

ฤทธิ์ต้านอนุมูลอิสระและยับยั้งการอักเสบของเปปไทด์จากหอยหวาน *Babylonia areolata*



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จุฬาลงกรณ์มหาวิทยาลัย

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ANTIOXIDANT AND ANTI-INFLAMMATORY ACTIVITIES OF PEPTIDE FROM
SPOTTED BABYLON *Babylonia areolata*

Mr. Komson Techoaphiwatanakun



A Thesis Submitted in Partial Fulfillment of the Requirements
for the Degree of Master of Science Program in Biotechnology

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ระดับอนุมูลอิสระที่ไม่เหมาะสมถือว่าเป็นหนึ่งในสาเหตุหลักของโรคต่างๆ ในชีวิต เมื่ออนุมูลอิสระอยู่ในระดับที่มากเกินไปและสารต้านอนุมูลอิสระไม่เพียงพอจนเกิดภาวะความเครียดออกซิเดชันนำไปสู่ความเสียหายของเซลล์และเนื้อเยื่อซึ่งสามารถลดความเสียหายได้จากการบริโภคสารต้านอนุมูลอิสระที่เพิ่มขึ้น ในการศึกษาเปปไทด์ที่ได้จากหอยหวาน (*Babylonia areolata*) ถูกย่อยด้วยเอนไซม์โปรตีเอส 3 ชนิด (อัลคาเลส นิวเตรสและเฟลเวอร์ไซม์) และเปปไทด์ที่ได้จากการย่อยด้วยเฟลเวอร์ไซม์เป็นเวลา 3 ชั่วโมง แสดงค่าการยับยั้ง DPPH ABTS NO SOD Catalase และ GPx ได้ค่าที่ดีที่สุดเมื่อเทียบกับการย่อยด้วยเอนไซม์อื่นๆ จากนั้นทำการแยกเปปไทด์ด้วยเทคนิคอัลตราฟิลเตรชัน และเทคนิคโครมาโตกราฟีแบบเจลฟิลเตรชันและพบว่า F3 มีการต้านอนุมูลอิสระที่ดีที่สุด หลังจากนั้นนำ F3 มาทดสอบการยับยั้ง NO และ MTT ในเซลล์ RAW 264.7 ทำบริสุทธิ์โดยเทคนิคโครมาโตกราฟีของเหลวสมรรถนะสูงซึ่งแสดงผล 4 พิก และทั้งหมดถูกวิเคราะห์ด้วยเทคนิคแมสสเปกโตรเมตรี พบสายของเปปไทด์ 6 สาย

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Inappropriate free radical levels are considered to be one of the major causes of various syndromes in living systems. Oxidative stress, which occurs when free radicals and antioxidant levels are in excess and insufficient, respectively, leading to cell and tissue damage, can be alleviated in some circumstances by the consumption of additional antioxidants. In this study, peptide derived from spotted babylon (*Babylonia areolata*) was hydrolysed using three kinds of proteases (alcalase, neutrase and flavozyyme), and the flavozyyme hydrolysate obtained by 3-h hydrolysis exhibited the highest DPPH, ABTS, NO, SOD, Catalase and GPx activities assay compared to other hydrolysates. By using ultrafiltration and gel filtration chromatography, the F3 fraction from the flavozyyme hydrolysate of spotted Babylon was highest antioxidant activity. After that, F3 fraction from gel filtration chromatography was tested in RAW 264.7 cells by inhibition of NO production assay and MTT assay, and the F3 fraction was purified using HPLC technique. The chromatogram showed the profile which contained 4 main peaks. These 4 fractions will analyzed using mass spectrometry which was obtained 6 sequence in 4 peak.

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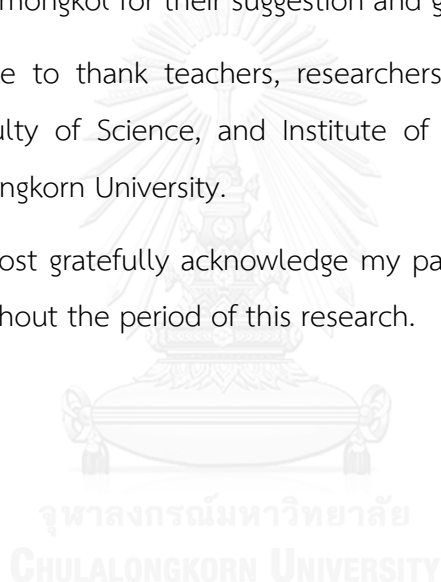
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CONTENTS

| | Page |
|---|------|
| THAI ABSTRACT | iv |
| ENGLISH ABSTRACT | v |
| ACKNOWLEDGEMENTS | vi |
| CONTENTS | vii |
| LIST OF TABLE | x |
| LIST OF FIGURE..... | xii |
| LIST OF ABBREVIATIONS | xiii |
| CHAPTER I INTRODUCTION..... | 1 |
| CHAPTER II LITERATURE REVIEWS | 4 |
| 2.1 Free radicals | 4 |
| 2.2 Antioxidant activity | 5 |
| 2.2.1 Non-enzymatic antioxidant..... | 6 |
| 2.2.1.1 Vitamin C (Ascorbic acid)..... | 6 |
| 2.2.1.2 Vitamin E (tocopherol) | 6 |
| 2.2.2 Enzyme antioxidant..... | 7 |
| 2.2.2.1 Superoxide dismutase (SOD)..... | 7 |
| 2.2.2.2 Catalase (CAT) | 7 |
| 2.2.2.3 Glutathione peroxidase (GPX)..... | 7 |
| 2.3 Anti-inflammation activity | 8 |
| 2.3.1 Inflammation..... | 8 |
| 2.3.2 Biological of nitric oxide | 9 |
| 2.3.3 Nitric oxide activity | 11 |

| | Page |
|--|------|
| 2.3.4 Cytotoxic activity..... | 12 |
| 2.3.5 Anti-inflammation protein..... | 13 |
| 2.4 Preparation Protein hydrolysate | 13 |
| 2.5 Bioactive activity from marine source..... | 14 |
| 2.6 Protein hydrolysate from Mollusca | 16 |
| 2.7 Spotted babylon (<i>Babylonia areolata</i>)..... | 17 |
| CHAPTER III MATERIALS AND METHODOLOGY..... | 21 |
| 3.1 Peptide preparation..... | 21 |
| 3.2 Purification and identification..... | 21 |
| 3.2.1 Ultrafiltration..... | 21 |
| 3.2.2 Gel filtration chromatography..... | 21 |
| 3.2.3 Reversed-phase high-performance liquid chromatography (RP-HPLC)..... | 22 |
| 3.2.4 Mass spectrometry | 22 |
| 3.3 Protein concentration assay..... | 24 |
| 3.4 DPPH radical scavenging assay | 24 |
| 3.5 ABTS radical scavenging assay | 24 |
| 3.6 Nitric oxide radical scavenging..... | 24 |
| 3.7 Superoxide radical scavenging activity assay..... | 25 |
| 3.8 Catalase activity assay..... | 25 |
| 3.9 Glutathione peroxidase activity assay..... | 25 |
| 3.10 The percentage inhibition | 26 |
| 3.11 RAW 264.7 cell culture and pretreatment..... | 26 |
| 3.12 Inhibition of nitric oxide (NO) production From RAW 264.7 Cells | 27 |

| | Page |
|---|------|
| 3.13 MTT assay for measuring cell proliferation | 27 |
| CHAPTER IV RESULTS AND DISCUSSION | 28 |
| 4.1 DPPH radical scavenging activity | 28 |
| 4.2 ABTS radical scavenging activity..... | 28 |
| 4.3 Nitric oxide scavenging activity..... | 29 |
| 4.4 Superoxide dismutase radical scavenging activity..... | 31 |
| 4.5 Catalase activity..... | 31 |
| 4.6. Glutathione peroxidase activity..... | 32 |
| 4.7 Gel filtration chromatography | 33 |
| 4.8 Effects of spotted babylon hydrolysate on NO production in RAW 264.7 cells | 34 |
| 4.9 Cell viability in Raw 264.7 cells..... | 35 |
| 4.10 RP-HPLC..... | 36 |
| 4.11 Mass spectrometry..... | 36 |
| CHAPTER V CONCLUSION..... | 41 |
| REFERENCES | 42 |
| APPENDIX..... | 49 |
| APPENDIX A | 50 |
| APPENDIX B | 53 |
| VITA..... | 59 |

LIST OF TABLE

| | Page |
|---|------|
| Table 1 Beneficial effects and harmful effects of inflammation..... | 9 |
| Table 2 Classification of mammalian nitric oxide synthase..... | 10 |
| Table 3 The advantages and disadvantages of enzymatic hydrolysis..... | 14 |
| Table 4 Proteolytic enzymes, characteristics and optimum conditions | 14 |
| Table 5 Some bioactive activity of protein hydrolysates from marine source | 16 |
| Table 6 Bioactive activity of protein hydrolysate of Mollusca..... | 17 |
| Table 7 Comparison of nutritional values of spotted babylon with other economically important marine organisms..... | 18 |
| Table 8 Amino acid content (mg/100mg) in small and big size of spotted Babylon.. | 19 |
| Table 9 Amino acid composition of spotted babylon <i>Babylonia areolata</i> (mg/100mg)..... | 20 |
| Table 10 IC ₅₀ values of DPPH, ABTS, nitric oxide activity from spotted babylon protein hydrolysate. Antioxidant activity assay by DPPH, ABTS, nitric oxide activity. Values are mean ± standard deviation (SD) (n = 3)..... | 30 |
| Table 11 Ultrafiltration separation (MW < 10 kDa) of protein hydrolysate from spotted babylon prepared by alcalase, flavourzyme and neutrase. Antioxidant activity assay was determined by DPPH, ABTS, nitric oxide activity. Values are the mean ± standard deviation (SD) (n = 3)..... | 30 |
| Table 12 Crude protein and MW < 10 kDa of protein hydrolysate from spotted babylon prepared by alcalase, flavourzyme and neutrase. was measured percent inhibition of superoxide radical..... | 31 |
| Table 13 Crude protein and MW < 10 kDa of protein hydrolysate from spotted babylon prepared by alcalase, flavourzyme and neutrase. was measured unit/ml of catalase activity..... | 32 |

| | |
|---|----|
| Table 14 Crude protein and MW < 10 kDa of protein hydrolysate from spotted babylon prepared by alcalase, flavourzyme and neutrase. was measured unit/ml of glutathione peroxidase activity | 33 |
| Table 15 The antioxidant activities of fractions from a column of Sephacryl S-200 gel filtration chromatography | 34 |
| Table 16 Peptide sequence of peak 1 identified by LC-MS/MS Q-TOF | 37 |
| Table 17 Peptide sequence of peak 2 identified by LC-MS/MS Q-TOF | 38 |
| Table 18 Peptide sequence of peak 3 identified by LC-MS/MS Q-TOF | 39 |
| Table 19 Peptide sequence of Peak 4 identified by LC-MS/MS Q-TOF | 40 |



LIST OF FIGURE

| | Page |
|--|------|
| Figure 1 Free radicals chain reactions | 5 |
| Figure 2 Vitamin C (Ascorbic acid) | 6 |
| Figure 3 Vitamin E (tocopherol)..... | 7 |
| Figure 4 Superoxide dismutase(SOD)..... | 7 |
| Figure 5 Catalase (CAT)..... | 7 |
| Figure 6 Glutathione peroxidase (GPX)..... | 8 |
| Figure 7 Acute and chronic inflammation | 9 |
| Figure 8 Chemical reaction of NO ₂ using the Griess Reagent System..... | 12 |
| Figure 9 MTT assay | 13 |
| Figure 10 Spotted babylon (<i>Babylonia areolata</i>). (Source; http://www.ku.ac.th/e-magazine/jan51/agri/Babylonia.htm) | 17 |
| Figure 11 The entire process of this work. | 23 |
| Figure 12 Chromatogram of flavourzyme hydrolysate protein (MW < 10 kDa) from Sephacryl S-200 gel filtration chromatography. Each fraction of the eluted solution was monitored at 280 nm..... | 34 |
| Figure 13 Inhibitory effect of spotted babylon hydrolysate on NO production in LPS stimulated RAW 264.7 cells and effect of spotted babylon hydrolysate on cell viability in RAW 264.7 cells..... | 36 |
| Figure 14 Chromatogram of fraction 4 from protein hydrolysate of spotted babylon (UV 280)..... | 36 |

LIST OF ABBREVIATIONS

| | |
|-------------------------------|---|
| Abs | Absorbance |
| ABTS | 2,2'-azinobis-(3-ethylbenzothiazoline-6-sulfonic acid) |
| BSA | Bovine serum albumin |
| CO ₂ | Carbon dioxide |
| DMSO | Dimethylsulfoxide |
| DPPH• | 2,2-diphenyl-1-picrylhydrazyl radical |
| <i>et al.</i> | and others |
| eNOS | Endothelial nitric oxide synthase |
| FBS | Fetal bovine serum |
| GPX | Glutathione peroxidase |
| GSH | Glutathione |
| h | Hour |
| H | hydrogen |
| H ₂ O | water |
| H ₂ O ₂ | Hydrogen peroxide |
| IC ₅₀ | Median inhibitory concentration, 50% maximum inhibition |
| iNOS | Inducible nitric oxide synthase |
| kDa | Kilodalton |
| LPS | Lipopolysaccharide |
| mg | Milligram |
| min | Minute |
| ml | Milliliter |
| mM | Millimolar |
| MTT | 3-[4,5-dimethylthiazol-2-yl]-2,5- |

| | |
|-------------------|---------------------------------|
| | diphenyltetrazolium bromide |
| MW | Molecular weight |
| NaCl | Sodium chloride |
| NED | N-(1-naphthyl) ethylene diamine |
| nm | Nanometer |
| nNOS | Neuron nitric oxide synthase |
| NO• | Nitric oxide |
| O ₂ | oxygen |
| O ₂ •- | Superoxide anion |
| O.D. | Optical Density |
| PBS | Phosphate buffered saline |
| PGE2 | Prostaglandin E2 |
| Rpm | Round per minute |
| TNF-μ | Tumor necrosis factor alpha |
| UV | Ultraviolet |
| α | Alpha |
| β | Beta |
| °C | Degree Celsius |
| γ | Gamma |
| g | Microgram |
| μl | Microliter |
| μM | Micromolar |
| / | Per |
| % | Percentage |
| : | Ratio |

CHAPTER I

INTRODUCTION

Nowadays, humans are exposed to elevated levels of free radicals from external sources such as UV rays, pollution, stress and poor nutrition. Free radical appears to play a major role and a cause of many diseases such as inflammation, cancer, ageing, heart attack, diabetes, dermatitis and other health complications. However, antioxidants are compounds that can be used to inhibit the free radicals. The compounds help prevent free radical damage by donation of electron. Normally, the antioxidants can be derived from the diet, such as vegetables and meat. The body is a substance that can inhibit and control free radical including antioxidant such as ceruloplasmin, transferrin, superoxide, dismutase, catalase, glutathione peroxidase and others substance.

