



**UNIVERSITI PUTRA MALAYSIA**

**CRYSTALLOGRAPHIC ANALYSIS OF GROUND AND  
SPACE-GROWN THERMOSTABLE T1 LIPASE  
CRYSTAL**

**SAYANGKU NOR ARIATI BT MOHAMAD ARIS**

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AND SPACE-GROWN THERMOSTABLE T1 LIPASE**



**SAYANGKU NOR ARIATI BT MOHAMAD ARIS**

**MASTER OF SCIENCE  
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**2013**



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THERMOSTABLE T1 LIPASE CRYSTAL**

**SAYANGKU NOR ARIATI BT MOHAMAD ARIS**

**By**

**Thesis Submitted to the School of Graduate Studies,  
Universiti Putra Malaysia, in Fulfillment of the  
Requirements for the Degree of Master of Science**

**May 2013**

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment  
of the requirement for the degree of Master of Science

**CRYSTALLOGRAPHIC ANALYSIS OF GROUND- AND SPACE-GROWN  
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**SAYANGKU NOR ARIATI BT MOHAMAD ARIS**

**May 2013**

**Chair: Professor Raja Noor Zaliha Raja Abd Rahman, D.Eng.**

**Faculty: Biotechnology and Biomolecular Sciences**

X-ray crystallography is a major tool to provide three dimensional structures. High resolution protein crystal data is important in revealing a highly accurate structure at atomic level. This is essential in order to understand the properties and function of the protein. In crystallization process, convection and sedimentation is thought to be detrimental for growth of high quality protein crystals. Both aspects can be avoided by either working in gelled systems, working in systems of small dimensions, or in the absence of gravity. In this research, crystallization by using counter diffusion method in space was performed with the aim to obtain high resolution diffracting crystals with better internal order to improve the accuracy of the structure.

Recombinant T1 Lipase from *Geobacillus zalihae* was successfully purified to homogeneity via two step affinity chromatography followed by ion exchange chromatography with 8.9 % yield. Purified T1 lipase was then crystallized in microbatch and vapour diffusion methods. The best crystal growth was obtained in Formulation 21 (Crystal Screen 2) with optimum growth temperature of 20 °C. The crystallization set up condition was applied to counter diffusion method for space experiment as well as ground control. Crystallization of T1 lipase under microgravity condition experiment was done in collaboration with JAXA (Japanese Aerospace Exploration Agency) under the JAXA-UPM Protein Crystal Growth (PCG) #2 Flight 2 program. The synchrotron diffraction data set were collected to 1.3 Å and 1.1 Å resolutions and belonged to monoclinic C2 Space group for ground grown and space grown crystal, respectively.

The major difference between the two crystal growth systems is the lack of convection and sedimentation in microgravity environment resulted in the growth of much higher quality crystals of T1 lipase. The structural analysis of T1 lipase was performed using molecular replacement method with final R factor 0.134 ( $R_{free}$  0.162) for ground-grown crystal and 0.129 ( $R_{free}$  0.150) for space-grown crystal, respectively. The structure of T1 lipase crystal contains two molecules per asymmetric unit with 387 amino acids each. Overall topology showed of  $\alpha/\beta$  hydrolase fold containing catalytic triad active site and covered by  $\alpha$ -helix 6 and  $\alpha$ -helix 7 as a ‘lid’. The structure contained zinc and calcium binding site which was important for the structural stabilization. Comparative crystallographic analysis revealed that the space-grown crystal structure has improved as compared to ground-

grown crystal. This study has shown that crystallization in counter diffusion method using microgravity environment improved the internal order of crystals thus gave a more precise three dimensional structure.



Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai  
memenuhi keperluan untuk ijazah Master Sains

