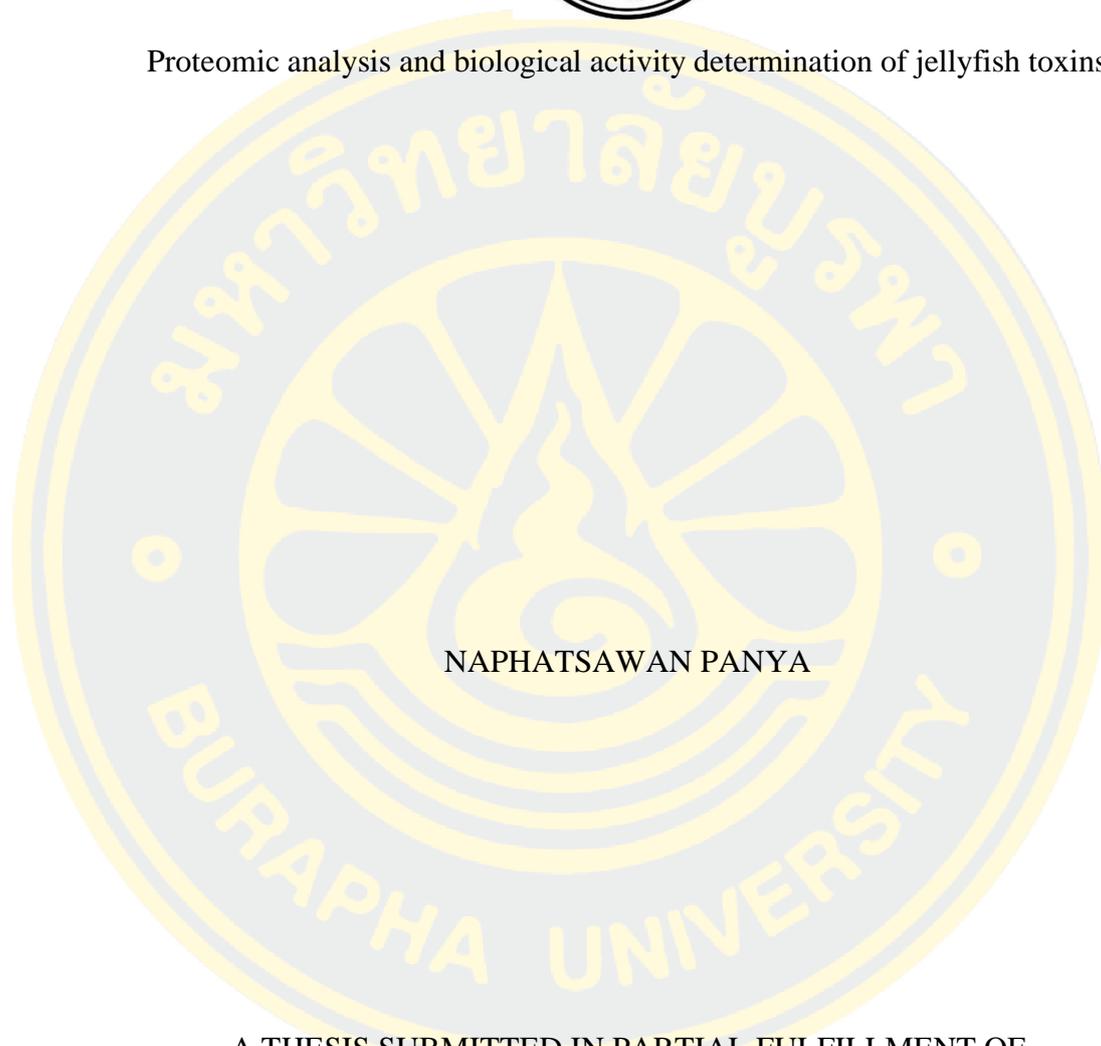




Proteomic analysis and biological activity determination of jellyfish toxins



NAPHATSAWAN PANYA

A THESIS SUBMITTED IN PARTIAL FULFILLMENT OF
THE REQUIREMENTS FOR MASTER OF SCIENCE

IN BIOCHEMISTRY

FACULTY OF SCIENCE

BURAPHA UNIVERSITY

2021

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การวิเคราะห์โปรตีนโอมิกส์และการศึกษาฤทธิ์ทางชีวภาพของพืชแมงกะพรุน



นภัสวรรณ ปัญญา

วิทยานิพนธ์นี้เป็นส่วนหนึ่งของการศึกษาตามหลักสูตรวิทยาศาสตรมหาบัณฑิต

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ลิขสิทธิ์เป็นของมหาวิทยาลัยบูรพา

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The Thesis of Naphatsawan Panya has been approved by the examining committee to be partial fulfillment of the requirements for the Master of Science in Biochemistry of Burapha University

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NAPHATSAWAN PANYA : PROTEOMIC ANALYSIS AND
BIOLOGICAL ACTIVITY DETERMINATION OF JELLYFISH TOXINS.

ADVISORY COMMITTEE: WAEOWALEE CHOKSAWANGKARN, , SALIL
CHANROJ 2021.