In addition, the free radical damages endothelial cell and increases vascular permeability. Then, it is stimulating adhesion of neutrophil on endothelial cell, and motivated endothelial cell create up superoxide. Moreover, the free radical inhibits antiprotease which destructs extracellular matrix and cell tissue by enzyme from the lysosome. Therefore, the pharmaceutical industry is giving more attention to the new classes of protein drugs with the stability and bioavailability of small molecules. Peptide drugs, especially the short synthetic, fewer side-effects, low toxicity and long-acting ones, are quickly increasing in the global market. Inflammation is a protective immunovascular response that involves immune cells, blood vessels, and molecular mediators. The inflammation signs are pain, heat, redness, swelling, and loss of function. There is the need to consider new sources of drug to cure this effect. During inflammation, macrophages cells release chemical mediators such as nitric oxide and prostaglandins E₂. These substances built from leukocytes by enzymes Cyclooxygenase-2 (COX-2) and Inducible Nitric oxide synthase (iNOS). Nitric oxide and prostaglandins E₂ Will be induced to create up a large number of cytokine and endotoxin. Nitric oxide is a chemical compound with chemical formula of NO which has an important role in the disease of inflammation. Then, it is an effective molecule in many biological systems such as immunological, neuronal,

cardiovascular, tissues, blood circulatory system and others. Then, the effect of prostaglandin E2 (PGE2) renders vasodilation and Increased vascular permeability.

Protein hydrolysis is a product of the protein digestion by digesting polypeptide chains into short-peptide chains which have antioxidant activity (Taherzadeh and Karimi 2007, Samaranayaka and Li-Chan 2011, Pokora, Eckert *et al.* 2013). There are 2 methods for the preparation of protein hydrolysate; acid-base extraction and enzymatic hydrolysis. This study will focus on enzymatic hydrolysis (Kim, Lee *et al.* 2009). The advantages of enzyme hydrolysis are the high conversion yield, nontoxic, biodegradable, high specificity and utilization of soft conditions. Recently, active peptides are the interesting sources of drug development (Moure, Cruz *et al.* 2001). So, this study will focus on new sources of protein hydrolysate from marine spotted babylon.

Spotted babylon (*Babylonia areolata*) (Chaitanawisuti and Kritsanapuntu 1999), belonging to the family Buccinidae, genus Babylonia, is an important gastropod consumption in Thailand. Spotted babylon has a high nutrition which contains 18.78% of protein, 17 amino acids (glutamic acid arginine and alanine up to 80.18% of the total free amino acid contents), fat 2.86%, carbohydrate 5.18%, ash 5.27%, and moisture 67.91%. meat and intestines of spotted babylon includes 17 amino acids. Spotted babylon could be a precious material for the new production of protein hydrolysates because their rich in many nutrients which show a good results of anti-inflammation activity and antioxidant activity. Prior to this study have little education about anti-inflammatory activity and antioxidant activity in family Mollusca. In this study, protein hydrolysate extract from spotted Babylon by using 3 enzyme and then survey effect of antioxidant activity and anti-inflammatory activity such as DPPH radical scavenging assay, ABTS radical scavenging assay, nitric oxide radical scavenging, Superoxide radical scavenging activity assay, glutathione peroxidase activity assay and others assay.

This study, therefore, proposed that spotted babylon might be the main source of protein hydrolysate. The objective of this study was to impose antioxidant scavenging activity and anti-inflammation of protein hydrolysate obtained from peptide of spotted babylon. So, spotted babylon hydrolysates are new peptides

which have a significant bioactive and interesting. Antioxidant activity and anti-inflammatory activity containing peptides from spotted babylon could be further developed for commercial products. Then, development is a good dosage form and low side effects by using compensates anti-inflammatory medicine which effects to digestive and expensive.



CHAPTER II

LITERATURE REVIEWS

2.1 Free radicals

Free radicals are atoms or molecule with an unpaired electrons and can be interacts with other molecules. Once formed these highly reactive radicals can start a chain reaction. Free radicals can be produced from endogenous or exogenous sources. Endogenous sources generating free radicals from normal cell metabolisms occur during aerobic respiration in the mitochondria. Exogenous source from air pollution, cigarette smoke, Ozone (O_3), alcohol, industrial solvents, cooking (smoked meat) medication and radiation(Pham-Huy, He et al. 2008). Free radicals include hydroxyl (OH^\bullet), superoxide ($O_2^{\bullet-}$), nitric oxide (NO^\bullet), hydrogen peroxide (H_2O_2), peroxy (ROO^\bullet) and hypochlorous acid ($HOCl$) (Lü, Lin et al. 2010). These free radicals may oxidize nucleic acids, proteins, lipids or DNA. For example, hydroxyl radical and peroxy nitrite can damage cell membranes and lipoproteins by a process called lipid peroxidation, which are cytotoxic and mutagenic. Lipid peroxidation occurs by a radical chain reaction. Proteins may also be damaged by free radical, leading to structural changes and loss of enzyme activity. Oxidative damage to DNA leads to the formation of different oxidative DNA lesions which can cause mutations(Pham-Huy, He et al. 2008). So, free radicals appears to be a major role to many diseases such as cancer, autoimmune disorders, aging, cardiovascular diabetes mellitus, pathogenesis of inflammatory and neurodegenerative diseases (Valko, Leibfritz et al. 2007).

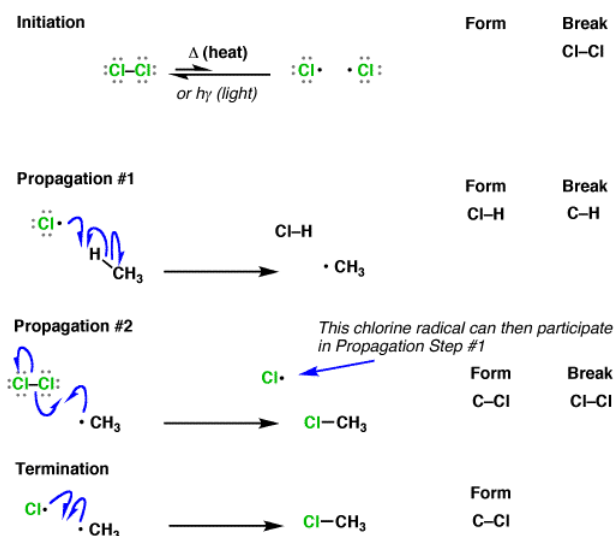


Figure 1 Free radicals chain reactions

The mechanism of free radicals chain reactions is chemical reaction. Radical chain reactions have three: initiation, propagation, and termination shown in Figure 1. The initiation phase describes initially creates a radical species. It is a hemolytic cleavage event and takes place very rarely due to the high energy barriers involved by the application of light, heat, UV radiation or a metal-containing catalyst is necessary to overcome the energy barrier. The propagation phase describes create the chain of chain reactions. Once a reactive free radical is generated, it can react with stable molecules to form new free radicals. These new free radicals go on to generate more free radicals, and start over again. Chain termination occurs when two free radical species react with each other to form a stable, non-radical adduct(Gordon 1990).

2.2 Antioxidant activity

An antioxidant is a molecule that inhibits the oxidation of free radicals. Antioxidants are molecules that can neutralize free radicals by accepting or donating electron(s) to eliminate the unpaired condition of the radical. The human body systems have antioxidants including enzyme and non-enzymatic compounds. The function of antioxidant is varied mechanisms of each compound including acting as radical scavenging, hydrogen donor, reducing agent, enzyme inhibitor and metal

chelating (Lobo, Patil et al. 2010). For example, non-enzymatic antioxidants have aromatic ring structures and are able to delocalize the unpaired electron such as vitamin C, vitamin E, B-carotene and uric acid. Enzymes antioxidant are superoxide dismutase (SOD), catalase (CAT) and glutathione peroxidase (GPX) (Lü, Lin et al. 2010). These produced in the body provide an important defence against free radicals. Moreover, synthetic antioxidants such as butylated hydroxyanisole (BHA) and butylated hydroxytoluene (BHT) are widely used in the food industry. However, synthetic antioxidants is strictly regulated because of effects in some animals at high levels (Shahidi and Zhong 2010). Therefore, natural antioxidants from various natural sources as alternatives to synthetic as protein hydrolysate from plant and animal.

2.2.1 Non-enzymatic antioxidant

2.2.1.1 Vitamin C (Ascorbic acid)

Vitamin C is a water-soluble vitamin and can be found in a number of foods, such as fruits and vegetables. Vitamin C is not an enzyme, but classified as electron donor. Ascorbic acid is a reducing agent and can reduce by neutralize free radical such as hydrogen peroxide (Shigeoka, Ishikawa et al. 2002). Ascorbic acid play an important protective role in the body against the damaging effects of free radicals through its ability as an antioxidant to scavenge free radicals and to regenerate vitamin E (Bendich, Machlin et al. 1986).

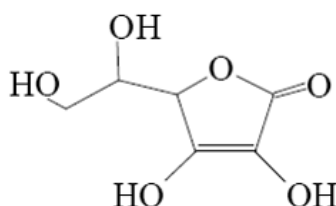


Figure 2 Vitamin C (Ascorbic acid)

2.2.1.2 Vitamin E (tocopherol)

Vitamin E is fat-soluble vitamin and can be found in wheat germ oil, sunflower, and safflower oils. It protects membranes from oxidation by reacting with lipid radicals produced in the lipid peroxidation chain reaction. This reaction

produces oxidized α -tocopheroxyl radicals that can be recycled back to the active reduced form (Traber and Atkinson 2007).

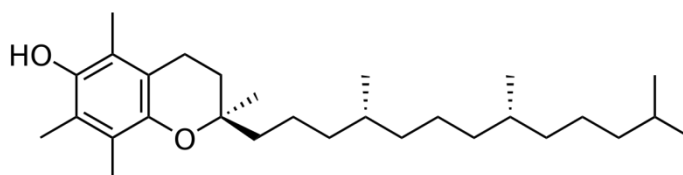


Figure 3 Vitamin E (tocopherol)

2.2.2 Enzyme antioxidant

2.2.2.1 Superoxide dismutase (SOD)

Superoxide dismutase (SOD) is an enzymes antioxidant that catalyze the breakdown of the superoxide anion (O_2^-) into oxygen and hydrogen peroxide (H_2O_2). SOD is essential enzyme present in almost all aerobic cells and in extracellular fluids which is located in every part of living systems. There are three major families of superoxide dismutase, depending on the metal cofactor: Cu/Zn (which binds both copper and zinc) (Zelko, Mariani et al. 2002).

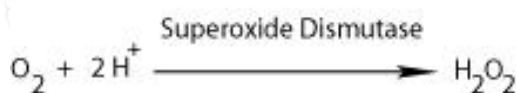


Figure 4 Superoxide dismutase(SOD)

2.2.2.2 Catalase (CAT)

Catalase (CAT) is the ferroporphyrin (heme) containing enzyme, found in nearly all living organisms. This enzyme functions to catalyze the decomposition of hydrogen peroxide into less reactive water and oxygen (Chelikani, Fita et al. 2004).

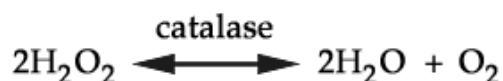


Figure 5 Catalase (CAT)

2.2.2.3 Glutathione peroxidase (GPX)

Glutathione peroxidase is an enzyme containing four selenium-cofactors that catalyze the breakdown of hydrogen peroxide(H_2O_2) and organic hydroperoxides

(ROOH) to water, using the tripeptide glutathione as a hydrogen donor (Brigelius-Flohé 1999).

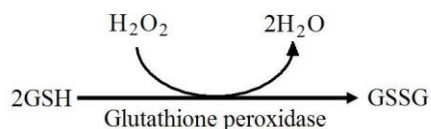


Figure 6 Glutathione peroxidase (GPX)

2.3 Anti-inflammation activity

2.3.1 Inflammation

The inflammation signs are pain, heat, redness, swelling, and loss of function. Inflammation can be classified into 2 cases including acute and chronic. Acute inflammation is the initial response of the body to harmful stimuli and is achieved by the increased movement of plasma and leukocytes (especially granulocytes) from the blood into the injured tissues. Chronic inflammation or prolonged inflammation, leads to a progressive shift in the type of cells present at the site of inflammation and is characterized by simultaneous destruction and healing of the tissue from the inflammatory process (Calder, Albers et al. 2009). During inflammation, macrophages cells release chemical mediators such as nitric oxide and prostaglandins E2. These substances built from leukocytes by enzymes Cyclooxygenase-2 (COX-2) and Inducible Nitric oxide synthase (iNOS). Nitric oxide and prostaglandins E2 Will be induced to create up a large number of cytokine and endotoxin. However, inflammations have both beneficial effects and harmful effects as shown in Table 1. And an important role in the disease of inflammation such as rheumatoid arthritis, atherosclerosis and asthma. (Hanada and Yoshimura 2002) Therefore, determination of anti-inflammatory properties has been proposed as a good way for preventing it.

