAO, RAA & OAT

Execution: BTF, BAO, RAA, OAT, RNO & OAB

Interpretation: BTF, BAO, RAA, OAT, RNO & OAB

Writing the paper: BTF, BAO, RAA, OAT & OAB

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