In recent years, incidence of jellyfish expansion has been increasing by several factors, including global warming, overfishing, and adjustment environment for aquaculture. Jellyfish envenomation can cause many symptoms, such as inflammation, swelling, pain, and lethal, depending on the jellyfish species. These symptoms are caused by the toxin proteins released from the jellyfish nematocyst. This study focuses on proteomic analysis of the venom proteins from nematocysts of edible (*Rhopilema hispidum*) and highly venomous (*Sanderia malayensis*) jellyfish to understand the causes of clinical symptoms. In addition, three biological activities (hemolytic, angiotensin I-converting enzyme (ACE) inhibitory and acetylcholinesterase (AChE) inhibitory activities) of the venoms from both jellyfish species were also investigated. In this work, proteins obtained from two different extraction methods, including SDS coupled with sonication and PBS buffer coupled with ultrasonication were used prior to LC-MS/MS analysis. The results showed that using PBS extraction was a better method for protein extraction than SDS extraction. Difference in protein profiles of edible jellyfish and highly venomous jellyfish was observed. However, biological functions of proteins identified from these two species were mostly similar, including metalloprotease, neurotoxic, and hydrolase functions. Interestingly, pore-forming proteins were only identified from highly toxic jellyfish. Moreover, higher number of proteins identified was obtained from highly venomous jellyfish (883 proteins), as compared to edible jellyfish (809 proteins). These might be important factors causing stronger toxicity. For biological activities determination, hemolytic and AChE inhibitory activities were only observed from edible jellyfish. The toxin CaTX-A identified from edible jellyfish was possible cause of hemolytic activity. However, the ACE inhibitory activity of toxins from both jellyfish was not presented. This study provided more understanding about the toxin components from

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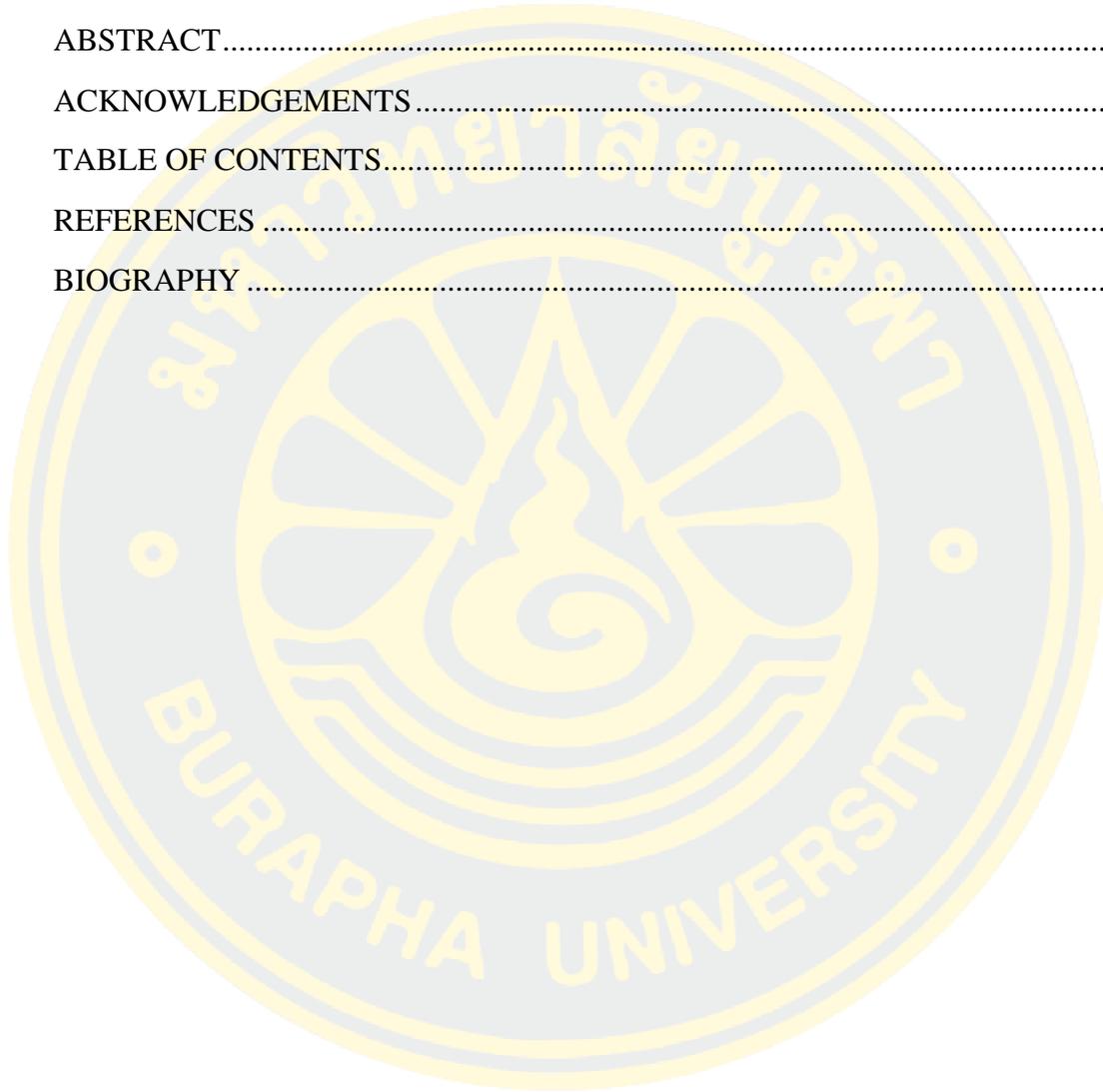
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This study was mainly supported by Research Grant of Burapha University, Thailand through the National Research Council of Thailand (Grant No. 45.4/2562). And I would like to acknowledge Faculty of Science, Burapha University and the Center of Excellence for Innovation in Chemistry (PERCH-CIC), Commission on Higher Education, Ministry of Education, and Bangkok, Thailand, for their financial supports. In addition, this work was partially supported by Science Innovation Facility, Faculty of Science Burapha University (SIF-IN-620918) and Graduate School, Burapha University, Fiscal Year 2020.