Components of acute and chronic inflammation

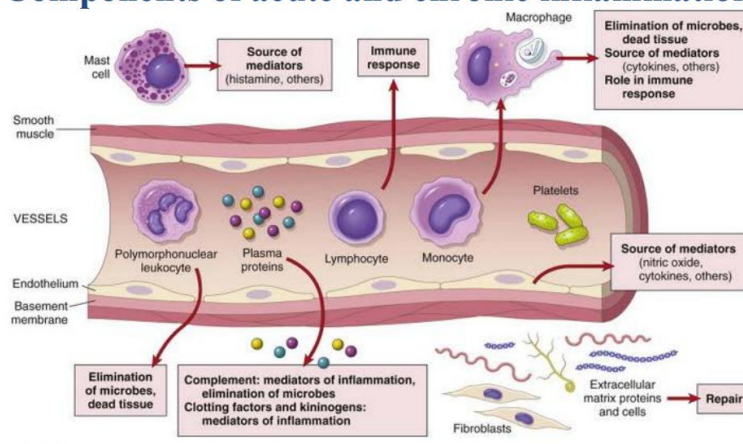


Figure 7 Acute and chronic inflammation

Table 1 Beneficial effects and harmful effects of inflammation

| Beneficial effects of inflammation | Harmful effects of inflammation |
|---------------------------------------|-------------------------------------|
| Dilution of toxins | Persistent cytokine release |
| Entry of antibodies | Destruction of normal tissues |
| Fibrin formation | Swelling |
| Delivery of nutrients | Inappropriate inflammatory response |
| Oxygen Stimulation of immune response | |

2.3.2 Biological of nitric oxide

Nitric oxide is a chemical compound with chemical formula of NO which has an effective molecule in many biological systems such as immunological, neuronal, cardiovascular, tissues, blood circulatory system. NO is one of the inflammatory mediators that have been implicated in a variety of pathophysiological conditions including inflammation, 4 carcinogenesis and atherosclerosis. NO acts as a host defense by damaging pathogenic DNA, and as a regulatory molecule with homeostatic activities (Kou and Schroder, 1995). Moreover, the potentially lethal substances released from microglia, overproduction of NO has been reported to cause oxidative damages and cell death (Minghetti and Levi, 1998). In animal cells,

NO is produced by the oxidation of L-arginine catalyzed by NO synthase (NOS). Three NOS isoforms have been identified neuronal NOS (nNOS), inducible NOS in macrophages (iNOS), and endothelial NOS (eNOS) (Table 2) (Nathan and Xie, 1994). The nNOS and the eNOS are referred to as constitutive NOSs, whereas iNOS gene expression is induced in macrophages and many other cell types in response to inflammatory agents and cytokines (Mayer and Hemmens, 1997).

Table 2 Classification of mammalian nitric oxide synthase

| Isoform | Typical localization | Cellular localization | Monomer molecular mass (kDa) |
|---------|----------------------|-------------------------|------------------------------|
| nNOS | Neuron | Soluble and particulate | -160 |
| eNOS | Endothelial cells | Particulate | -135 |
| iNOS | Macrophages | Soluble | -130 |

Inducible NOS (iNOS) is induced in response to various pro-inflammatory cytokines, including interferon- γ (IFN- γ), tumor necrosis factor- α (TNF- α), and interleukin-6 (IL-6), and mediates several inflammatory responses. NO synthesized by iNOS has also been considered as an important mediator of carcinogenesis. Overproduction of NO has been reported to cause oxidative damage cell death. Inhibition of NO overproduction has been proved to increase cell survival in several models. For example, NO has been correlated with the inflammatory process, in which multiple cytotoxic effects are related to the ability to increase vascular permeability and edema. This involves changes in local blood flow and increases in pro-inflammatory prostaglandins (Lantz et al., 2005). The macrophages can be activated by lipopolysaccharide (LPS) and interferon- γ (IFN- γ). LPS is one of the major constituents of the outer membrane of Gram-negative bacteria, and the immune system is constantly exposed to low levels of LPS through infections. LPS recognition and signal transmission are the key events aimed at eliminating an invading pathogen. The LPS-induced activation of macrophages results in the production of bioactive lipids, reactive oxygen species, and in particular,

inflammatory cytokines to fight and clear the bacterial infection. However, LPS mediates both the beneficial and deleterious reaction to the host. The excessive and uncontrolled production of inflammatory mediators triggered by LPS is harmful, and can lead to potentially lethal systemic disorders such as septic shock (Cho et al., 2008). The antigen can activate macrophages to release some inflammatory mediators such as NO, TNF- α , PGE2 and others. Therefore, the inhibition of NO, PGE2 and TNF- α production is an important therapeutic consideration in the development of anti-inflammatory agents.

2.3.3 Nitric oxide activity

Measurement of NO generation can be performed by different experimental setups. The rate of conversion of 3 H- or 14C- labeled L-arginine into the respective labeled L-citrulline and subsequent spectrophotometry is a standard procedure for indirect confirmation of NO production. L-citrulline can be readily detected using ionexchange procedures to separate substrate and product (Chan et al., 1997). In addition, there are many spectrophotometric assays available for the determination of NO metabolites. In oxygenated solution, NO reacts with O₂ to form nitrite and nitrate which can be measured using the Griess reaction (Kelm et al., 1997). The Griess Reagent System is based on the chemical reaction shown in Figure 8, which uses sulfanilamide and N-1-napthylethylenediamine dihydrochloride (NED) under acidic (phosphoric acid) conditions. This system detects NO₂ in a variety of biological and experimental liquid matrices such as plasma, serum, urine and tissue culture medium (Griess, 1879).

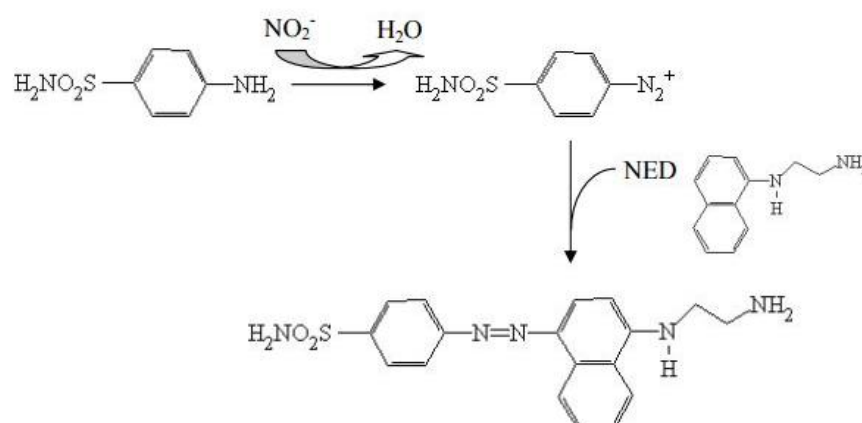


Figure 8 Chemical reaction of NO₂ using the Griess Reagent System

2.3.4 Cytotoxic activity

The predictive value of in vitro cytotoxicity tests is based on the idea of “basal” cytotoxicity – that toxic chemicals affect basic functions of cells which are common to all cells, and that the toxicity can be measured by assessing cellular damage. The development of in vitro cytotoxicity assays has been driven by the need to rapidly evaluate the potential toxicity of large numbers of compounds, to limit animal experimentation whenever possible, and to carry out tests with small quantities of compound. Evidence for the utility of in vitro cytotoxicity tests (Barile et al., 1994; Davila et al., 1990; Todd et al., 1999). The general principles for the detection of cell growth or cell kill via the MTT cytotoxicity assay (Figure 9). This method has been proven to be user friendly, rapid and highly sensitive (Promega, 2005; Bakand et al., 2006; Potera, 2007). MTT (3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide, a yellow tetrazole), is reduced to purple formazan in living cells. A solubilization solution (usually dimethyl sulfoxide, an acidified ethanol solution, or a solution of the detergent sodium dodecyl sulfate in diluted hydrochloric acid) is added to dissolve the insoluble purple formazan product into a colored solution. The absorbance of this colored solution can be quantified by measuring at a certain wavelength (usually between 500 and 600 nm) by a spectrophotometer. The absorption maximum is dependent on the solvent employed (Mosmann, 1983).

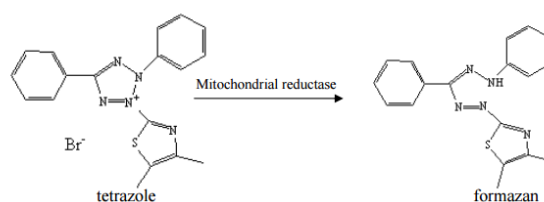


Figure 9 MTT assay

2.3.5 Anti-inflammation protein

The anti-inflammatory activity of several protein hydrolysate and isolated compounds has already been reported. Protein hydrolysate of tuna cooking juice showed the peptide fractions with the molecular weight ranging from 204 to 1672.9 Da possessed the highest anti-inflammatory activity. The amino acid sequences of the two anti-inflammatory peptides were Pro-Arg-Arg-Thr-Arg-Met-Met-Asn-Gly-Gly-Arg (1543.8 Da) and Met-Gly-Pro-Ala-Met-Met-Arg-Thr-Met-Pro-Gly (1211.5 Da) (Cheng, Wang et al. 2015). The peptic hydrolysates from salmon byproduct protein showed anti-inflammatory activity by inhibiting nitric oxide production and proinflammatory cytokines including tumor necrosis factor- α , interleukin-6 and - 1β in RAW264.7 macrophage cells. The peptides contained amino acids such as Tyr, Phe, Pro, Ala, His, and Leu (Ahn, Je et al. 2012). In 2013, Wang and co-workers were reported that blue mussel protein hydrolysed by neutrase exhibited the highest DPPH radical scavenging activity. BNH-P7, the fraction departed from HPLC, exhibited good scavenging activity on DPPH radical, hydroxyl radical, and superoxide anion radical with IC₅₀ of 2.62, 0.228, and 0.072 mg/ml, respectively. In 2015, Ahn and co-workers were reported the anti-inflammatory peptide from salmon hydrolysed by pepsin. The purified peptide inhibited the production of NO by 63.80% and PGE₂ by 45.33%.

2.4 Preparation Protein hydrolysate

Protein hydrolysate from plant and animal containing peptide or amino acid 3-20 amino acids. The protein hydrolysate can be produced by acid-base extraction or enzymatic hydrolysis. In this thesis, enzymatic hydrolysis was chosen to selectively hydrolyze protein because enzymatic hydrolysis is non-toxic chemicals in the

products. The advantages and disadvantages of enzymatic hydrolysis as shown in Table 3. Protein hydrolysis by enzyme including protease such as protease from animal (trypsin, pepsin and pancreatin), protease from plant (papain and protease), protease from microorganism (alcalase, , flavourzyme and neutrase) under mild condition of pH (6-8) and temperature (40-60 °C) (Table 4) (Ahn, Cho et al. 2015).

Table 3 The advantages and disadvantages of enzymatic hydrolysis

| Advantages | Disadvantages |
|-----------------------------------|----------------|
| 1. Not-consumed during reaction | 1. Instability |
| 2. High conversion yield | 2. High cost |
| 3. Nontoxic and biodegradable | |
| 4. High specificity | |
| 5. Utilization in soft conditions | |
| 6. Large-scale production | |

Table 4 Proteolytic enzymes, characteristics and optimum conditions

| Enzyme | Source of origin | Condition | |
|-------------|-------------------------------------|-----------|-----------|
| | | pH | Temp (°C) |
| Alcalase | <i>Bacillus licheniformis</i> | 7.0 | 50 |
| Flavourzyme | <i>Bacillus stearothermophilus</i> | 7.0 | 50 |
| Neutrase | <i>Bacillus amyloliquefaciens</i> | 7.0 | 50 |
| Pepsin | Porcine gastric mucosa | 2.0 | 37 |
| Trypsin | Bovine, porcine or human pancreas | 8.0 | 37 |
| Papain | <i>Carica papaya</i> (papaya latex) | 6.0 | 37 |

2.5 Bioactive activity from marine source

Although, synthetic antioxidants, such as butylated hydroxyanisole (BHA) and butylated hydroxytoluene (BHT) are strictly regulated because of effects in toxicity

(Shahidi and Zhong 2010). Therefore, natural antioxidants from various natural sources as alternatives to synthetic such as protein hydrolysate from plant and animal. The marine source, which makes up more than 70% of the earth's surface, represents a vast with diverse biological activities have been identified in mollusk, algae, fish and shellfish, which represents a good candidate raw material for protein hydrolysate peptide.

In 2012, Bougatef and co-workers were studied sardine fish '*Sardinella aurita*'. They hydrolyzed the crude protein by NH1 protease enzyme for 3 hours. The antioxidant activity is about 87 percentages.

In 2013, Wang and co-workers were studied blue mussel shell '*Mytilus edulis*'. They hydrolyzed the crude protein by neutrase enzyme for 3 hours. The antioxidant activity is about 28 percentages.

In 2014, Jiang and co-workers were studied round scad fish '*Decapterus maruadsi*'. They hydrolyzed the crude protein by alcalase enzyme for 5 hours. The antioxidant activity is about 39 percentages.

There are many proteins hydrolysate from marine sources including plants and animals which represent antioxidant activity such as *Ecklonia cava* (microalgae) (Heo, Jeon et al. 2003), *Porphyra tenera*(macroalgae) (Lee, You et al. 2005). *Penaeus japonicus* (prawn) (Suetsuna 2000). *Mytilus edulis*(mussel) (Rajapakse, Mendis et al. 2005) and *Dosidicus eschrichtii* (squid) (Lin and Li 2006). Moreover, proteins hydrolysate from marine sources shown bioactive activity including antihypertensive, ACE inhibitory, anti-inflammation, antimicrobial, antityrosinase and antitumor. Such as *Harengula zunasi*(sardine) (Shang-gui, Zhi-ying et al. 2004), *Tachypleus tridentatus* (Crab) (Masuda, Nakashima et al. 1992), *Parasilurus asotus*(cat fish) (Park, Park et al. 1998), *Scomber austriasicus*(maceral) (Masaaki and Hiroyuki 2007), *Dolabella auricularia*(sea hare) (Madden, Tran et al. 2000) and *Pomatomus saltatrix* (Trout) (Bauchart, Chambon et al. 2007).

