**Chapter 7**

**Depolymerization of polymers**

Abokitse, K. *et al*. (2022). A novel actinobacterial cutinase containing a noncatalytic polymer-binding domain. *Applied & Environmental Microbiology* **88**(1), e01522-21. <https://journals.asm.org/doi/abs/10.1128/AEM.01522-21>

Ameri, R. *et al*. (2022). Genome sequence and Carbohydrate Active Enzymes (CAZymes) repertoire of the thermophilic *Caldicoprobacter algeriensis* TH7C1T. *Microbial Cell Factories* **21**, 91. <https://doi.org/10.1186/s12934-022-01818-0>

Arnling Bååth, J. *et al*. (2022). Structure-function analysis of two closely related cutinases from *Thermobifida cellulosilytica*. *Biotechnology & Bioengineering* **119**(2), 470-481. <https://doi.org/10.1002/bit.27984>

Atiwesh, G. *et al*. (2022). Lignin degradation by microorganisms: A review. *Biotechnology Progress* **38**(2), e3226. <https://doi.org/10.1002/btpr.3226>

Chaput, G. *et al*. (2022). *Sodalis ligni* strain 159R isolated from an anaerobic lignin-degrading consortium. *Microbiology Spectrum* **10**(3), e02346-21. <https://journals.asm.org/doi/abs/10.1128/spectrum.02346-21>

Ding, S. *et al*. (2022). Boosting enzymatic degradation of cellulose using a fungal expansin: Structural insight into the pretreatment mechanism. *Bioresource Technology* **358**, 127434. <https://doi.org/10.1016/j.biortech.2022.127434>

Dominelli, N. *et al*. (2022). The insect pathogen *Photorhabdus luminescens* protects plants from phytopathogenic *Fusarium graminearum* via chitin degradation. *Applied & Environmental Microbiology* **88**(11), e00645-22. <https://journals.asm.org/doi/abs/10.1128/aem.00645-22>

Gao, L. *et al*. (2022). A type IX secretion system substrate involved in crystalline cellulose degradation by affecting crucial cellulose binding proteins in *Cytophaga hutchinsonii*. *Applied & Environmental Microbiology* **88**(2), e01837-21. <https://journals.asm.org/doi/abs/10.1128/AEM.01837-21>

Ichikawa, S. *et al*. (2022). The expression of alternative sigma-I7 factor induces the transcription of cellulosomal genes in the cellulolytic bacterium *Clostridium thermocellum*. *Enzyme & Microbial Technology* **156**, 110002. <https://doi.org/10.1016/j.enzmictec.2022.110002>

Jiang, C. *et al*. (2022). Enzymatic verification and comparative analysis of carrageenan metabolism pathways in marine bacterium *Flavobacterium algicola*. *Applied & Environmental Microbiology* **88**(7), e00256-22. <https://journals.asm.org/doi/abs/10.1128/aem.00256-22>

Li, Z. *et al*. (2022). Toward understanding the alginate catabolism in *Microbulbifer* sp. ALW1 by proteomics profiling. *Frontiers in Bioengineering & Biotechnology* **10**, 829428. <https://www.frontiersin.org/article/10.3389/fbioe.2022.829428>

Lima, B. P. *et al*. (2022). *Streptococcus gordonii* poised for glycan feeding through a MUC5B-discriminating, lipoteichoic acid-mediated outside-In signaling circuit. *Journal of Bacteriology* **204**(6), e00118-22. <https://journals.asm.org/doi/abs/10.1128/jb.00118-22>

Moon, M. *et al*. (2022). Lytic polysaccharide monooxygenase (LPMO)-derived saccharification of lignocellulosic biomass. *Bioresource Technology* **359**, 127501. <https://doi.org/10.1016/j.biortech.2022.127501>

Nnolim, N. E. & Nwodo, U. U. (2020). *Bacillus* sp. CSK2 produced thermostable alkaline keratinase using agro-wastes: keratinolytic enzyme characterization. *BMC Biotechnology* **20**, 65. <https://doi.org/10.1186/s12896-020-00659-2>

Shen, N. *et al*. (2022). Isolation and identification of a feather degrading *Bacillus tropicus* strain Gxun-17 from marine environment and its enzyme characteristics. *BMC Biotechnology* **22**, 11. <https://doi.org/10.1186/s12896-022-00742-w>

Tran, D. M. *et al*. (2022). Molecular analysis of genes involved in chitin degradation from the chitinolytic bacterium *Bacillus velezensis*. *Antonie van Leeuwenhoek* **115**(2), 215-231. <https://doi.org/10.1007/s10482-021-01697-2>