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KEYWORD: JELLYFISH VENOM/ *R. hispidum*/ *S. malayensis*/ PROTEOMICS/
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NAPHATSAWAN PANYA: PROTEOMIC ANALYSIS AND
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CHAPTER 1

INTRODUCTION

Nowadays, the jellyfish population has been increasing and causes serious global issues in marine environment. It could be resulted from global warming, eutrophication, overfishing and modification of the marine environment for fishery (Dong, Liu, & Keesing, 2010). Jellyfish is a venomous animal which contains various toxins that can be harmful to the tourist in a coastal area. Jellyfish envenomation could cause many clinical symptoms to human such as pain, itch, swelling, skin inflammation, and hypotension. Toxins from some jellyfish species could interfere with the nervous system, and even cause fatality. Jellyfish venoms are located in a specialized organelle, which contains harpoon-like structures of toxic strings, called nematocyst. The major active components in the jellyfish venoms are various types of proteins (Li et al., 2016; Li et al., 2018). Discharge of venom-containing sting in the nematocyst can be triggered by skin rubbing or tentacle traction resulted from external stimulation. After the nematocyst discharge, venom can be injected and penetrated into the tissues, causing inflammation, pain, swelling and itching and leading to skin necrosis in more severe cases (Cegolon, Heymann, & Mastrangelo, 2013). There was previous report about first aid guideline to decrease the nematocyst discharge by using seawater or acetic acid in order to remove sting on the skin. However, acetic acid should be avoided in some species, such as *Nemopilema nomurai*, *Physalia physalis*, and *Chrysaora quinquecirrha*. Using ethanol and ammonia can cause more severe damage due to nematocyst discharging induced by those chemicals (Pyo et al., 2016; Birsa, Verity, & Lee, 2010). Currently, antivenom is available for only the box jellyfish (*Chironex fleckeri*) sting treatment (Currie, 2003). For other jellyfish species, there are no effective procedure to treat the patients with jellyfish poisoning, only symptomatic treatment is available. Further studies are needed for discovering jellyfish venom drug target for more effective treatment (Lakkis, Maalouf, & Mahmassani, 2015).

This study focuses on proteomic analysis of edible jellyfish (*Rhopilema hispidum* Vanhöffen, 1888) found in Bangsaen coastal area and highly venomous

jellyfish or Amakusa jellyfish (*Sanderia malayensis*). Currently, there are no information about proteome of the venom from these two species. It is interesting and necessary to characterize the types of toxic proteins in the jellyfish, in order to use them as a target for treatment, such as development of antivenom to neutralize the specific toxin. In additions, proteins identified from the jellyfish could potentially be developed as novel drugs for medical applications, as found in previous reports about other protein-based drugs from the cone snail and sea anemone. Ziconotide is a commercial name for proteins isolated from cone snail, which has been used as pain reliever for patient with severe pain from neurological damage and cancer progression. It is known to be more effective than morphine (McGivern, 2007). And another study indicated that venom proteins from sea anemone has been continuously developed to use as a drug for autoimmune disease (Prentis, Pavasovic, & Norton, 2018).

There are several challenges for analysis of jellyfish venom proteome, including optimization of sample preparation techniques, optimization of separation and detection methods for proteins with various molecular weight ranges, and implementation of data analysis workflow without a complete protein database. Bottom-up proteomics is a commonly used method for protein identification. With this technique, proteins are digested with proteases to produce peptides with specific amino acid residue at the N- or C-termini prior to the analysis by LC-MS/MS. The MS/MS spectra of peptides can be searched against a chosen protein database to identify the peptide sequences, with the criteria of specific enzyme treatment. In the absence of enzyme-specific residue in the venoms, small proteins could not be digested by proteases, leading to no identification from the mass spectra. Moreover, with protein separation by SDS-PAGE, small peptides can pass through the gel matrix and fall-off gel, resulting in no peptide identification. To overcome these limitations, top-down proteomic experiment was employed for studying small proteins, in addition to the bottom-up approach. Top-down proteomics is an approach for identification of intact protein without digestion, so complete sequence coverage of the protein can be obtained. Moreover, there are previous reports about small proteins or peptides from several venomous animals that possess biological functions, such as antimicrobial peptides from wasp and scorpion venom, anticoagulants from leech

venom, analgesic peptides from cone snail venom, and antitumor proteins from scorpion venom (Beeton, 2013). It is plausible that small proteins from the jellyfish could be developed as drugs for medical application in the future.