**ANALISIS KRISTALOGRAFI TERHADAP LIPASE TERMOSTABIL T1 DI  
BUMI DAN ANGKASA**

Oleh

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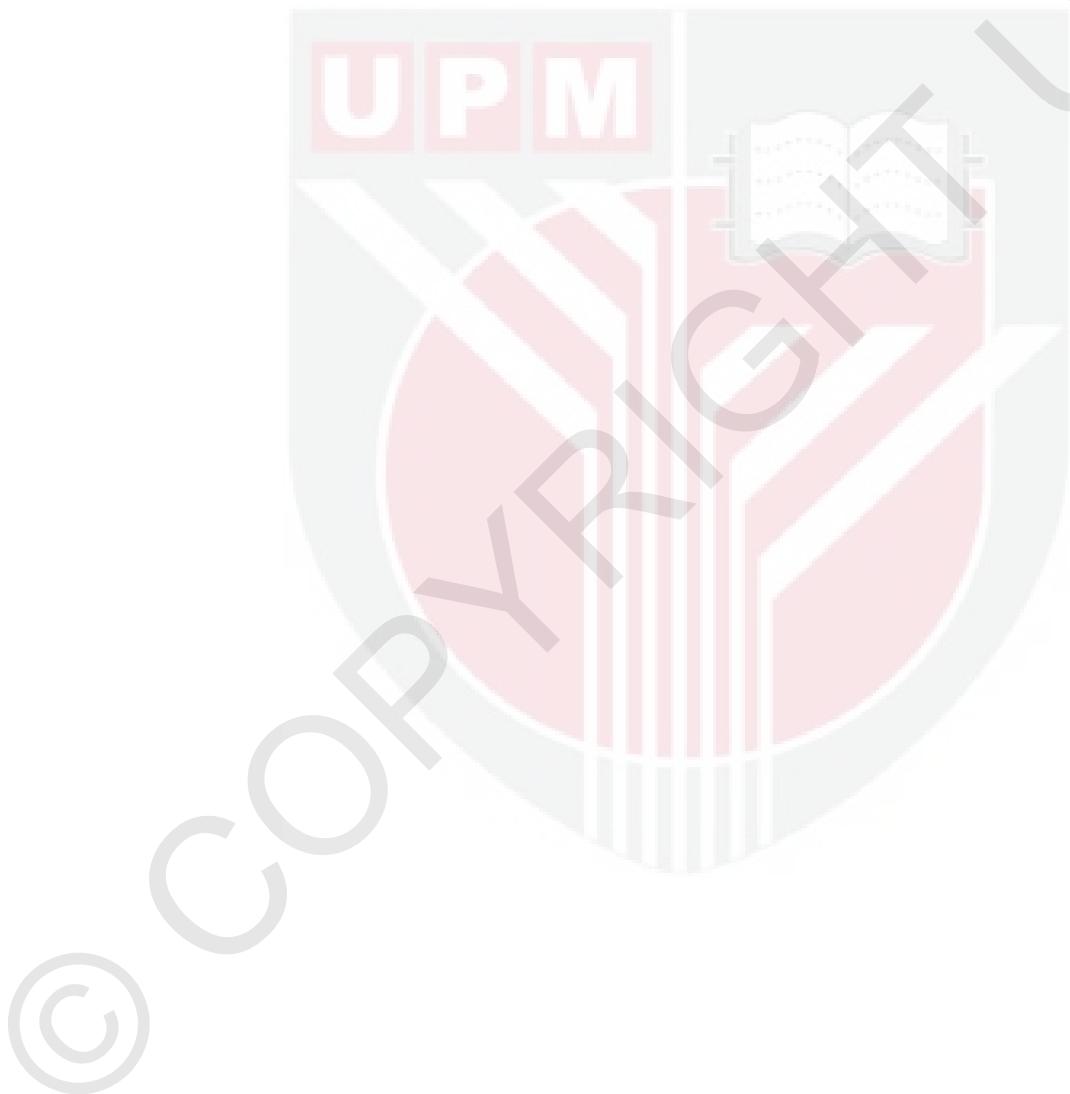
**Fakulti: Bioteknologi dan Sains Biomolekul**

Kristalografi sinar-X adalah alat utama dalam memberikan struktur tiga dimensi. Data dari hablur protein yang beresolusi tinggi adalah penting untuk mendedahkan struktur yang lebih tepat pada tahap atom. Ini adalah penting dalam memahami ciri-ciri dan fungsi protein. Perolakan dan pemendapan dikatakan memudaratkan dalam pertumbuhan hablur berkualiti tinggi. Kedua-dua aspek tersebut boleh diatasi samada dengan melakukan proses penghabluran di dalam sistem gel, di dalam dimensi yang kecil atau keadaan ketiadaan graviti. Di dalam kajian ini, penghabluran menggunakan kaedah resapan lawan di angkasa telah dijalankan bertujuan untuk memperolehi hablur yang mempunyai susunan dalaman yang lebih teratur untuk mendapatkan ketepatan struktur.

T1 lipase rekombinan dari *Geobacillus zalihae* telah berjaya ditulenkan melalui dua kaedah kromatografi affiniti diikuti dengan kromatografi pertukaran ion dengan peratus perolehan 8.9 %. T1 lipase tulen kemudiannya dihablurkan dengan kaedah ‘microbatch’ dan difusi wap. Pertumbuhan hablur yang terbaik diperolehi dari formulasi 21 (Crystal Screen 2) dengan suhu optimum pada 20°C. Kondisi terbaik penghabluran diaplikasikan kepada kaedah resapan lawan untuk eksperimen di angkasa dan eksperimen di bumi sebagai kawalan. Kajian penghabluran T1 lipase dibawah persekitaran mikrograviti telah dijalankan dengan kolaborasi pihak JAXA (Agensi Angkasa Jepun) di bawah program JAXA-UPM Pertumbuhan Penghabluran Protein (PCG) #2 penerbangan kedua. Set data pembelauan oleh Synchrotron dikumpulkan sehingga resolusi 1.3 Å dan 1.1 Å dan tergolong dalam kumpulan ruang C2 monoklinik untuk hablur yang tumbuh di bumi dan angkasa setiap satunya.