Zhang, J. *et al*. (2022). Characterization of a novel type of glycogen-degrading amylopullulanase from *Lactobacillus crispatus*. *Applied Microbiology & Biotechnology* **106**(11), 4053-4064. <https://doi.org/10.1007/s00253-022-11975-2>

**Utilization of carbohydrates and related compounds**

Anbalagan, S. *et al*. (2022). Regulation of mannitol metabolism in *Enterococcus faecalis* and association with *par*EF0409 toxin-antitoxin locus function. *Journal of Bacteriology* **204**(5), e00047-22. <https://journals.asm.org/doi/abs/10.1128/jb.00047-22>

Bhayani, J. *et al*. (2022). Carbohydrate metabolism in bacteria: Alternative specificities in ADP-glucose pyrophosphorylases open novel metabolic scenarios and biotechnological tools. *Frontiers in Microbiology* **13**, 867384. <https://www.frontiersin.org/article/10.3389/fmicb.2022.867384>

Centeno-Leija, S. *et al*. (2022). Mining for novel cyclomaltodextrin glucanotransferases unravels the carbohydrate metabolism pathway via cyclodextrins in *Thermoanaerobacterales*. *Scientific Reports* **12**, 730. <https://doi.org/10.1038/s41598-021-04569-x>

Heistinger, L. *et al*. (2022). Genotypic and phenotypic diversity among *Komagataella* species reveals a hidden pathway for xylose utilization. *Microbial Cell Factories* **21**, 70. <https://doi.org/10.1186/s12934-022-01796-3>

Kumano, T. *et al*. (2021). FAD-dependent C-glycoside–metabolizing enzymes in microorganisms: Screening, characterization, and crystal structure analysis." *Proceedings of the National Academy of Sciences of the USA* **118**(40), e2106580118. <https://www.pnas.org/content/pnas/118/40/e2106580118.full.pdf>

Orellana, L. H. *et al*. (2022). *Verrucomicrobiota* are specialist consumers of sulfated methyl pentoses during diatom blooms. *The ISME Journal* **16**(3), 630-641. <https://doi.org/10.1038/s41396-021-01105-7>

Sharma, M. *et al*. (2022). Oxidative desulfurization pathway for complete catabolism of sulfoquinovose by bacteria. *Proceedings of the National Academy of Sciences of the USA* **119**(4), e2116022119. <https://www.pnas.org/doi/abs/10.1073/pnas.2116022119>

**Organic acid utilization**

**Alcohol utilization**

Kumar, G. et al. (2022). A major shell protein of 1,2-propanediol utilization microcompartment conserves the activity of Its signature enzyme at higher temperatures. *ChemBioChem* **23**(9), e202100694. <https://doi.org/10.1002/cbic.202100694>

**Amino acid and nucleic acid base utilization**

**Hydrocarbon utilization**

Williams, S. C. & Austin, R. N. (2022). An overview of the electron-transfer proteins that activate alkane monooxygenase (AlkB). *Frontiers in Microbiology* **13**, 845551. <https://www.frontiersin.org/article/10.3389/fmicb.2022.845551>

**Utilization of natural and anthropogenic xenobiotics**

Erickson, E. *et al*. (2022). Comparative performance of PETase as a function of reaction conditions, substrate properties, and product accumulation. *ChemSusChem* **15**(1), e202101932. <https://doi.org/10.1002/cssc.202101932>

Fuentes-Jaime, J. *et al*. (2022). Concerted action of extracellular and cytoplasmic esterase and urethane-cleaving activities during Impranil biodegradation by *Alicycliphilus denitrificans* BQ1. *Biodegradation* **33**(4), 389-406. <https://doi.org/10.1007/s10532-022-09989-8>

Gricajeva, A. *et al*. (2022). Insights into polyester plastic biodegradation by carboxyl ester hydrolases. *Journal of Chemical Technology & Biotechnology* **97**(2), 359-380. <https://onlinelibrary.wiley.com/doi/abs/10.1002/jctb.6745>

Ke, Z. *et al*. (2022). Two LysR family transcriptional regulators, McbH and McbN, activate the operons responsible for the midstream and downstream pathways, respectively, of carbaryl degradation in *Pseudomonas* sp. strain XWY-1. *Applied & Environmental Microbiology* **88**(4), e02060-21. <https://journals.asm.org/doi/abs/10.1128/aem.02060-21>

Lu, H. *et al*. (2022). Machine learning-aided engineering of hydrolases for PET depolymerization. *Nature* **604**(7907), 662-667. <https://doi.org/10.1038/s41586-022-04599-z>