Furthermore, various toxic effects of the jellyfish venom have been investigated, such as hemolytic, cytotoxic, neurotoxic, and cardiotoxic activities. It was previously reported that the venom of some jellyfish, such as *Rhopilema esculentum*, *Cyanea nozakii*, and *Stomolophus meleagris* showed hemolytic effect (Yu et al., 2007; Li et al., 2011; Feng et al., 2010). In the same genus of *Rhopilema hispidum*, hemolytic activity was found from the toxins of *Rhopilema spp.* (Jafari, Honari, Zargan, & Jahromi, 2019). And in the close family of *Sanderia malayensis*, hemolytic activity was previously reported from the venoms of *Pelagia noctiluca* (Marino, Morabito, Pizzata, & La Spada, 2008). Therefore, hemolytic activity was determined from the toxins of *R. hispidum* and *S. malayensis* in this study.

In addition, other biological activities of angiotensin I-converting enzyme (ACE) inhibitory activity were investigated from jellyfish venoms to find new drug for application in hypertension treatment. Inhibition of angiotensin I-converting enzyme was previously reported from the venom peptide of box jellyfish (*Chiropsalmus quadrigatus*) (So et al., 2016). Moreover, ACE inhibitory activity had been found from the protein hydrolysate of *R. hispidum* (Sun et al., 2018). Thus, we were interested in ACE inhibitory activity from the venom of edible and highly venomous jellyfish.

Moreover, inhibition of acetylcholinesterase (AChE) was also evaluated from venoms of edible and highly venomous jellyfish. Since there was previous report about anticholinesterase activities from crude venom of *Pelagia noctiluca*, which butyrylcholinesterase had similar function as acetylcholinesterase (Ayed et al., 2012). This biological activity could be beneficial for medical application to treatment of Alzheimer's disease.

1.1 Objective

1. To identify proteins from the nematocyst of edible jellyfish (*Rhopilema hispidum* Vanhöffen, 1888) and highly venomous jellyfish (*Sanderia malayensis*).

2. To evaluate biological activities, including hemolytic, acetylcholinesterase inhibitory, and angiotensin I-converting enzyme inhibitory activities of the venoms from both species.

1.2 Hypothesis

1. Proteome of *Rhopilema hispidum*, (Vanhöffen, 1888) and *Sanderia malayensis* are different.

2. Nematocyst proteins from *Rhopilema hispidum*, (Vanhöffen, 1888) and *Sanderia malayensis* possess biological activities.

1.3 Advantage

1. Identification of venom proteome from edible jellyfish (*Rhopilema hispidum* Vanhöffen, 1888) and highly venomous jellyfish (*Sanderia malayensis*) can be beneficial for development of antivenom to treatment of jellyfish envenomation.

2. Toxin proteins from jellyfish with biological activity could be applied in medical application.

1.4 Scope of research

The proposes of this study are to identify proteins from nematocyst of two jellyfish species (*Rhopilema hispidum*, (Vanhöffen, 1888) and *Sanderia malayensis*. Mass spectrometry-based proteomic approach was employed to identify proteins. Autolysis method was used to extract nematocysts from jellyfish tentacles. Toxin proteins were extracted from nematocyst by using two methods, including using 2% SDS coupled with sonication, and PBS buffer coupled with ultrasonication. After extraction, proteins were subjected to either bottom-up and top-down proteomic analysis using the nanoHPLC interfaced with the Q-Exactive Orbitrap mass analyzer. The bottom-up approach was used for identification of venom proteins with high complexity. And the top-down approach was employed for analysis of small proteins. Database searching was performed to identify proteins from the mass spectra. In addition, small proteins derived from top-down proteomics were identified using De Novo sequencing. Gene ontology annotation of those proteins was also carried out to categorize the functions of identified proteins. Furthermore, biological activities of

jellyfish toxin proteins were evaluated, including, hemolytic, acetylcholinesterase inhibitory, and angiotensin I-converting enzyme inhibitory activity activities.



CHAPTER 2

LITERATURE REVIEWS

2.1 Jellyfish

Jellyfish is marine invertebrate belonging to the phylum of Cnidaria. Two major groups of Cnidaria consists of Anthozoa and Medusozoa. The Anthozoa shows the characteristics of solitary polyps attached to the seabed, such as sea anemones, true corals and sea pens; while Medusozoa are mostly live as a free-swimming medusa and polyps forms (Technau & Steele, 2011). The Medusozoa is the main group of jellyfish, which can be classified into four classes, including Hydrozoa, Scyphozoa, Cubozoa, and Staurozoa (Technau, Genikhovich, & Kraus, 2015) (Figure 2-1). Hydroids and Portuguese Man O' War are in the class of Hydrozoa. True jellyfish are in the class of Scyphozoa. Box jellyfish were considered in the class of Cubozoa. And stalked jellyfish was classified in the Staurozoa class. The body of jellyfish can be divided into two parts, bell body and tentacles (Cegolon et al., 2013). Bell body part is used for their movement. Tentacle part is used for catching the preys. Jellyfish venom can be found in both parts of their body, but mostly found in the tentacles. The longest part of jellyfish life cycle is in the form of free-floating medusa (Badré, 2014). Jellyfish venoms are located in the special organelle called nematocyst, containing active toxin components (Kang et al., 2009). Some species of jellyfish with mild stings can be consumed as seafood (Hsieh, Leong, & Rudloe, 2001) and applied as biomarker for scientific research by using their green fluorescence proteins (Tsien, 1998; Technau et al., 2015).