Table 5 Some bioactive activity of protein hydrolysates from marine source

| Marine source | Bioactive activity | Peptide sequence | References |
|--|--------------------|-------------------|-------------------------------|
| <i>Porphyra yezoensis</i> | Antihypertensive | AKYSY | Saito and Hagino 2005 |
| <i>Gadus microcephalus</i> (Cod) | Antioxidant | TGGGNV | Ngo, Ryu et al. 2011 |
| <i>Pinctadafucata martencii</i> (Oyster) | ACE inhibitory | PY | Katano, Oki et al. 2003 |
| <i>Mytilus edulis</i> (Mussel) | Antihypertensive | EVMAGNLYPG | Je, Park et al. 2005 |
| <i>Dosidicus giga</i> (Squid) | antioxidant | NADFGLNGLE GLA | Rajapakse, Mendis et al. 2005 |
| <i>Meretrix lusoria</i> (Clam) | ACE inhibitory | VRK | Tsai, Chen et al. 2008 |
| <i>Homarus gammarus</i> (Lobster) | Antimicrobial | - | Hauton, Brockton et al. 2006 |
| <i>Bryopsis sp.</i> (Trout) | Antitumor | - | Ciruelos, Trigo et al. 2002 |

2.6 Protein hydrolysate from Mollusca

Mollusca is one of the most diverse groups of marine animals with at least 50,000 living species includes snails, octopuses, squid, clams, scallops, oysters, and chitons. Some of Mollusca have report about bioactivity activity such as antioxidant activity, anticoagulant, antihypertensive and antimicrobial as shown in Table 6. Antioxidant activity of protein hydrolysates relies on amino acid composition of sequence and molecular weight of a peptide. Peptides containing hydrophobic amino acids, such as Pro, Leu, Ala, Trp and Phe, are possess high antioxidant activity (Mendis, Rajapakse et al. 2005). Peptides containing aromatic amino acid such as Trp, Tyr and Met also show the highest antioxidant activity, followed by Cys, His and Phe (Dávalos, Miguel et al. 2004).

Table 6 Bioactive activity of protein hydrolysate of Mollusca

| Source | Bioactive activity | Amino acid sequence | Referent |
|--|------------------------|---------------------|-------------------------------|
| Oyster | Antioxidant | LKQELEDLLEKQE | Qian, Jung et al. 2008 |
| <i>Mytilus edulis</i> (Blue mussel) | Antioxidant | HFGDPFH | Rajapakse, Mendis et al. 2005 |
| <i>Mytilus edulis</i> | Anticoagulant | EADIDGDGQVAMMTSK | Jung and Kim 2009 |
| Hard clam | Antihypertensive | YN | Tsai, Chen et al. 2008 |
| <i>Crassostrea gigas</i> (Oyster) | Inhibit HIV-1 protease | LLEYSL | Lee and Maruyama 1998 |
| <i>Crassostrea gigas</i> (Oyster) | Antimicrobials | LLEYSI | Liu, Dong et al. 2008 |
| <i>Mytilus galloprovincialis</i> . | Antimicrobial | - | Mitta, Hubert et al. 1999 |

2.7 Spotted babylon (*Babylonia areolata*)



Figure 10 Spotted babylon (*Babylonia areolata*). (Source; <http://www.ku.ac.th/e-magazine/jan51/agri/Babylonia.htm>)

Babylonia areolata or Spotted babylon, belonging to the family Buccinidae, genus *Babylonia*, is an important gastropod consumption in Thailand. Then, spotted

babylon's shell has heavy and oval which has white color and brown stripes on shell. They have highlights organ such as 2 eyes, 2 tentacle, shell, big foot uses moment like snail. Afterwards these shells eat feed by using organ same as white tubing releases fluid which digests and suck feed. After that, it moves in the sandy. The feed of these ones are carrion from the sea, and then that grows by about 40-100 mm. Habitat of spotted Babylon is according to the sandy sea floor or Sandy mud from the depths 2 to 20 m which founds in Gulf of thailand. Spotted babylon has a high nutrition which contains 18.78% of protein, 17 amino acids (glutamic acid arginine and alanine up to 80.18% of the total free amino acid contents), fat 2.86%, carbohydrate 5.18%, ash 5.27%, and moisture 67.91% (Chaitanawisuti and Kritsanapuntu 1999). meat and intestines of spotted babylon includes 17 amino acids. Nowadays, spotted Babylon is a kind of economic animals and eats together in both domestic and foreign. Therefore, the promotion of aquaculture is a career.

Table 7 Comparison of nutritional values of spotted babylon with other economically important marine organisms

| Organism | Composition of nutritional value (%) | | | | |
|----------------------------|--------------------------------------|------|------|--------------|----------|
| | Protein | Fat | Ash | Carbohydrate | Moisture |
| Natural spotted babylon | 18.03 | 2.39 | 2.38 | 3.33 | 73.87 |
| Cultivated spotted babylon | 20.01 | 6.33 | 2.04 | 0.79 | 70.83 |
| Mussel | 11.90 | 2.24 | 1.59 | 3.69 | 80.58 |
| Oyster | 9.45 | 2.30 | 1.23 | 4.95 | 82.06 |
| Abalones | 17.10 | 0.76 | 1.57 | 6.01 | 74.56 |
| Tiger prawn | 20.31 | 1.73 | 1.20 | 0.90 | 75.86 |

Taken from (Prakot, Chaitanawisuti et al. 2014).

Table 8 Amino acid content (mg/100mg) in small and big size of spotted Babylon

| Amino acid | Big size of spotted babylon | Small size of spotted babylon |
|---------------|--------------------------------|----------------------------------|
| Threonine | 731.55 | 502.07 |
| Isoleucine | 1,071.44 | 767.10 |
| Leucine | 2,211.60 | 1,948.33 |
| Lysine | 2,792.39 | 2,714.73 |
| Methionine | 300.32 | 303.42 |
| Cystine | 35.54 | 18.55 |
| Phenylalanine | 1,171.00 | 1,851.35 |
| Tyrosine | 1,624.58 | 1,321.69 |
| Valine | 1,031.18 | 725.92 |
| Arginine | 229.81 | 131.89 |
| Histidine | 1,540.16 | 1,212.00 |
| Alanine | 1,149.63 | 788.54 |
| Aspartic acid | 1,006.29 | 477.89 |
| Glutamic acid | 1,133.58 | 1,433.07 |
| Glycine | 1,274.81 | 874.41 |
| Proline | 1,749.84 | 1,147.63 |
| Serine | 22.06 | 17.31 |

Translated from (Chaitanawisuti and Kritsanapuntu 1999).

Table 9 Amino acid composition of spotted babylon *Babylonia areolata* (mg/100mg).

| Amino acid profile | Results (%) |
|--------------------|--------------|
| Alanine | 4.36 |
| Arginine | 5.85 |
| Glycine | 4.30 |
| Aspartic Acid | 7.09 |
| Valine | 3.03 |
| Cystine | 0.64 |
| Glutamic Acid | 11.70 |
| Leucine | 5.27 |
| Isoleucine | 2.36 |
| Histidine | 1.20 |
| Threonine | 3.15 |
| Proline | 3.12 |
| Lysine | 4.42 |
| Methionine | 1.65 |
| Hydroxyproline | Not Detected |
| Serine | 3.12 |
| Phenylalanine | 2.43 |
| Hydroxylysine | Not Detected |
| Tyrosine | 2.37 |
| Tryptophan | 0.40 |

Taken from; (Prakot, Chaitanawisuti et al. 2014)

CHAPTER III

MATERIALS AND METHODOLOGY

3.1 Peptide preparation

Spotted babylon (Sichang Marine Science Research, Chulalongkorn University in Cholburi province of Thailand) was asphyxiated with ice. Then, Spotted babylon removes shell by hammer. The muscle of spotted babylon was separated manually and washed with cold distilled water. After that the muscle of spotted babylon was pounded to homogenate (Kim, Kim et al. 2013). Crude protein was extracted from spotted babylon using 20 mM phosphate buffer (pH 7.2). Three proteases; alcalase, flavourzyme and neutrase, were used in the hydrolysis process. Five percentages of enzymes were mixed with crude protein and incubated at 50 °C for 4 h prior to inactivation of the protein by boiling at 90 °C for 20 min. Finally, all protein hydrolysis was silted by centrifugation. Afterward, protein hydrolysis was collected from supernatant and remove sediment. Spotted babylon hydrolysate (SBH) was kept in a cold storage at -20 °C until desired for using.

3.2 Purification and identification

3.2.1 Ultrafiltration

All protein hydrolysates were fractionated by ultrafiltration using the molecular weight cut-off membrane of 10 (Amersham Biosciences, Sweden). Protein hydrolysates were initially processed in a 10 kDa membrane to generate a retentate (MW > 10 kDa) and permeate (MW < 10 kDa). The permeate proteins (MW < 10 kDa) were collected for antioxidant activity assay and purification (Jiang, Tong et al. 2014).

3.2.2 Gel filtration chromatography

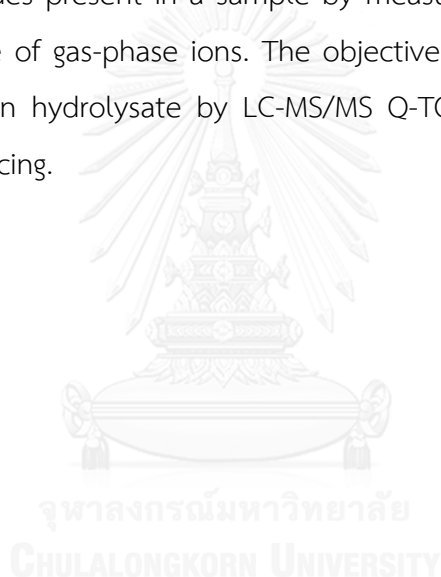
The fraction with the best antioxidant activities was further purified by injection into a Sephacryl S-200 gel filtration column (2.6 × 80 cm) equilibrated with ultrapure water, and the loaded proteins were eluted with ultrapure water at a flow rate of 1.0 ml/min (Ahn, Cho et al. 2015). Each fraction of the eluted solution was detected at 280 nm. Their antioxidant activities were examined. The fractions with the highest antioxidant activities was subjected to the next purification step.

3.2.3 Reversed-phase high-performance liquid chromatography (RP-HPLC)

The fraction with the highest antioxidant activities from the gel filtration chromatography was further purified by reversed phase high performance liquid chromatography on Shimpack C-18 column (250×46 mm), using a linear gradient of acetonitrile containing 0.05% trifluoroacetic acid (TFA) (Bougatef, Ali et al. 2010). The elution solution was detected at 280 nm and 3 purified peptides, namely F1, F2, and F3, were analyzed by mass spectrometry.

3.2.4 Mass spectrometry

Mass spectrometry is an analytical chemistry technique to identify compounds or peptides present in a sample by measuring the mass-to-charge ratio (m/z) and abundance of gas-phase ions. The objective of this study was to identify compounds in protein hydrolysate by LC-MS/MS Q-TOF data were analyze by de novo peptide sequencing.



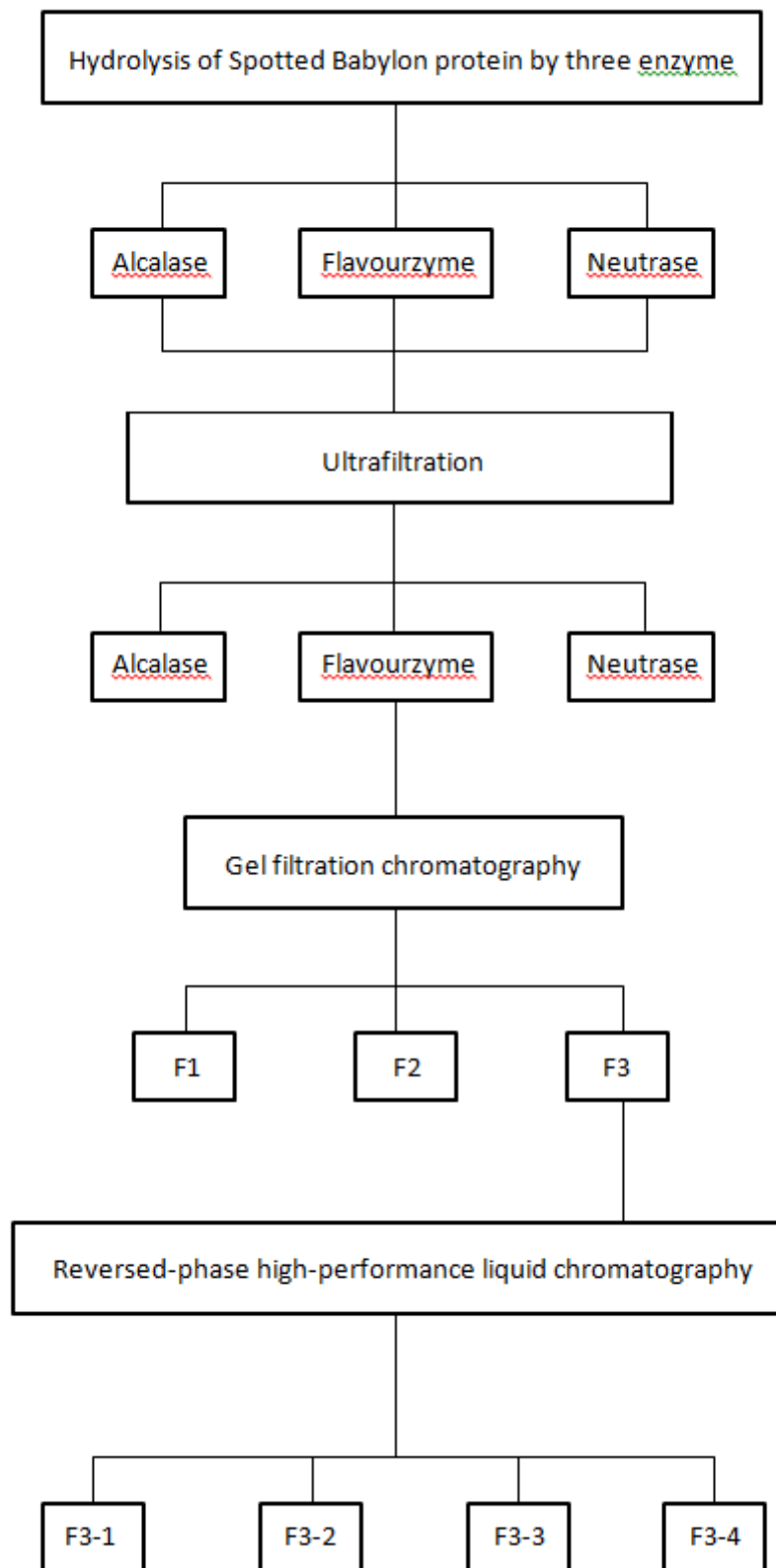


Figure 11 The entire process of this work.

3.3 Protein concentration assay

Protein contents of the sample were determined using the Bradford assay. Various concentrations of bovine serum albumin (BSA) were used as the standard for the constructing of calibration curve (Bradford 1976).