Perbezaan utama antara dua sistem pertumbuhan hablur adalah pengurangan perolakan dan pemendapan pada keadaan persekitaran kekurangan mikrograviti menghasilkan hablur T1 lipase yang lebih berkualiti tinggi. Hablur yang tumbuh di angkasa mempamerkan darjah ketidak aturan yang lebih rendah berbanding dengan hablur yang tumbuh di bumi dan data-data pembelauannya juga mempunyai nilai faktor-B yang lebih rendah. Analisis struktur T1 lipase dilakukan dengan menggunakan kaedah penggantian molekul dengan nilai akhir faktor-R 0.134 ( $R_{free}$  0.162) untuk hablur yang tumbuh di bumi dan 0.129 ( $R_{free}$  0.150) untuk hablur yang tumbuh di angkasa. Struktur T1 lipase mengandungi dua molekul di setiap unit asimetri dengan mempunyai 387 asid amino setiap satunya. Topologi keseluruhan menunjukkan lipatan  $\alpha/\beta$  hidrolase mengandungi triad katalitik sebagai tapak aktif

diliputi dengan  $\alpha$ -helix 6 dan  $\alpha$ -helix 7 sebagai penutup. Struktur juga mengandungi tapak mengikat untuk zink dan kalsium yang mana ianya penting untuk penstabilan struktur. Analisis perbandingan kristalografi menunjukkan bahawa struktur hablur yang tumbuh di angkasa adalah lebih baik berbanding dengan yang tumbuh di bumi. Kajian ini menunjukkan penghabluran menggunakan kaedah resapan lawan dengan menggunakan keadaan mikrograviti telah memperbaiki susunan dalaman hablur dan telah menghasilkan struktur tiga dimensi protein yang lebih tepat.



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I certify that a Thesis Examination Committee has met on 30<sup>th</sup> May 2013 to conduct the final examination of Sayangku Nor Ariati Bt Mohamad Aris on her thesis entitled "Crystallographic Analysis of Ground and Space Thermostable T1 lipase Crystal" in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U.(A) 106] 15 March 1998. The Committee recommends that the student be awarded the Master of Science.

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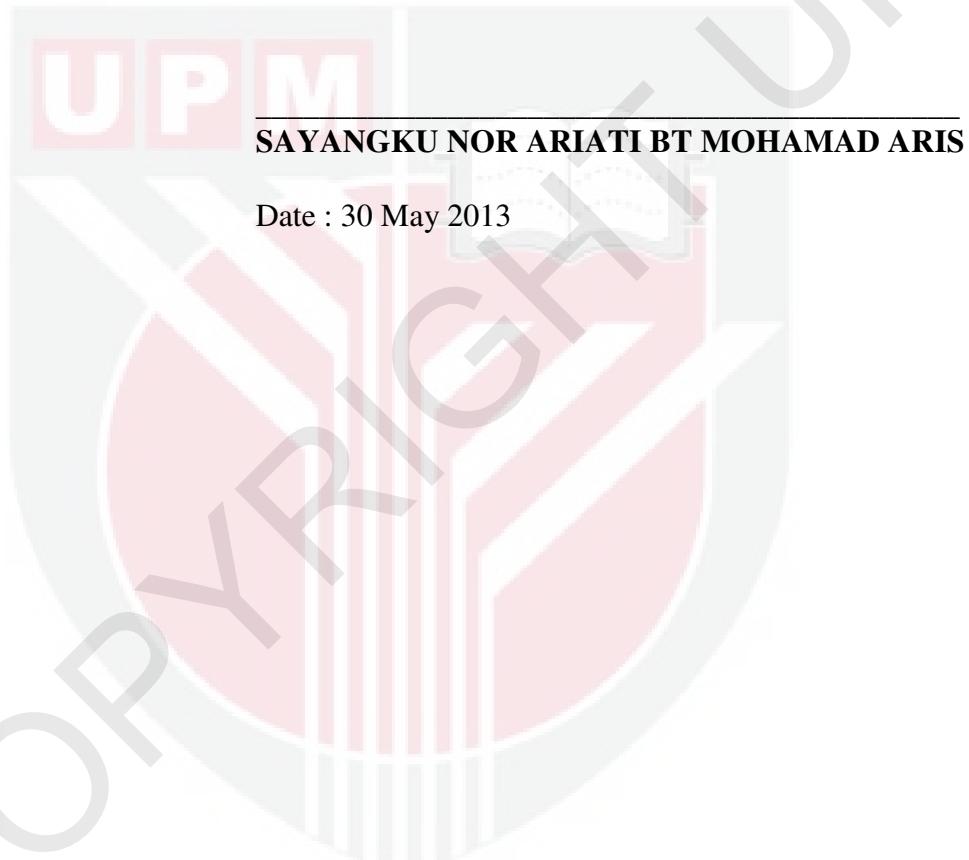
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## **DECLARATION**

I declare that the thesis is my original work except for quotations and citations which have been duly acknowledged. I also declare that it has not been previously, and is not concurrently, submitted for any other degree at Universiti Putra Malaysia or at any other institution.



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