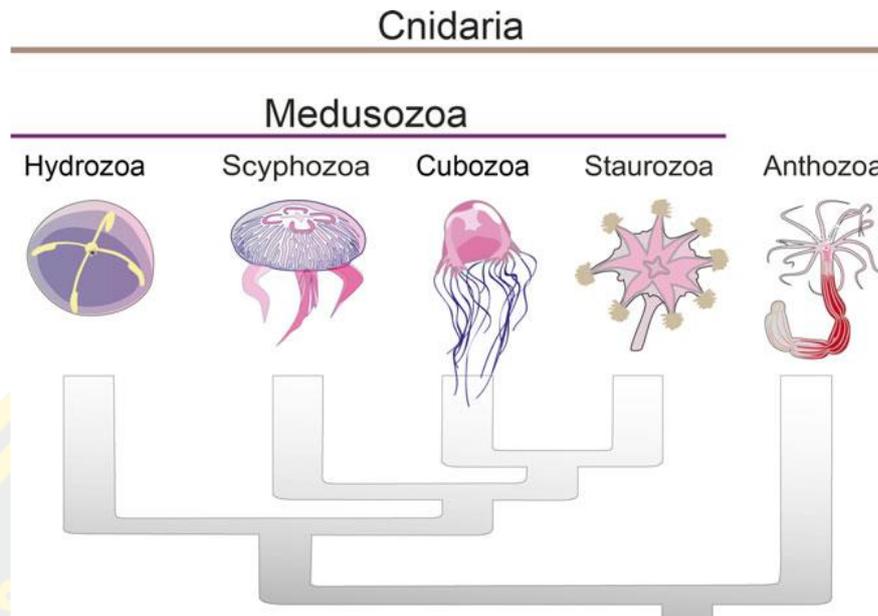


Figure 2-1. The phylogenetic tree of Cnidaria (Technau et al., 2015).

2.1.1 *Rhopilema hispidum*

Rhopilema hispidum (Vanhöffen, 1888) or edible jellyfish are in the class of Scyphozoa. Their toxins have a mild effect to human. Their bell bodies have rough surface with the diameters in a range of 120 to 650 mm. There are brown spots on the bell body, as shown in the figure 2-2A (Gul & Morandini, 2015). This species was found in many countries, such as Pakistan, Vietnam, China, Malaysia, and Japan (Gul & Morandini, 2015; Nishikawa, Thu, Ha, & Thu, 2008; Rizman-Idid, Farrah-Azwa, & Chong, 2016; Omori & Kitamura, 2004). Particularly, *Rhopilema hispidum* is the main species for commercial harvest in the Gulf of Thailand (Kondo et al., 2020).

2.1.2 *Sanderia malayensis*

Sanderia malayensis (Goette, 1886) or Amakusa jellyfish is a highly venomous jellyfish (Figure 2-2B). They are members of Scyphozoa class. Their bell diameters are in a range of 3 to 8 cm. Sixteen long tentacles are located at the edge of bell. The bell body of this species is colorless or light-yellow. There are four mouth-arms located in the middle of the bell. Reddish spots may found over the bell and mouth-arms (Morandini & Gul, 2016; Fenner, Burnett, & Rifkin, 1996). They were found in the coast of many countries, including Singapore, Pakistan, China, and Japan

(Kramp, 1961; Morandini & Gul, 2016; Xian, Kang, & Liu, 2005; Wakabayashi et al., 2012).

2.1.3 Jellyfish expansion and incidence of jellyfish envenomation

Currently, it was found that jellyfish population have been expanding in the coastal areas, which could be resulted from overfishing, eutrophication, global warming, translocation and aquatic animal habitat modification for fishery (Dong et al., 2010; Dong, 2019). The blooming of *Sanderia malayensis* had been reported in Yangtze Estuary, China. Jellyfish blooms affect the fishery, fish habitat and breeding due to consumption of fish eggs and larvae by the jellyfish. (Xian, Kang, & Liu, 2005).

Due to the jellyfish expansion worldwide, the incidence of jellyfish envenomation increases every year. After human skin is in contact with the stings, the nematocysts can be discharged and the toxins are injected into the skin (Figure 2-4). The toxin envenomation leads to various symptoms, such as pain, inflammation, swelling, itching, skin necrosis, and death. (Cegolon et al., 2013). Kawahara, Uye, Burnett, and Mianzan (2006) reported that three species of edible jellyfish, which were *Rhopilema hispidum*, *Rhopilema esculentum* and *Nemopilema nomurai*, could cause eruption, pruritus, and cutaneous symptoms, respectively. In July 2013, there was another report stated that toxins from *Rhopilema hispidum* can cause dermatitis and oedema on the skin (Kondo et al., 2020). In 2001, there were 136 victims including 18 persons who have serious symptoms stung by *Aurelia aurita* around the coast of Changdong province of China (Dong et al., 2010). Furthermore, ranging from 2010 to 2016 in Guadeloupe (French), there were 211 patients being stung by jellyfish, which 95 patients had Irukandji syndrome, probably relevant to *Alatina alata* (Bouyer-Monot, Pelczar, Ferracci, & Boucaud-Maitre, 2017). Another reported showed that the number of patients from envenomation was up to 1500 cases in Korea during 2009-2013. For instance, in 2012, there was a child died within 4 hours after envenomation by *Nemopilema nomurai*, which caused pulmonary oedema (Kim, Han, & Durey, 2018). Moreover, from 1994, up to 63 cases were died after being stung by the most dangerous jellyfish (*Chironex fleckeri*) in the region of Australian waters (Tibballs, 2006).

