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# PlasticDB: a database of microorganisms and proteins linked to plastic biodegradation

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## Abstract

The number of presumed plastic-degrading microorganisms reported is rapidly increasing, making it possible to explore the conservation and distribution of plastic-degrading traits across the diverse microbial tree of life. After assessing the international scientific literature, we centralised information on known plastic-degrading microorganisms in an interactive and updatable phylogenetic tree and database (<http://plasticdb.org/>). The database currently has 564 species of microorganisms reported in the scientific literature to have plastic-degrading capabilities and 165 enzymes described to break down plastics. With these data, we verify that plastic degradation is, in general, not phylogenetically conserved. Instead, plastic-degrading microorganisms are widely distributed across the bacterial and fungal branches of the tree of life, although polylactic acid (PLA) degradation is dominated by the bacterial family Pseudonocardiaceae. Our database is freely available to the scientific community in the form of a web server, such that researchers can now analyse various aspects of plastic biodegradation via genome and metagenome annotation and comparison, species identification in taxonomic tables, and metabolic pathway analysis. We predicted *in silico* the structures of all presumed plastic degrading enzymes in the database. These can now be visualised in the user's browser or downloaded and incorporated into any downstream analysis. Our database and the tree are regularly updated, reflecting rapid developments in this area of science. Our research benefits the field by providing an updated 'library' of presumed plastic-degrading taxa and traits. Further, it expands our understanding of microbial plastic-degrading traits' genetic diversity and evolution

**Keywords:** Plastic, Biodegradation, Database, Microorganisms, Enzymes

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