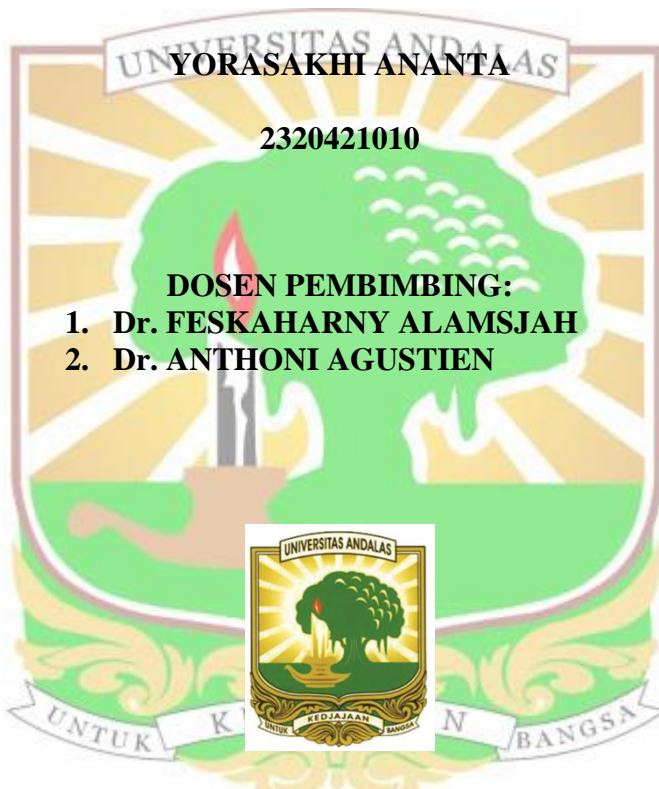


**OPTIMASI PRODUKSI DAN IDENTIFIKASI MOLEKULER ISOLAT
BAKTERI PUA-14 PENGHASIL PROTEASE DARI PERAIRAN
MANGROVE**

TESIS

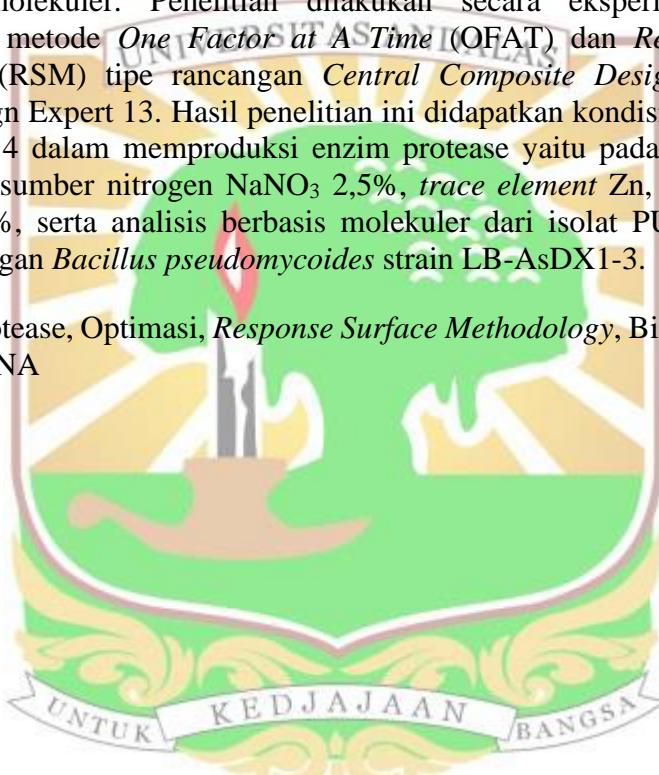


**PROGRAM STUDI MAGISTER
DEPARTEMEN BIOLOGI
FAKULTAS MATEMATIKA DAN ILMU PENGETAHUAN ALAM
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ABSTRAK

Enzim protease termasuk ke dalam kelompok enzim hidrolase yang memecah protein menjadi molekul yang lebih sederhana dan banyak digunakan dalam industri makanan, farmasi, dan industri kimia lainnya. Pemilihan mikroorganisme sebagai penghasil enzim dapat dijadikan solusi atas tingginya kebutuhan enzim yang menuntut produksi berkelanjutan. Tujuan dari penelitian ini untuk menganalisis sumber karbon, sumber nitrogen, *trace element*, konsentrasi sumber karbon, konsentrasi sumber nitrogen, dan konsentrasi inokulum optimum terhadap isolat bakteri PUA-14 dalam memproduksi protease; serta menganalisis jenis isolat bakteri PUA-14 penghasil protease dari perairan mangrove dengan identifikasi berbasis biomolekuler. Penelitian dilakukan secara eksperimental dengan menggunakan metode *One Factor at A Time* (OFAT) dan *Response Surface Methodology* (RSM) tipe rancangan *Central Composite Design* (CCD) pada software Design Expert 13. Hasil penelitian ini didapatkan kondisi optimum isolat bakteri PUA-14 dalam memproduksi enzim protease yaitu pada sumber karbon laktosa 0,5%, sumber nitrogen NaNO_3 2,5%, *trace element* Zn, dan konsentrasi inokulum 2,5%, serta analisis berbasis molekuler dari isolat PUA-14 memiliki similaritas dengan *Bacillus pseudomycoides* strain LB-AsDX1-3.

Keywords: Protease, Optimasi, *Response Surface Methodology*, Biomolekuler, 16S rRNA



ABSTRACT

Protease enzymes belong to the group of hydrolase enzymes which break down proteins into simpler molecules and are widely used in the food, pharmaceutical and other chemical industries. Selection of microorganisms as enzyme producers can be used as a solution to the high demand for enzymes which demands sustainable production. The aim of this research was to analyze carbon sources, nitrogen sources, trace element carbon source concentrations, nitrogen source concentrations, and optimum inoculum concentrations for PUA-14 bacterial isolates in producing protease; and analyzing the type of protease-producing PUA-14 bacterial isolate from mangrove waters using biomolecular-based identification. The research was carried out experimentally using the One Factor at A Time (OFAT) method and Response Surface Methodology (RSM) Central Composite Design (CCD) design type on Design Expert 13 software. The results of this research showed that PUA-14 bacterial isolates had optimal conditions in producing enzymes. protease, namely the carbon source lactose 0.5%, nitrogen source NaNO₃ 2.5%, trace element Zn, and inoculum concentration 2.5%, as well as molecular-based analysis of isolate PUA-14 which has similarities with *Bacillus pseudomyoides* strain LB-AsDX1- 3.

Keywords: Protease, Optimization, Response Surface Methodology, Biomolecular, 16S rRNA