This project focuses on characterization of toxin proteins from edible jellyfish (*Rhopilema hispidum*) and highly venomous jellyfish (*Sanderia malayensis*) (Figure 2-2). These two species are in Scyphozoa class and can be harmful to the human. (Adler & Jarms, 2009; Gul & Morandini, 2015).

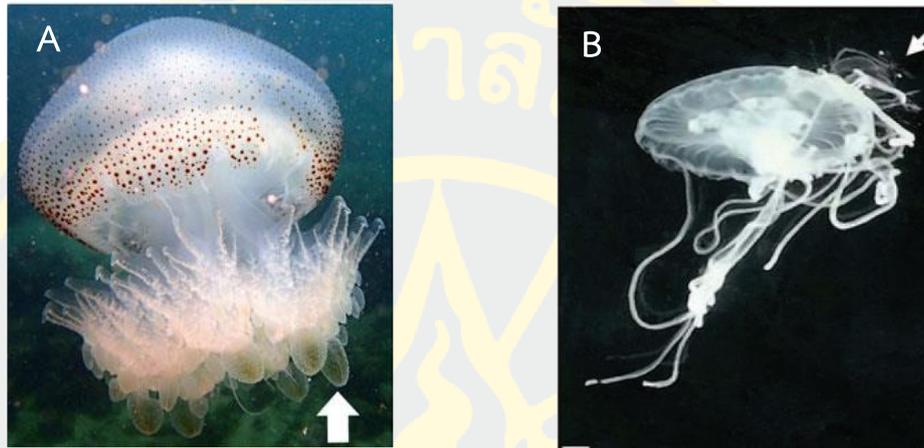


Figure 2-2. (A) Edible jellyfish (*Rhopilema hispidum*) (Gul & Morandini, 2015) and (B) amakusa jellyfish (*Sanderia malayensis*) (Wakabayashi et al., 2012)

2.1.4 Nematocyst

The specialized cells called cnidocyte are present among organisms in the phylum of Cnidaria, such as corals, sea anemones, and jellyfish. Nematocyst is considered as the secretory organelles with various sizes (5-100 μm) and shapes, within the cnidocyte. This organelle can be used to capture the prey and to prevent the predator because it contains a mixture of toxin proteins. There are 25-30 types of nematocysts (Figure 2-3), which were classified from their morphologies and the character of nematocyst discharge (Kass-Simon & Scappaticci, 2002; David et al., 2008; Beckmann & Özbek, 2012). The types of nematocysts have been considered by shape along with the tube characters of nematocyst releasing toxins. (Kass-Simon & Scappaticci, 2002).

For the jellyfish, there are many types of nematocysts from various species of jellyfish. Previous study reported about four types of nematocysts, small ellipsoid isorhiza, medium round isorhiza, large round isorhiza, and rhopaloid, which were

found from *Rhopilema hispidum* (Kondo et al., 2020). Currently, there is a lack of information about nematocyst types of *Sanderia malayensis*.

