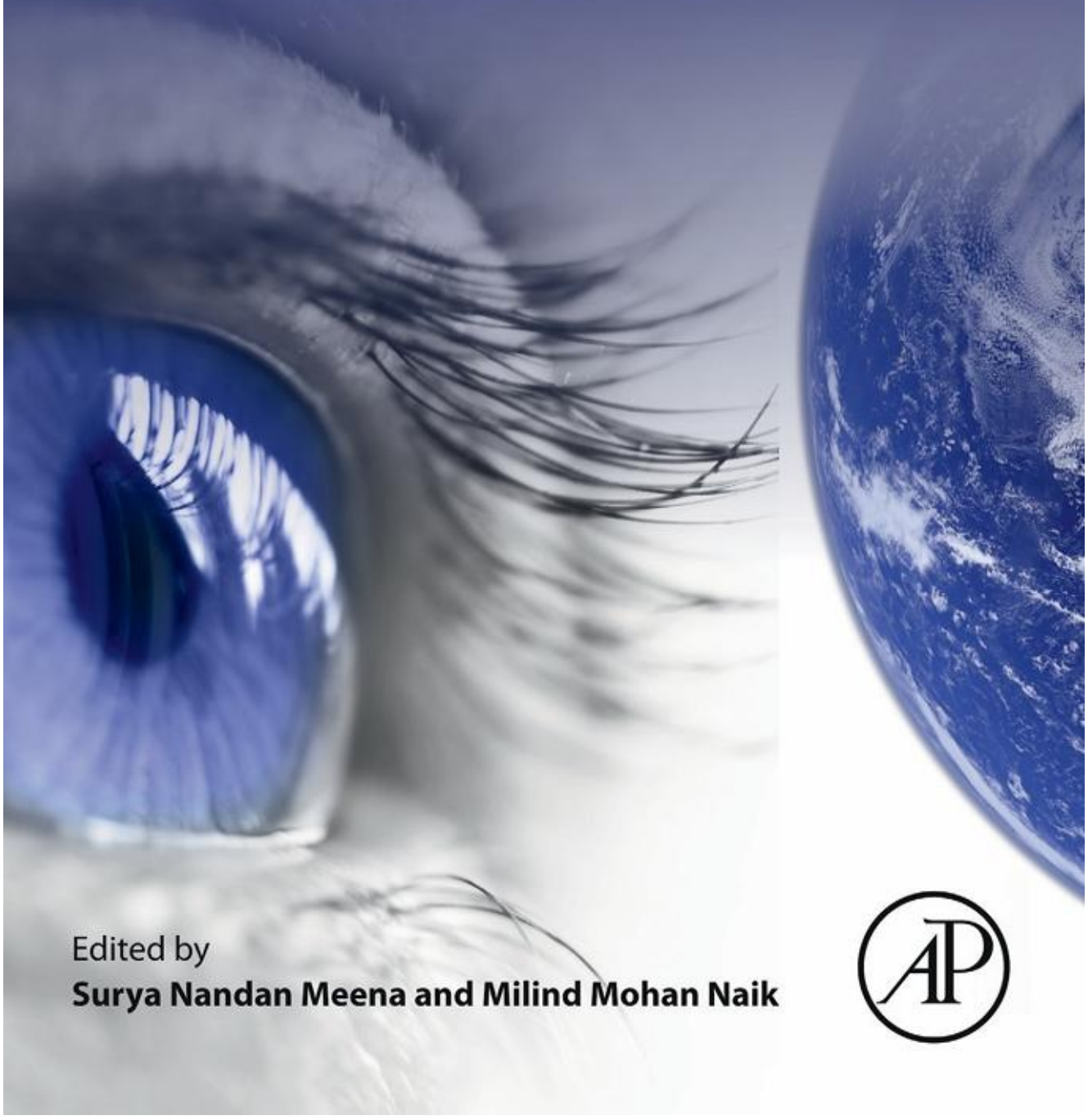
# Advances in Biological Science Research

## A Practical Approach



Edited by
**Surya Nandan Meena and Milind Mohan Naik**

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## A Practical Approach

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Chapter 2

# Genome sequence analysis for bioprospecting of marine bacterial polysaccharide-degrading enzymes

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## 2.1 Introduction

Complex polysaccharides (CPs) are composed of repeating units of homo/hetero monosaccharides linked by various glycosidic linkages and having diverse functional groups. CPs are widely present in plants, animals, and microorganisms. They promote structural integrity and shield organisms from predators [1]. In marine ecosystems, seaweeds and crustaceans are the main source of CPs. Additionally, the mangrove ecosystem receives a lot of plant litter rich in CPs. Agar, alginate, carrageenan, xylan, pullulan, pectin, cellulose, chitin, etc. are the predominant CPs that are widely present in marine organisms. The repeating units of monosaccharides are heavily substituted by various functional groups rendering CPs recalcitrant, and hence they are also referred to as insoluble complex polysaccharides (ICPs). Conversion of these ICPs into simpler oligosaccharides/metabolizable sugars requires the synergistic action of various polysaccharide-degrading enzymes that hydrolyzes CPs into their respective oligosaccharides/metabolizable sugars. Marine bacteria are the major sources of polysaccharide-degrading enzymes.

Polysaccharide-degrading enzymes demonstrate a wide range of applications in various industries such as paper, pulp, textiles, cosmetics, as well as in pharmacology. Therefore, various polysaccharide-degrading enzymes, such as agarase, alginate lyase, carrageenase, chitinase, and xylanase, were purified from various sources including marine bacteria. The polysaccharide-degrading enzymes producing bacteria are ubiquitous in marine ecosystems and have been reported from costal water, sediments, deep sea, seaweeds, and exoskeleton of crustacean [2–8]. Traditionally, the polysaccharide-degradation capability

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