3.4 DPPH radical scavenging assay

The DPPH radical scavenging activity was performed according to the method of Mohsen and Ammar (Mohsen and Ammar 2009) with slight modifications. Protein hydrolysate (40 μ l) was added to 160 μ l of DPPH solution (1M in 100% of ethanol). The mixtures were incubated in the dark at room temperature for 30 min, and reduction of DPPH radicals was measured at 517 nm using a microplate reader. L-ascorbic acid (Vitamin C) was used as a standard control .

3.5 ABTS radical scavenging assay

The ABTS radical scavenging activity was determined according to the method of Cai et al (Cai, Luo et al. 2004) with slight modifications. ABTS solution was prepared from 7 mM ABTS in potassium persulphate solution. ABTS solution was incubated in the dark at room temperature for 12 h. The ABTS solution (300 μ l) was mixed with 10 μ l of protein hydrolysate, and the mixtures were incubated at room temperature for 5 min. The reduction of ABTS radicals was measured at 734 nm using a microplate reader.

3.6 Nitric oxide radical scavenging

The nitric oxide radical scavenging was performed according to the method of Govindarajan et al (Govindarajan, Rastogi et al. 2003). Protein hydrolysate was mixed with Griess containing 10 mM sodium nitroprusside in 20 mM buffer solution (pH 7.2). The total volume was then adjusted to 40 μ l, and the mixtures were incubated at room temperature for 150 min. of The mixtures (0.5 ml) were added to 100 μ l of sulfanilamide solution (0.33% sulfanilamide in 20% acetic acid), and incubated for 5 min at 37 °C. 100 μ l of N-(1-naphthyl) ethylene diamine dichloride (NED) was added and incubated at at room temperature for 30 min, then the absorbance at 540 nm was measured by a microplate reader.

3.7 Superoxide radical scavenging activity assay

The assay of superoxide dismutase was measured the method of 19160 SOD determination kit by sigma-aldrich. In this method, 20 μ l of each protein hydrolysate were mixed with 200 μ l WST working solution (WST-1 (2-(4-Iodophenyl)-3-(4-nitrophenyl)-5-(2,4-disulfophenyl)-2Htetrazolium, monosodium salt). Add 20 μ l Enzyme working solution and mix thoroughly. The mixture incubated at 37°C for 20 min. The absorbance was measured at 450 nm.

3.8 Catalase activity assay

Catalase activity was assayed by the method of Catalase assay kit by sigma-aldrich. Catalase is an antioxidant enzyme that is present in living organisms. Catalase activity can be determined in the measurement of the hydrogen peroxide substrate remaining after the action of catalase (Catalase change hydrogen peroxide (H_2O_2) to water and oxygen) In this method, add 20 μ l of protein hydrolysate to quartz plate mixing with 80 μ l of 1x Assay Buffer. The reaction was started by the addition of 100 μ l of UV Assay Substrate Solution (20 mM H_2O_2). Follow the decrease of A240 for 30 sec with the kinetic program, the following parameters: Initial delay = 3 seconds, interval = 5 seconds, readings = 7

The activity was calculated as follow:

$$\text{Unites/ml} = \frac{[\Delta A / \min(\text{Blank}) - \Delta A / \min(\text{Sample})] \times d \times 1}{V \times 0.0436}$$

d = dilution of original sample, V= sample volume (x μ l = 0.00x ml), 0.0436 = ϵ^{mM} for hydrogen peroxide , 1= reaction volume in ml

3.9 Glutathione peroxidase activity assay

Glutathione peroxidase activity was assayed by the method of Glutathione peroxidase cellular activity assay kit sigma-aldrich. The assay kit uses an indirect determination method base on GPx converts reduced glutathione (GSH) to oxidized glutathione (GSSG). In this method, add 180 μ l into quartz plate. Then, add 10 μ l of NADPH Assay Reagent and 8 μ l of protein hydrolysate and mix by inversion. The reaction was started by the addition of 2 μ l of 30 mM tert-Butyl Hydroperoxide

Solution. And mix by inversion. Follow the decrease in absorbance at 340 nm with the kinetic program, the following parameters:

Initial delay = 15 seconds, Interval = 10 seconds, Readings = 6

The activity was calculated as follow:

$$\text{Unites/ml} = \frac{(\Delta A_{340}/\text{min}(\text{blank}) - A_{340}/\text{min}(\text{sample})) \times DF}{6.22 \times V}$$

DF = dilution factor of original sample, V= sample volume in ml, 6.22 = ϵ^{mM} for NADPH

3.10 The percentage inhibition

The percentage inhibition of antioxidant activity was calculated as follows:

$$\left[\frac{(\text{Abs control} - \text{Abs blank}) - (\text{Abs sample} - \text{Abs background})}{(\text{Abs control} - \text{Abs blank})} \right] \times 100$$

where Abs control is the absorbance of control (no sample), Abs sample is the absorbance of sample, Abs background is the color absorbance of the sample, and Abs blank is the absorbance of deionized water. The IC50 was calculated using GraphPad Prism version 6. All tests were performed in triplicate. The values are expressed as mean \pm standard deviation of the triplicate data.

3.11 RAW 264.7 cell culture and pretreatment

The RAW 264.7 cell line cultured in DMEM medium added with 10% (v/v) fetal bovine serum (FBS) (Chantaranothai, Palaga et al. 2013). RAW 264.7 cells were incubated at 37°C in the presence of 5% CO₂ in Forma™ 310 Direct Heat CO₂ Incubators. Cell culture uses times about 3-4 day. After that, the medium was pulled and the cells were rinsed out with 0.5 ml of trypsin at 30-40 minutes. Trypsin was removed and added new DMEM medium. Then, all cells in DMEM medium were collected in tube for determination of nitric oxide and MTT assay. The viable cell numbers were calculated following equation.

Total cell count (cells/mL)

$$= \text{the number of cell counted in 4 large squares} \times 10 \times 10^4$$

After that, total cell count mix new DMEM medium in sterilized bottle. Then, total cell from bottle were suck to 180 μl /well of 96-well plates which were incubated overnight at 37°C in 5% CO_2 . Therefrom preparation of sample and LPS (lipopolysaccharide), sample was mixed DMEM medium at the ratio 1:2 to 1:1,000 (v/v) and 1 $\mu\text{g}/\text{ml}$ of LPS was prepared from 500 $\mu\text{g}/\text{ml}$ of stock LPS. Next day, DMEM medium was removed from 96-well plates and then 96-well plates was added at 190 μl /well of sample and 10 μl /well of LPS. 96-well plates were incubated overnight at 37°C in 5% CO_2 .

3.12 Inhibition of nitric oxide (NO) production From RAW 264.7 Cells

RAW264.7 macrophage cells were incubated overnight at 37°C in 5% CO_2 . with different concentrations of sample in the absence or presence of 10 μl of LPS. After that, 100 μl of culture medium was collected and used to NO assay. Then, 100 μl of culture medium was mixed with 100 μL of Griess reagent (0.33% sulfanilamide in 1% acetic acid and 0.1% N-(1-naphthyl) ethylene diamine dichloride), and further incubated for 15 min, then the absorbance at 540 nm was measured by a microplate reader. The Sodium nitrite dissolved in DMEM was. using a standard curve of NO concentration in the media of sample healed cells.

3.13 MTT assay for measuring cell proliferation

The MTT assay (Yang, Kang et al. 2014) was assessed cytotoxicity of sample from RAW264.7 macrophage cells were grown in 96-well plates at a density of 1.6×10^4 cells/well. After overnight, RAW264.7 macrophage cells were treated with control medium (medium containing only different concentration sample) and medium containing different concentration sample and LPS which were collected overnight or 24 h at 37°C in 5% CO_2 . After that, The MTT solution (1 mg/mL) was added 10 μl /well in 96-well plates cell culture, and incubated for 4 h. Finally, dimethyl sulfoxide (DMSO) was added 100 μl /well in 96-well plates due to DMSO solubilizes the formed formazan crystals. The volume of formazan crystals was determined by measuring the absorbance at 540 nm.

CHAPTER IV

RESULTS AND DISCUSSION

4.1 DPPH radical scavenging activity

DPPH radical scavenging activity was determined by mixing of the protein sample and DPPH solution, and measured the reduction of DPPH radicals at 517 nm. In DPPH scavenging activity, the violet compound of DPPH radical turns yellow when neutralized by antioxidant. The DPPH radicals scavenged and the absorbance was reduced. The reduction in absorbance is therefore used to determine radical scavenging activity. The results of DPPH radical scavenging activity from spotted babylon protein were shown as changes of IC_{50} values (Tables 10 and 11). All protein hydrolysate were found to have the efficacy to scavenge the DPPH radical and showed no significant difference ($p > 0.05$). The protein hydrolysates that were passed to ultrafiltration membrane (MW < 10 kDa) flavozyme hydrolysate was found to have the highest scavenging activity ($0.75 \pm 0.04 \mu\text{g/ml}$) which have scavenging activity more than protein hydrolysate from *Decapterus maraudsi* (Jiang et al., 2014) and *Mytilus edulis* (Wang et al., 2013), while alcalase hydrolysate was found to have the lowest DPPH radical-scavenging activity ($1.27 \pm 0.24 \mu\text{g/ml}$).

4.2 ABTS radical scavenging activity

ABTS radical can be determined by monitoring the absorbance at 734 nm. Antioxidants suppress this reaction by electron donation radical scavenging and inhibit ABTS radical. The results of ABTS radical scavenging activity expressed as IC_{50} values are shown in the Table 10. All protein hydrolysate had the efficacy to scavenge. The highest ABTS scavenging activities were obtained from alcalase and flavozyme hydrolysate (5.28 ± 0.21 and $3.78 \pm 0.08 \mu\text{g/ml}$, respectively), whereas the lowest ABTS radical-scavenging activity was obtained from neutrase hydrolysate ($8.00 \pm 0.28 \mu\text{g/ml}$). Table 11 shows that the IC_{50} values of protein hydrolysate whose molecular mass was less than 10 kDa and with the highest IC_{50} values of ABTS radical scavenging activity were alcalase and flavozyme hydrolysate (2.47 ± 0.11 and $2.90 \pm 0.12 \mu\text{g/ml}$, respectively), whereas neutrase hydrolysate had the lowest ABTS radical scavenging activity ($1.27 \pm 0.24 \mu\text{g/ml}$). The results of ABTS scavenging activity in

many researchers found EC₅₀ of LPF (1.014 mg/ml), LLPF (1.031 mg/ml), from the protein hydrolysate of scalloped hammerhead, (Luo et al., 2013) and corn gluten meal (Zhuang et al., 2013), respectively.

4.3 Nitric oxide scavenging activity

Nitric oxide was formed from sodium nitropusside. All protein hydrolysates exhibited antioxidant activity. Nitric oxide was decreased and could be measured by monitoring the absorbance at 540 nm. The nitric oxide scavenging activity was shown as IC₅₀ values in Tables 10 and 11. The highest nitric oxide scavenging activity of crude protein was from flavourzyme hydrolysate and neutrase hydrolysate (0.005 ± 0.17 and 0.007 ± 0.19 $\mu\text{g/ml}$, respectively), but alcalase hydrolysate exhibits lowest nitric oxide scavenging activity which is 0.056 ± 0.068 $\mu\text{g/ml}$. The protein hydrolysate (MW < 10 kDa) with the highest nitric oxide scavenging activity were those from flavozyme and neutrase hydrolysate (0.0017 ± 0.00037 and 0.002 ± 0.0004 $\mu\text{g/ml}$, respectively). Then, alcalase hydrolysate shows lowest nitric oxide scavenging activity look like control. Eun-Kyung Kim et al. (2013) report the effect of flavourzyme hydrolysate from *Mytilus coruscus* on the viability of RAW264.7 cells was examined by MTT assay and NO-inhibitory effect assay. The cell viability was not reduced by Flavourzyme hydrolysate up to 1.0 mg/ml and NO reduced.

Table 10 IC₅₀ values of DPPH, ABTS, nitric oxide activity from spotted babylon protein hydrolysate. Antioxidant activity assay by DPPH, ABTS, nitric oxide activity. Values are mean ± standard deviation (SD) (n = 3).

| Enzyme | IC ₅₀ (µg/ml) | | |
|----------------------------------|--------------------------|---------------------------|----------------------------|
| | DPPH* | ABTS** | NO*** |
| Control | 6.56 ± 2.78 ^a | 12.88 ± 1.09 ^c | 0.016 ± 0.09 ^{ab} |
| Alcalase | 2.54 ± 0.34 ^a | 5.28 ± 0.21 ^a | 0.056 ± 0.068 ^b |
| Flavourzyme | 1.87 ± 0.98 ^a | 3.78 ± 0.08 ^a | 0.005 ± 0.17 ^a |
| Neutrase | 2.41 ± 2.66 ^a | 8.00 ± 0.28 ^b | 0.007 ± 0.19 ^a |
| Ascorbic acid (positive control) | 38.21 | 125.7 | 260.2 |

Control = spotted babylon protein wasn't digested from enzyme.

*DPPH scavenging effects of proteins were digested from 3 enzymes.

**ABTS scavenging effects of proteins were digested from 3 enzymes.

***NO scavenging effects of proteins were digested from 3 enzymes.

Table 11 Ultrafiltration separation (MW < 10 kDa) of protein hydrolysate from spotted babylon prepared by alcalase, flavourzyme and neutrase. Antioxidant activity assay was determined by DPPH, ABTS, nitric oxide activity. Values are the mean ± standard deviation (SD) (n = 3).

| Enzyme | MW (kDa) | IC ₅₀ (µg/ml) | | |
|----------------------------------|----------|---------------------------|---------------------------|-------------------------------|
| | | DPPH* | ABTS** | NO*** |
| Control | < 10 kDa | 4.10 ± 0.05 ^c | 15.07 ± 0.62 ^c | 0.034 ± 0.0019 ^b |
| Alcalase | < 10 kDa | 1.27 ± 0.24 ^b | 2.47 ± 0.11 ^a | 0.04 ± 0.007 ^b |
| Flavourzyme | < 10 kDa | 0.75 ± 0.04 ^a | 2.90 ± 0.12 ^a | 0.0017 ± 0.00037 ^a |
| Neutrase | < 10 kDa | 1.12 ± 0.09 ^{ab} | 4.13 ± 0.33 ^b | 0.002 ± 0.0004 ^a |
| Ascorbic acid (positive control) | | 38.21 | 125.7 | 260.2 |

Control = spotted babylon protein wasn't digested from enzyme.