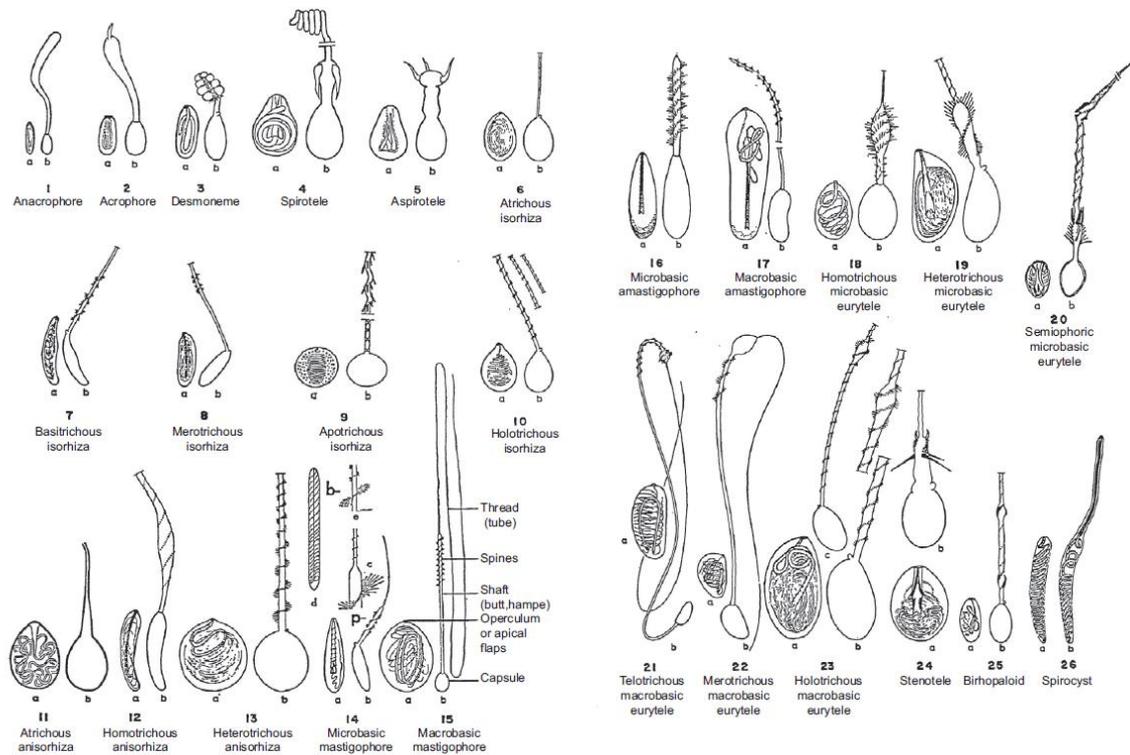


Figure 2-3. Characterization of nematocyst types (Folino-Rorem, 2015).

Rapid discharge of nematocyst can occur after stimulation by human skin contact. The discharge was proposed to be involved with removing calcium bound ions on the wall of nematocyst capsule. This calcium ion removing can increase osmotic pressure in the nematocyst and lead to nematocyst discharge, releasing toxins to the human skin (Figure 2-4) (Cegolon et al., 2013; Lubbock & Amos, 1981).

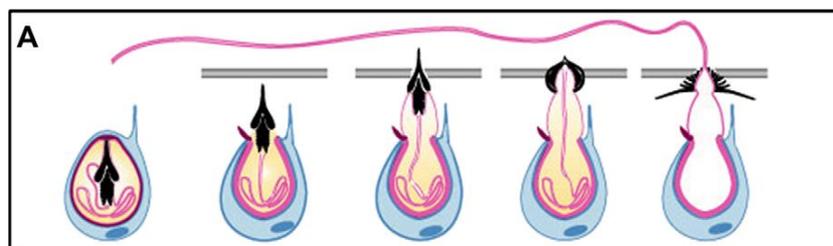


Figure 2-4. Mechanism of nematocyst discharge after being contacted with the prays (Özbek, Balasubramanian, & Holstein, 2009).

2.2 Proteomics

The name of “Proteome” is derived from a combination of protein and genome. Proteomics is a large-scale study of proteins produced by a cell, an organism or a tissue at a chosen timeframe for analysis of structure, expression and functions of the proteins (Ballesté, 2018; Suna & Mayr, 2018). Challenges in proteomic study resulted from complexity of proteins in the samples including post-translational modifications, such as glycosylation, phosphorylation and protein degradation (Suna & Mayr, 2018). Knowledge gained from proteomic studies, e.g., targeted protein quantitation, chemical proteomics, protein expression, protein-protein interactions and post-translational modification were widely used for applications in pharmaceutical and medical fields. (Yokota, 2018). The method for analyzing proteome can be divided to three important steps, including sample preparation, data acquisition from mass spectrometers and bioinformatics (Legg, McKiernan, & Reisdorph, 2017).

2.3 Mass spectrometry-based proteomics

High performance liquid chromatography followed by tandem mass spectrometry (HPLC-MS/MS) is useful tools for proteomic analysis. This instrument helps to identify thousand-number of proteins in a short time. After sample preparation step including, protein enrichment, digestion and pre-fractionation, proteins or peptides are subjected to HPLC for separation and injected to the mass spectrometer for mass measurement. (Legg et al., 2017). There are three main methods for data acquisition using the mass spectrometer (Noor, Mohamedali, & Ranganathan 2019, Suna & Mayr, 2018) (Figure 2-5).

1. Data dependent acquisition (DDA)

The DDA approach is commonly used for discovery proteomics. Using DDA, mass to charge ratio of the precursor are scanned with a certain mass range, then the most abundant precursor ions can be sequentially selected for fragmentation (MS/MS). Data acquired in form of ms/ms spectrum can be used for database searching or *de novo* sequencing and interpreted as peptide sequences.

2. Targeted proteomics

Targeted proteomics is an experiment for both quantification and identification of proteins of interest. This method is applicable for analysis of low abundant proteins. Previously known precursor ions can be selected for fragmentation in tandem mass spectrometry and the acquired spectra can be analyzed quantitatively and qualitatively.

3. Data independent acquisition (DIA)

DIA approach is a combination of DDA and targeted proteomics. All of precursor ions from MS1 spectrum are selected for fragmentation to identify both high and low abundant proteins. Sequentially, MS2 spectrum of all precursor ions are acquired by using tandem mass spectrometry with high mass accuracy.