Machona, O. *et al*. (2022). *Tenebrio molitor*: possible source of polystyrene-degrading bacteria. *BMC Biotechnology* **22**, 2. <https://doi.org/10.1186/s12896-021-00733-3>

Pinto, M. *et al*. (2022). Microbial consortiums of putative degraders of low-density polyethylene-sssociated compounds in the ocean. *mSystems* **7**(2), e01415-21. <https://journals.asm.org/doi/abs/10.1128/msystems.01415-21>

Priya, A. *et al*. (2022). A comprehensive biotechnological and molecular insight into plastic degradation by microbial community. *Journal of Chemical Technology & Biotechnology* **97**(2), 381-390. <https://doi.org/10.1002/jctb.6675>

Rakesh, M. *et al*. (2018). Metabolism and biodegradation of spacecraft cleaning reagents by strains of spacecraft-associated *Acinetobacter*. *Astrobiology* **18** (12), 1517-1527. <https://www.liebertpub.com/doi/abs/10.1089/ast.2017.1814>

Singh Jadaun, J. *et al*. (2022). Biodegradation of plastics for sustainable environment. *Bioresource Technology* **347**, 126697. <https://doi.org/10.1016/j.biortech.2022.126697>

Vidal-Verdú, À. et al. (2022). Living in a bottle: Bacteria from sediment-associated Mediterranean waste and potential growth on polyethylene terephthalate. *MicrobiologyOpen* **11**(1), e1259. <https://doi.org/10.1002/mbo3.1259>

Wackett, L. P. (2022). Nothing lasts forever: understanding microbial biodegradation of polyfluorinated compounds and perfluorinated alkyl substances. *Microbial Biotechnology* **15**(3), 773-792. <https://doi.org/10.1111/1751-7915.13928>

Zhou, X. *et al*. (2022). Whole genome sequencing and analysis of fenvalerate degrading bacteria *Citrobacter freundii* CD-9. *AMB Express* **12**(1), 51. <https://doi.org/10.1186/s13568-022-01392-z>

**Methylotrophy**

Chang, J. *et al*. (2022). Variable inhibition of nitrous oxide reduction in denitrifying bacteria by different forms of methanobactin. *Applied & Environmental Microbiology* **88**(7), e02346-21. <https://journals.asm.org/doi/abs/10.1128/aem.02346-21>

Crombie, A. T. (2022). The effect of lanthanum on growth and gene expression in a facultative methanotroph. *Environmental Microbiology* **24**(2), 596-613. <https://doi.org/10.1111/1462-2920.15685>

Good, N. M. *et al*. (2022). Hyperaccumulation of gadolinium by *Methylorubrum extorquens* AM1 reveals impacts of lanthanides on cellular processes beyond methylotrophy. *Frontiers in Microbiology* **13**, 820327. <https://www.frontiersin.org/article/10.3389/fmicb.2022.820327>

Koo, C. W. *et al*. (2022). Recovery of particulate methane monooxygenase structure and activity in a lipid bilayer. *Science* **375**(6586), 1287-1291. <https://www.science.org/doi/abs/10.1126/science.abm3282>

Leducq, J.-B. *et al*. (2022). Fine-scale adaptations to environmental variation and growth strategies drive phyllosphere *Methylobacterium* diversity. *mBio* **e13**(1), e03175-21. <https://journals.asm.org/doi/abs/10.1128/mbio.03175-21>

Palberg, D. *et al*. (2022). A survey of *Methylobacterium* species and strains reveals widespread production and varying profiles of cytokinin phytohormones. *BMC Microbiology* **22**, 49. <https://doi.org/10.1186/s12866-022-02454-9>

Quynh Le, H. T. *et al*. (2022). Development of *Methylorubrum extorquens* AM1 as a promising platform strain for enhanced violacein production from co-utilization of methanol and acetate. *Metabolic Engineering* **72**, 150-160. <https://doi.org/10.1016/j.ymben.2022.03.008>

Villada, J. C. *et al*. (2022). Integrative genome-scale metabolic modeling teveals versatile metabolic strategies for methane utilization in *Methylomicrobium album* BG8. *mSystems* **7**(2), e00073-22. <https://journals.asm.org/doi/abs/10.1128/msystems.00073-22>

**Incomplete oxidation**

Ernst, L. *et al*. (2022). Methane formation driven by reactive oxygen species across all living organisms. *Nature* **603**(7901), 482-487. <https://doi.org/10.1038/s41586-022-04511-9>