*DPPH scavenging effects of proteins were digested from 3 enzymes.

**ABTH scavenging effects of proteins were digested from 3 enzymes.

***NO scavenging effects of proteins were digested from 3 enzymes.

4.4 Superoxide dismutase radical scavenging activity

Another important free radical is superoxide radical which encourage oxidative reactions in body because superoxide radical scavenging activity stimulates the dismutation of the superoxide anion (O_2^-), and then particularly important as the product of the one-electron reduction of O_2 . Table 12 shows % inhibition superoxide radical. Flavourzyme hydrolysate of crude protein obtains highest % inhibition of superoxide radical scavenging activity that is 73.7 ± 0.92 . The second is $64.66 \pm 0.21\%$ inhibition of neutrase hydrolysate. Then percent inhibition of alcalase, and control are 59.45 ± 2.86 and 53.62 ± 2.79 , respectively. All MW < 10 kDa of protein hydrolysate have value about 60-30 %inhibition.

Table 12 Crude protein and MW < 10 kDa of protein hydrolysate from spotted babylon prepared by alcalase, flavourzyme and neutrase. was measured percent inhibition of superoxide radical

| Enzyme | SOD (%inhibition) | |
|-------------|--------------------|---------------------|
| | Crude protein | <10kDa |
| Alcalase | 59.45 ± 2.86^a | $59.4. \pm 4.45^a$ |
| Flavourzyme | 73.7 ± 0.92^b | 58.72 ± 4.61^a |
| Neutrase | 64.67 ± 4.27^a | 53.36 ± 4.73^b |
| Control | 53.62 ± 2.79^c | $34.81. \pm 7.73^c$ |

4.5 Catalase activity

Catalase is enzyme found in nearly all living organisms revealed to oxygen, and then. It stimulates the decomposition of hydrogen peroxide to oxygen and water. Catalase is also an important antioxidant activity in body. This experiment shows results of catalase activity in Table 13. The highest catalase activity is

49.40±4.59 unit/ml of alcalase hydrolysate. Then, the second is 46.56±2.23 unit/ml of flavourzyme hydrolysate. Other samples have less values than 30 unit/ml.

Table 13 Crude protein and MW < 10 kDa of protein hydrolysate from spotted babylon prepared by alcalase, flavourzyme and neutrase. was measured unit/ml of catalase activity

| Enzyme | Catalase (unit/ml) | |
|-------------|-------------------------|-------------------------|
| | Crude protein | <10kDa |
| Alcalase | 23.43±2.20 ^a | 49.40±4.59 ^a |
| Flavourzyme | 17.51±1.81 ^b | 46.56±2.23 ^a |
| Neutrase | 17.11±0.94 ^b | 29±3.13 ^b |
| Control | 8.88±1.31 ^c | 12±0.81 ^c |

4.6. Glutathione peroxidase activity

Glutathione peroxidase is peroxidase activity whose important biological role is to protect the organism from oxidative damage. Then, The function of glutathione peroxidase reduces lipid hydroperoxides to their corresponding alcohols and to reduce free hydrogen peroxide to water. As shown in Table 14, the highest value is 6.2625±0.93 unit/ml of neutrase hydrolysate (MW < 10 kDa). The second is 5.8625±2.31 unit/ml of alcalase hydrolysate (MW < 10 kDa). Crude protein have glutathione peroxidase activity less than MW < 10 kDa of protein hydrolysate.

Table 14 Crude protein and MW < 10 kDa of protein hydrolysate from spotted babylon prepared by alcalase, flavourzyme and neutrase. was measured unit/ml of glutathione peroxidase activity

| Enzyme | GPx (unit/ml) | |
|-------------|--------------------------|--------------------------|
| | Crude protein | <10kDa |
| Alcalase | 2.9±0.20 ^a | 5.8625±2.31 ^a |
| Flavourzyme | 0.7375±0.73 ^b | 3.6±1.41 ^b |
| Neutrase | 2.4875±0.94 ^a | 6.2625±0.93 ^a |
| Control | 0.6375±1.01 ^b | 3.475±1.98 ^b |

4.7 Gel filtration chromatography

As shown in Figure 12 and Table 15, flavourzyme hydrolysate (MW < 10 kDa) was divided into 3 subfractions including F1, F2 and F3. Among the 3 subfractions, F3 fraction exhibited the good scavenging activity on DPPH radical, ABTS radical and nitric oxide with IC₅₀ values of 0.0075 ± 0.0021, 0.008 ± 0.0027 and 0.004 ± 0.001 µg/ml, respectively. Then, F1 and F2 have specifically IC₅₀ values of ABTS radical scavenging activity which possess 0.023 ± 0.007 and 0.011 ± 0.002 µg/ml, respectively, but DPPH radical scavenging activity and nitric oxide scavenging activity were not show results due to too little concentration of protein was not calculated IC₅₀ values. The results of purification by gel filtration chromatography found small protein molecule which was better result than large protein molecule. The same as Bougatef et al. (2010) reports the smallest molecule yielded the best results and Wang et al. (2013) reports that high peak was provided the good effect because there are many amino acid.

Table 15 The antioxidant activities of fractions from a column of Sephacryl S-200 gel filtration chromatography

| Activity assay | IC ₅₀ (µg/ml) | | |
|----------------|--------------------------|---------------|-----------------|
| | F1 | F2 | F3 |
| DPPH | > 0.058 | > 0.052 | 0.0075 ± 0.0021 |
| ABTS | 0.023 ± 0.007 | 0.011 ± 0.002 | 0.008 ± 0.0027 |
| NO | > 0.058 | > 0.052 | 0.004 ± 0.001 |

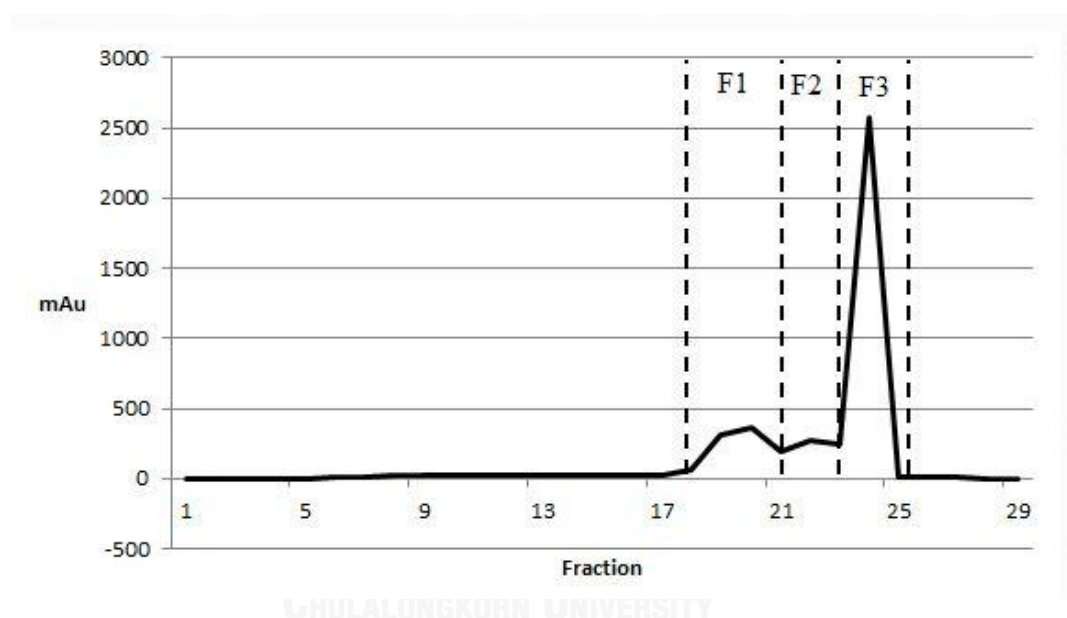


Figure 12 Chromatogram of flavourzyme hydrolysate protein (MW < 10 kDa) from Sephacryl S-200 gel filtration chromatography. Each fraction of the eluted solution was monitored at 280 nm.

4.8 Effects of spotted babylon hydrolysate on NO production in RAW 264.7 cells

The measurement of inhibited effect from spotted babylon hydrolysate on NO production and then RAW 264.7 cells were incubated with LPS (1 µg/ml) for overnight. The NO production in the culture medium was investigated by determination of the reduction of nitric oxide which is a stable metabolite of NO. As shown in Figure 13, the NO production of spotted babylon hydrolysate groups was

123.19 %, 281.02 %, 319.41 %, 323.47 %, 289.83 %, 272.15 %, 245.62 %, 221.63 %, 200.46 %, 180.62 %, 174.80 % and 164.03 % at the concentrations of 20, 10, 5, 2.5, 1.25, 0.63, 0.31, 0.16, 0.08, 0.04, 0.02 and 0.01 μM , respectively. The No production of control was 100 %. The results of this experiment was show inhibition of spotted babylon hydrolysate that was not inhibited NO production, but it stimulates to increase nitric oxide.

4.9 Cell viability in Raw 264.7 cells

The cytotoxic effect of spotted babylon hydrolysate in RAW 264.7 cells by using MTT assays. As shown in Figure 13, The control (treatment of LPS (1 $\mu\text{g}/\text{ml}$) alone) showed cytotoxic effect to RAW 264.7 cells which have differences between difference concentration of spotted babylon hydrolysate with control. When the macrophages cells were treated with 20, 10, 5, 2.5, 1.25, 0.63, 0.31, 0.16, 0.08, 0.04, 0.02 and 0.01 μM of spotted babylon hydrolysate which were found low cell viability is 36.71 % at concentration 20 μM and highest cell viability is 95.98 % at concentration 0.01 μM . The results indicated that up to the concentration about 0.63-0.01 μM of spotted babylon hydrolysate that did not affect RAW 264.7 cells. Combination the results of cell viability and NO production inhibitory effects was not exhibited the inhibitory effect of spotted babylon hydrolysate on NO production.

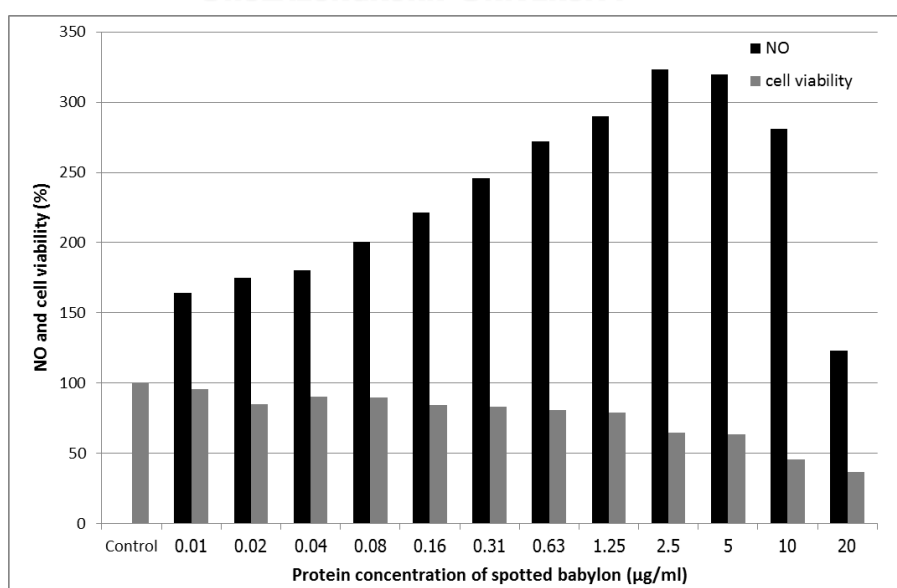


Figure 13 Inhibitory effect of spotted babylon hydrolysate on NO production in LPS stimulated RAW 264.7 cells and effect of spotted babylon hydrolysate on cell viability in RAW 264.7 cells.

4.10 RP-HPLC

The peptide fraction with the most active activity was further purified by reverse phase HPLC on a Shimpack C-18 column (250x46 mm) column with a linear gradient of acetonitrile 0.05% containing 0.1% trifluoroacetic acid (TFA) at a flow rate of 0.7 ml/min. The eluted peaks were monitored at 280 nm. As shown in Figure 14, The result showed 4 purified peaks. These peaks were collected for further characterization by mass spectrometer.

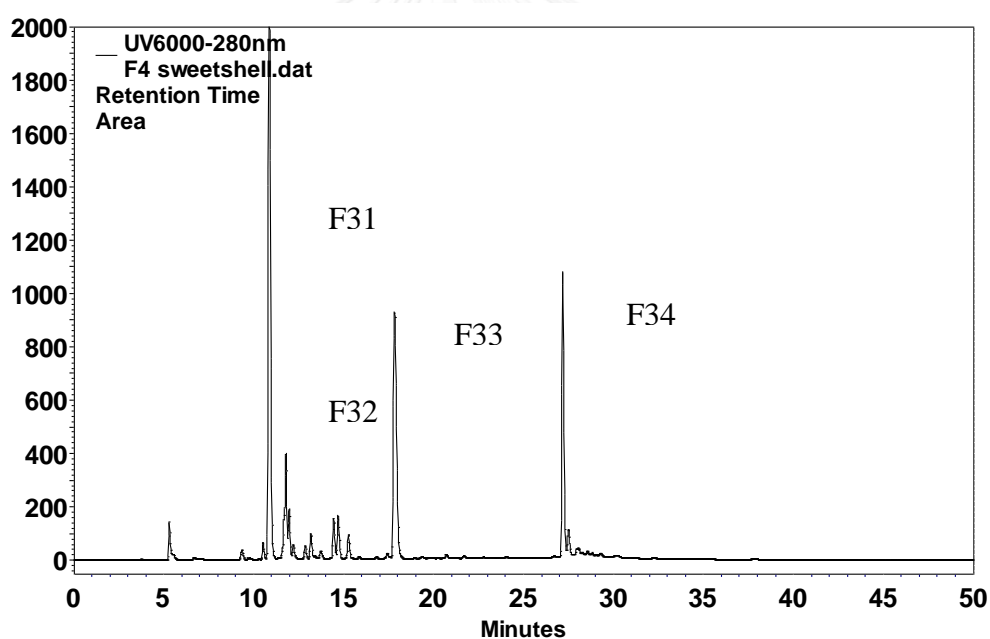


Figure 14 Chromatogram of fraction 4 from protein hydrolysate of spotted babylon (UV 280)

4.11 Mass spectrometry

The 4 bioactive peaks from RP-HPLC characterized by LC-MS/MS Q-TOF mass spectrometer. All peaks showed peptide sequence. In Table 16 showed 2 peptide chains of protein hydrolysate from peak 1. Peptide chains of protein hydrolysate

from peak 2, 3 and 4 showed in Table 17, 18 and 19, respectively. All peak had peptides that contain hydrophobic amino acid such as Pro, Leu, Ala, Trp and Phe, also show the highest antioxidant activity (Mendis, Rajapakse et al. 2005). In peak 1, 2 and 3, peptide chains contain aromatic amino acid Phe (F), Trp (W) and Tyr (Y) such as HTYHEVTKH (peak1) had Tyr (Y), WPVLAYHFT (peak2) had Phe (F), Trp (W) and Tyr (Y) and FAGRCKSTVE (peak3) contain Phe (F).

Hasegawa and co-worker (2012) study cysteine, histidine and glycine exhibit anti-inflammatory effects in human coronary arterial endothelial cells and Hasegawa and co-worker (2011) study exhibit anti-inflammatory effects in human monocytic leukemia cell line, THP-1 cells, there reports showed amino acids as Cys (C), His (H) and gly (G) possess anti-inflammation. Also, all peptide chains of protein hydrolysate contain amino acid (Cys(C), His(H) and gly (G) that show anti-inflammation. So, this purified peptide exhibited antioxidant and anti-inflammatory activity.

Table 16 Peptide sequence of peak 1 identified by LC-MS/MS Q-TOF

| Sequence | Organism | Mass | Query cover | Identity | Accession |
|---------------------|--|---------|-------------|----------|----------------|
| HTYHEVTKH | hypothetical protein LOTGIDRAFT_233146 [<i>Lottia gigantean</i>] | 1151.65 | 55% | 100% | XP_009056942.1 |
| | hypothetical protein OCBIM_22012557mg [<i>Octopus bimaculoides</i>] | 1151.65 | 55% | 100% | KOF89811.1 |
| | PREDICTED: myb-like protein W [Biomphalaria glabrata] | 1151.65 | 55% | 100% | XP_013080215.1 |
| | Pre-mRNA-splicing factor 38B [<i>Crassostrea gigas</i>] | 1151.65 | 55% | 100% | EKC31902.1 |
| | PREDICTED: ras-related protein Rab-18A isoform X2 [<i>Aplysia californica</i>] | 1151.65 | 55% | 100% | XP_005089064.1 |
| PSLDATVPS PVSAHA | cytochrome c oxidase subunit II (mitochondrion) | 1448.83 | 26% | 100% | AII23638.1 |

| | | | | | |
|--|---|---------|-----|------|----------------|
| | [<i>Babylonia areolata</i>] | | | | |
| | cytochrome c oxidase subunit II (mitochondrion) [<i>Babylonia areolata</i>] | 1448.83 | 26% | 100% | YP_008963244.1 |
| | NADH dehydrogenase subunit 5 (mitochondrion) [<i>Babylonia areolata</i>] | 1448.83 | 40% | 83% | AI23645.1 |
| | NADH dehydrogenase subunit 5 (mitochondrion) [<i>Babylonia areolata</i>] | 1448.83 | 40% | 83% | YP_008963252.1 |
| | Histone H3, partial [<i>Babylonia areolata</i>] | 1448.83 | 26% | 75% | AEP14878.1 |

Table 17 Peptide sequence of peak 2 identified by LC-MS/MS Q-TOF

| Sequence | Organism | Mass | Query cover | Identity | Accession |
|-----------|---|---------|-------------|----------|------------|
| WPVLAYHFT | cytochrome oxidase subunit I, partial (mitochondrion) [<i>Babylonia areolata</i>] | 1133.64 | 44% | 100% | ABS30401.1 |
| | cytochrome oxidase subunit I, partial (mitochondrion) [<i>Babylonia areolata</i>] | 1133.64 | 44% | 100% | ABS30400.1 |
| | cytochrome oxidase subunit I, partial (mitochondrion) [<i>Babylonia areolata</i>] | 1133.64 | 44% | 100% | ABS30390.1 |
| | cytochrome b (mitochondrion) [<i>Babylonia areolata</i>] | 1133.64 | 66% | 67% | AI23642.1 |

Table 18 Peptide sequence of peak 3 identified by LC-MS/MS Q-TOF

| Sequence | Organism | Mass | Query cover | Identity | Accession |
|---------------------|--|---------|-------------|----------|----------------|
| RGSTSSSRLN | NADH dehydrogenase subunit 4 (mitochondrion) [<i>Babylonia areolata</i>] | 1151.65 | 45% | 100% | AI23644.1 |
| | NADH dehydrogenase subunit 5 (mitochondrion) [<i>Babylonia areolata</i>] | 1151.65 | 81% | 67% | AI23645.1 |
| | ATP synthetase F0 subunit 8 (mitochondrion) [<i>Babylonia areolata</i>] | 1151.65 | 54% | 67% | AI23639.1 |
| | NADH dehydrogenase subunit 6 (mitochondrion) [<i>Babylonia areolata</i>] | 1151.65 | 18% | 100% | AI23641.1 |
| FAGRCKSTVE PVVKP | uncharacterized protein LOC106056025 [<i>Biomphalaria glabrata</i>] | 1617.97 | 52% | 100% | XP_013068028.1 |
| | PREDICTED: uncharacterized protein LOC101857057 [<i>Aplysia californica</i>] | 1617.97 | 40% | 100% | XP_012943224.1 |
| | Neurogenic locus notch-like protein 1 [<i>Crassostrea gigas</i>] | 1617.97 | 40% | 100% | EKC22858.1 |
| | hypothetical protein LOTGIDRAFT_230032 [<i>Lottia gigantea</i>] | 1617.97 | 40% | 100% | XP_009044487.1 |
| | hypothetical protein LOTGIDRAFT_158016 [<i>Lottia gigantea</i>] | 1617.97 | 73% | 60% | XP_009048841.1 |

Table 19 Peptide sequence of Peak 4 identified by LC-MS/MS Q-TOF

| Sequence | Organism | Mass | Query cover | Identity | Accession |
|------------|--|---------|-------------|----------|------------|
| RPSSSLPGKH | ATP synthetase F0 subunit 6 (mitochondrion) [<i>Babylonia lutosa</i>] | 1162.69 | 54% | 55% | AHH30668.1 |
| | ATP synthase F0 subunit 6 (mitochondrion) [<i>Babylonia lutosa</i>] | 1162.69 | 54% | 55% | ADU77469.1 |
| | NADH dehydrogenase subunit 2 (mitochondrion) [<i>Babylonia areolata</i>] | 1162.69 | 36% | 100% | AI23636.1 |
| | NADH dehydrogenase subunit 2 (mitochondrion) [<i>Babylonia lutosa</i>] | 1162.69 | 36% | 100% | AHH30665.1 |
| | NADH dehydrogenase subunit 4L (mitochondrion) [<i>Babylonia lutosa</i>] | 1162.69 | 18% | 100% | ADU77472.1 |

CHAPTER V

CONCLUSION

In this study, the best antioxidant activity peptide derived from spotted babylon was hydrolysed using flavozyyme hydrolysate compared to other enzymes by 2 testing. The first assay is non-enzymatic antioxidant by using DPPH, ABTS, and nitric oxide scavenging. Then, superoxide radical scavenging activity assay, catalase activity assay and glutathione peroxidase activity assay are enzymatic antioxidant of the second assay. Therefore, F3 fraction was purified by ultrafiltration (MW < 10 kDa) and gel filtration chromatography. 3 fractions were obtained from gel filtration chromatography. Thus, F3 fraction of gel filtration chromatography purification is the best fraction which was purified to RP-HPLC and mass spectrometry. RP-HPLC harvests 4 fraction that purified by mass spectrometry was obtained 6 sequence in 4 peak. After that, F3 fraction from gel filtration chromatography was tested in RAW 264.7 cells which are macrophage by inhibition of NO production assay and MTT assay. The results of cell viability and NO production inhibitory effects was not exhibited the inhibitory effect of spotted babylon hydrolysate on NO production.



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APPENDIX

จุฬาลงกรณ์มหาวิทยาลัย
CHULALONGKORN UNIVERSITY

APPENDIX A

Preparation of buffer and reagents

1. 20 mM Phosphate buffer pH 7.2

| | |
|-------------------------------|---------|
| 20mM KH_2PO_4 | 2.72 g |
| 20mM K_2HPO_4 | 8.71 g |
| 150mM NaCl | 8.77 g |
| Deionized water | 1000 ml |

Protocol: Mix 1000 ml deionized water with all reagents. Adjust the pH to 7.2 with KOH

2. Bradford solution

- Bradford stock solution

| | |
|---------------------|--------|
| 95% Ethanol | 100 ml |
| 88% Phosphoric acid | 200 ml |
| SERVA Blue G | 350 g |

- Bradford working buffer

| | |
|-------------------------|--------|
| Deionized water | 425 ml |
| 95% Ethanol | 15 ml |
| 88% Phosphoric acid | 30 ml |
| Bradford stock solution | 30 ml |

Note: Before using, Bradford working buffer must be filtered through the Whatman No.1 paper. It is stored in a brown glass bottle at room temperature.

Protocol: 1. Pipet protein solution into 96 well plates 20 μl .

2. Add Bradford working buffer 200 μl and shake.

3. Read A_{595} after 2 minutes but before 1 hour.

3. DPPH solution

| | |
|------------|----------|
| 0.1 M DPPH | 0.004 mg |
| Methanol | 100 ml |

Protocol: 1. Pipet protein solution into 96 well plates 40 μ l.
 2. Add DPPH solution 160 μ l and incubate 20 min in the dark room.
 3. Shake and Read the absorbance at 517 nm.

4. ABTS solution

- 7 mM ABTS (solution A)

Dissolve 0.096 g ABTS in 25 ml deionized water.

- 2.45 mM potassium persulphate (solution B).

Dissolve 0.016 g potassium persulphate in 25 ml deionized water

- ABTS solution

Mix solution A and solution B in the dark room for 12 – 16 hours before using. Before use it, dilute ABTS solution with distilled water to obtain an absorbance value of 0.7 ± 0.02 at 734 nm

Protocol: 1. Pipet protein solution into 96 well plates 10 μ l.
 2. Add ABTS solution 300 μ l and incubate 10 min.
 3. Shake and Read the absorbance at 734 nm

5. Nitric oxide method

- 0.1% (w/v) N- (1-Naphthyl) ethylenediamine dihydrochloride (NED)

Dissolve 0.1 g NED in 100ml deionized water.

- 10 mM sodium nitroprusside (SND) in PBS pH 7.2

Dissolve 0.29 g Sodium nitroprusside in 100 ml Phosphate buffer pH 7.2

- 0.33% (w/v) sulfanilamide in 20% acetic acid

Start with dissolve 0.33 g sulfanilamide in 100 ml 20% acetic acid (20 ml acetic in 80 ml distilled water.

Protocol : 1. Pipet protein solution into 96 well plates 25 μ l.
 2. Add SNP 25 μ l and incubate 2.5 h
 3. Add 0.33% (w/v) sulfanilamide 100 μ l and incubate 5 min
 4. Add 0.1% NED 100 μ l and incubate 30 min
 5. Shake and read the absorbance at 540 nm

6. Media: Complete DMEM

| | |
|--------------------------|------|
| DMEM | 100% |
| Fetal Bovine Serum (FBS) | 10% |

7. MTT solution

| | |
|----------------------|------|
| 5 mg/ml MTT solution | |
| MTT | 5 mg |
| Deionized water | 1 ml |

Protocol: dissolve 5 mg MTT with 1 ml deionized water.

8. LPS 1 μ g/ml

| | |
|--------------------|-----------|
| LPS 500 μ g/ml | 4 μ l |
| DMEM | 2 ml |

9. Mobile phase in RP-HPLC analysis**- Eluent A: 0.1% trifluoroacetic acid (TFA), 1000 ml**

start with add 1 ml TFA into 999 ml double deionized water followed by filtration using a cellulose acetate membrane.

- Eluent B: 70 % acetonitrile containing 0.05% TFA, 1000 ml

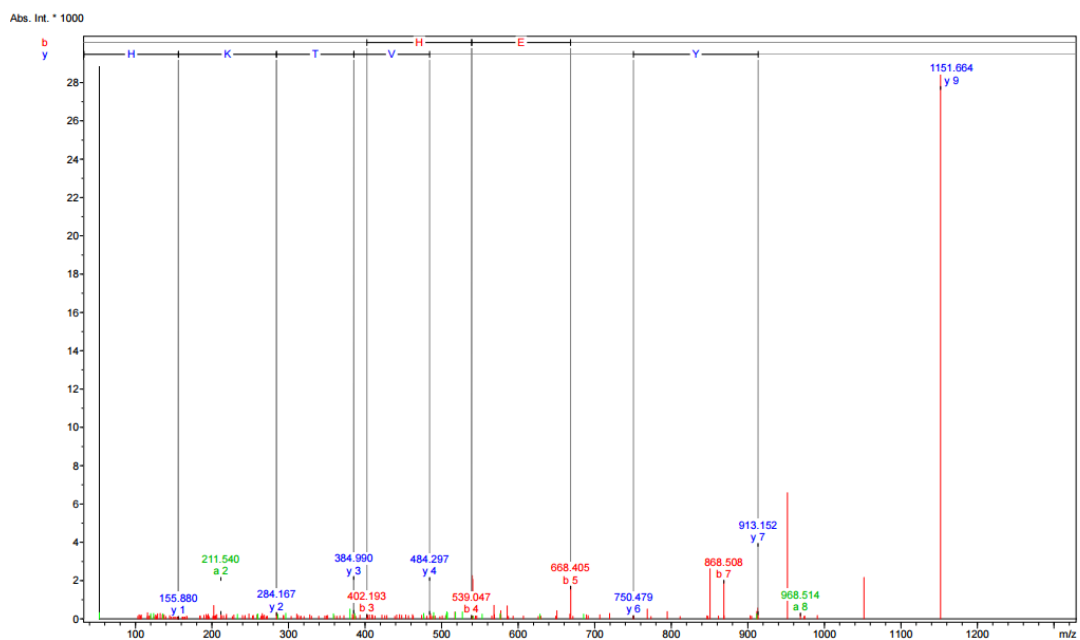
start with adding 300 ml 0.05% TFA in double deionized water into 700 ml 70% acetonitrile and mixing followed by filtration using PTFE membrane.

APPENDIX B

PEAK1

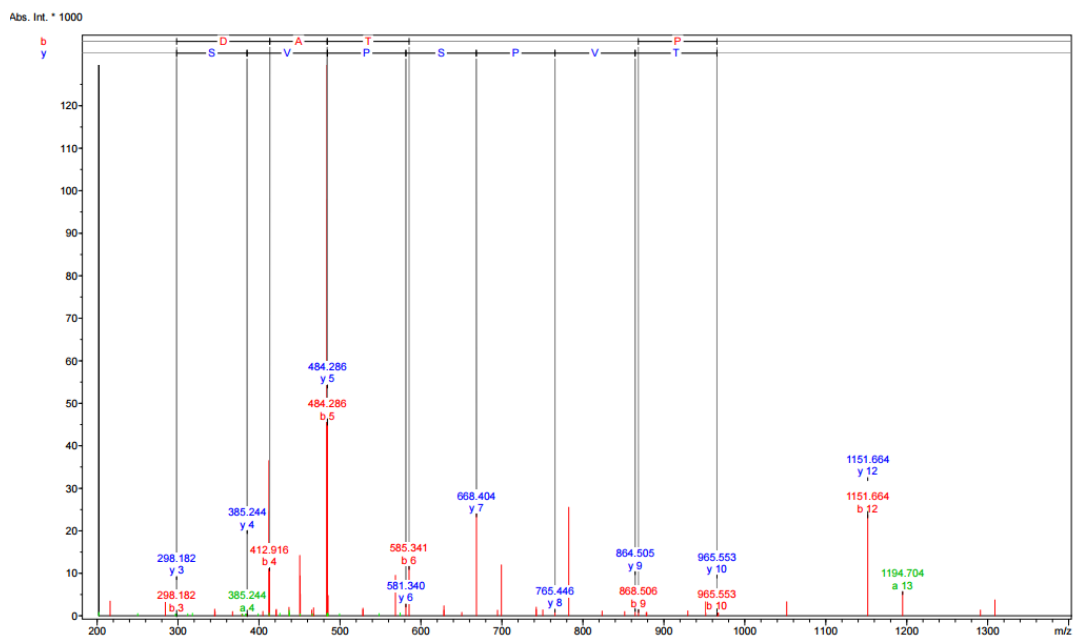
Sequence 1: .HTYHEVTKH

| | | | | |
|-------------------|-------|-----------------|-------------|-------------------------|
| | | | Parentmass: | 1151.658 |
| Mass Error: | 0.098 | MH+ (mono): | 1151.560 | MH+ (avg): 1152.242 |
| Threshold (a.i.): | 0.000 | Tolerance (Da): | 0.500 | Number of Peaks: 201 |
| Above Threshold: | 201 | Assigned Peaks: | 13 | Not assigned Peaks: 188 |



Sequence 2: PSLDATVPSPVSAHA

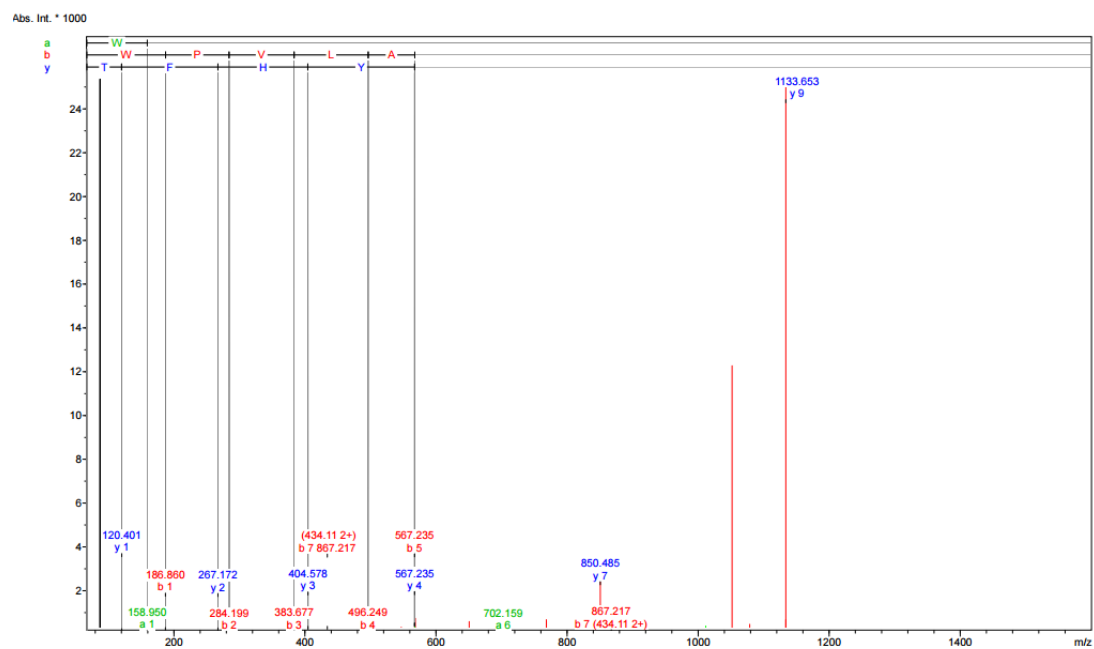
| | | |
|-------------------------|-----------------------|------------------------|
| Parentmass: | 1448.837 | |
| Mass Error: 0.098 | MH+ (mono): 1448.739 | MH+ (avg): 1449.588 |
| Threshold (a.i.): 0.000 | Tolerance (Da): 0.500 | Number of Peaks: 87 |
| Above Threshold: 87 | Assigned Peaks: 13 | Not assigned Peaks: 74 |



PEAK2

Sequence 1: WPVLAYHFT

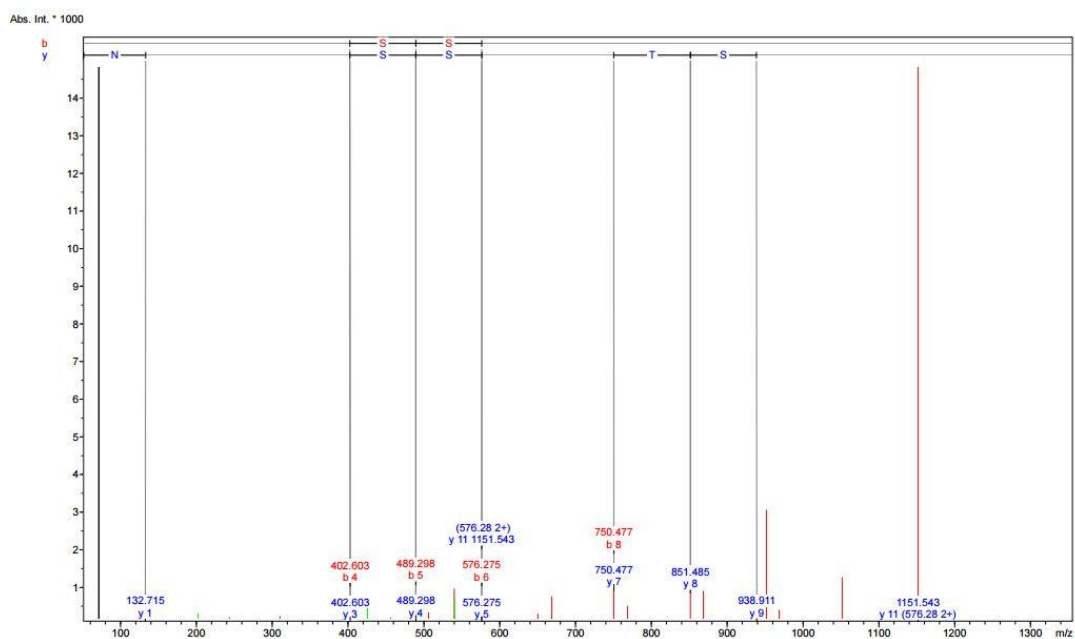
| | | | |
|-------------------|-------|---------------------|----------|
| | | Parentmass: | 1133.649 |
| Mass Error: | 0.071 | MH+ (mono): | 1133.578 |
| | | MH+ (avg): | 1134.308 |
| Threshold (a.i.): | 0.000 | Tolerance (Da): | 0.500 |
| | | Number of Peaks: | 161 |
| Above Threshold: | 161 | Assigned Peaks: | 13 |
| | | Not assigned Peaks: | 148 |



PEAK3

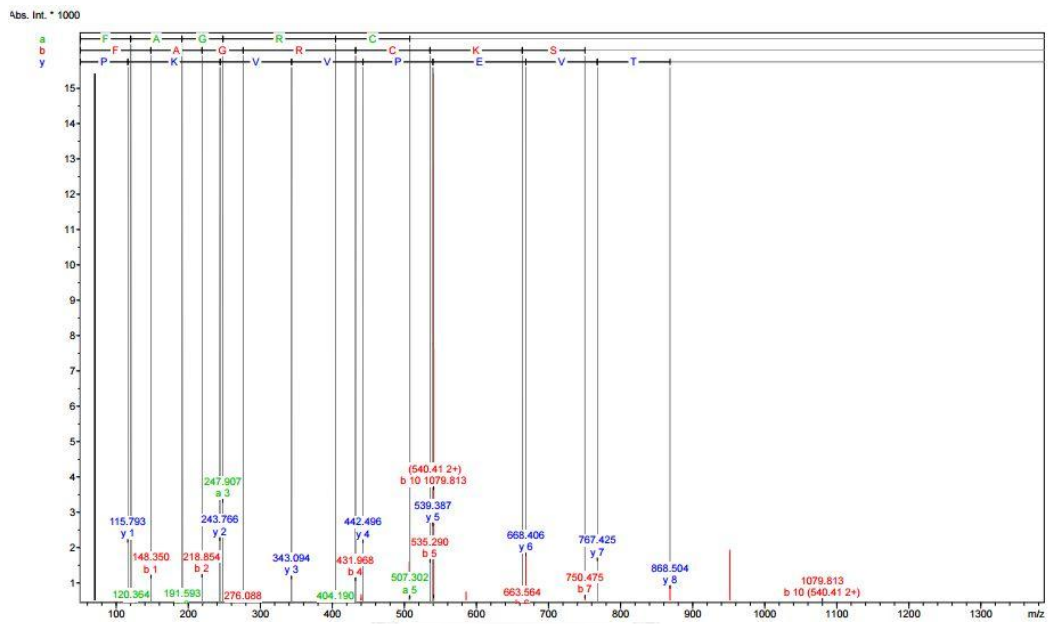
Sequence 1: RGSTSSSSRLN

| | | |
|-------------------------|-----------------------|------------------------|
| Parentmass: | 1151.659 | |
| Mass Error: 0.082 | MH+ (mono): 1151.577 | MH+ (avg): 1152.199 |
| Threshold (a.i.): 0.000 | Tolerance (Da): 0.500 | Number of Peaks: 55 |
| Above Threshold: 55 | Assigned Peaks: 8 | Not assigned Peaks: 47 |



Sequence 2: FAGRCKSTVEPVWKP

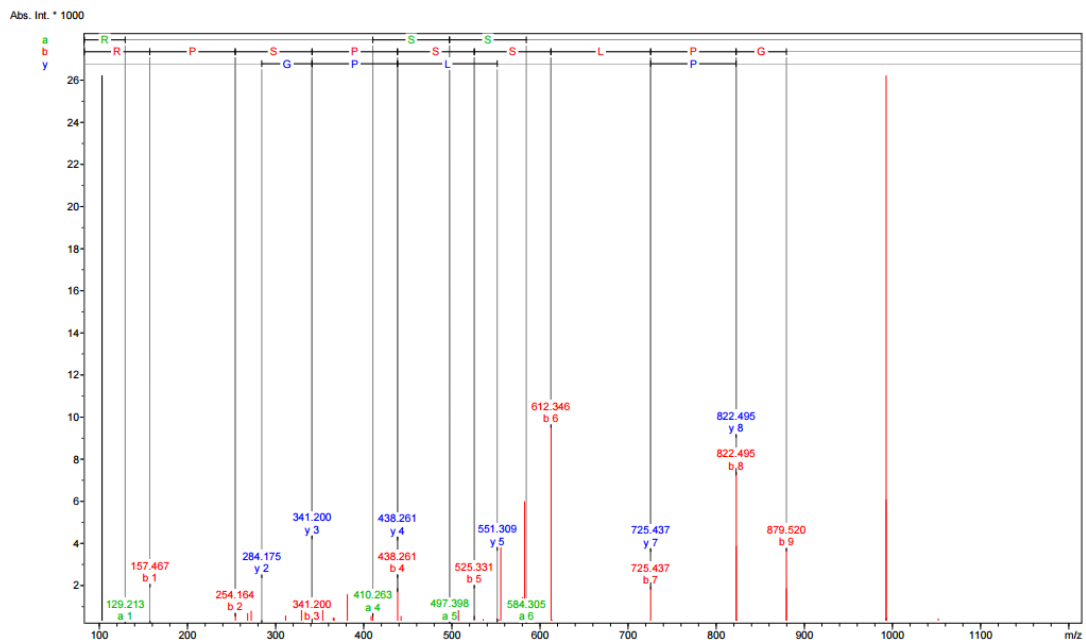
| | | | |
|-------------------|-------|-----------------------|-------------------------|
| | | | Parentmass: 1617.975 |
| Mass Error: | 0.096 | MH+ (mono): 1617.879 | MH+ (avg): 1618.923 |
| Threshold (a.i.): | 0.000 | Tolerance (Da): 0.500 | Number of Peaks: 198 |
| Above Threshold: | 198 | Assigned Peaks: 21 | Not assigned Peaks: 177 |



PEAK4

Sequence 1: RPSPSSLPGKH

| | | |
|-------------------------|-----------------------|-------------------------|
| Parentmass: | 1162.691 | |
| Mass Error: 0.058 | MH+ (mono): 1162.633 | MH+ (avg): 1163.310 |
| Threshold (a.i.): 0.000 | Tolerance (Da): 0.500 | Number of Peaks: 144 |
| Above Threshold: 144 | Assigned Peaks: 15 | Not assigned Peaks: 129 |



VITA

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