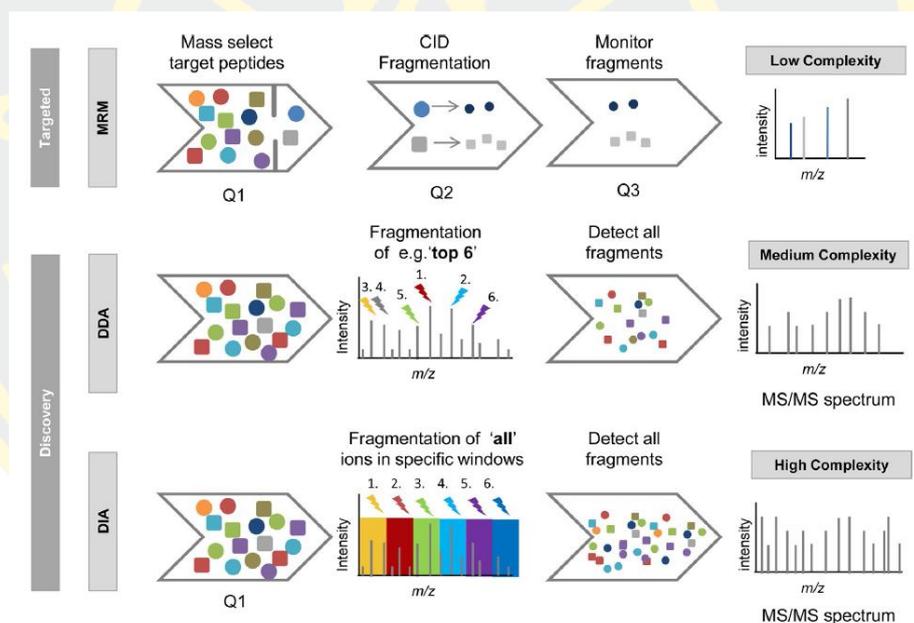


Figure 2-5. Three approaches for mass spectrometry-based proteomics (Suna & Mayr, 2018).

There are three main approaches for sample preparation and protein identification using mass spectrometry as categorized by masses of proteins or peptides, which are “bottom-up” (~500-3000 Da), “middle-down” (~3000 – 20000 Da) and “top-down” (~<50 kDa) approaches (Switzar, Giera, & Niessen, 2013) (Figure 2-6).

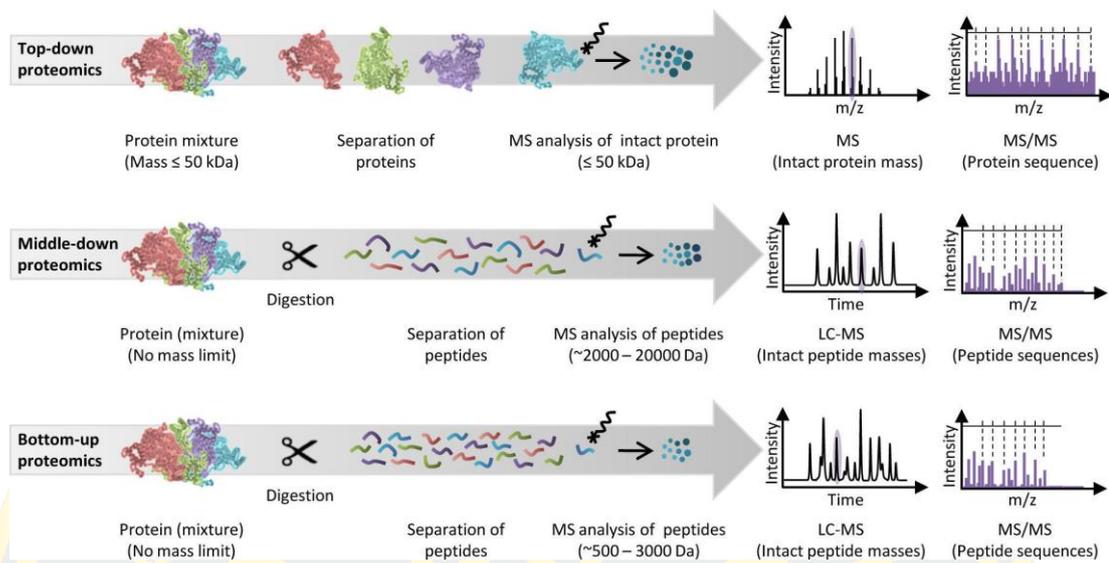


Figure 2-6. Three approaches for protein identification using mass spectrometry (Switzar et al., 2013).

In bottom-up proteomics, proteins are digested with proteases prior to separation by HPLC and analysis by MS/MS. This method is most commonly employed and suitable for the samples with high complexity (Suna & Mayr, 2018; Kennani, Crespo, Govin, & Pflieger, 2018) (Figure 2-7). In top-down proteomics, intact proteins without digestion are analyzed and fragmented using MS/MS. This method is suitable for analysis of samples with less complexity, and it is advantageous for characterization of the post-translational modifications. It is necessary to use the instrument with high mass accuracy for determination of complete protein sequences (Noor et al., 2019) (Figure 2-7). In middle-down proteomics, there is a process similar to bottom-up proteomics by digestion of the proteins; however, generated peptides from the middle-down approach are larger than those from bottom-up approach. Thus, these three experiments can be considered based on the size and complexity of the proteins.

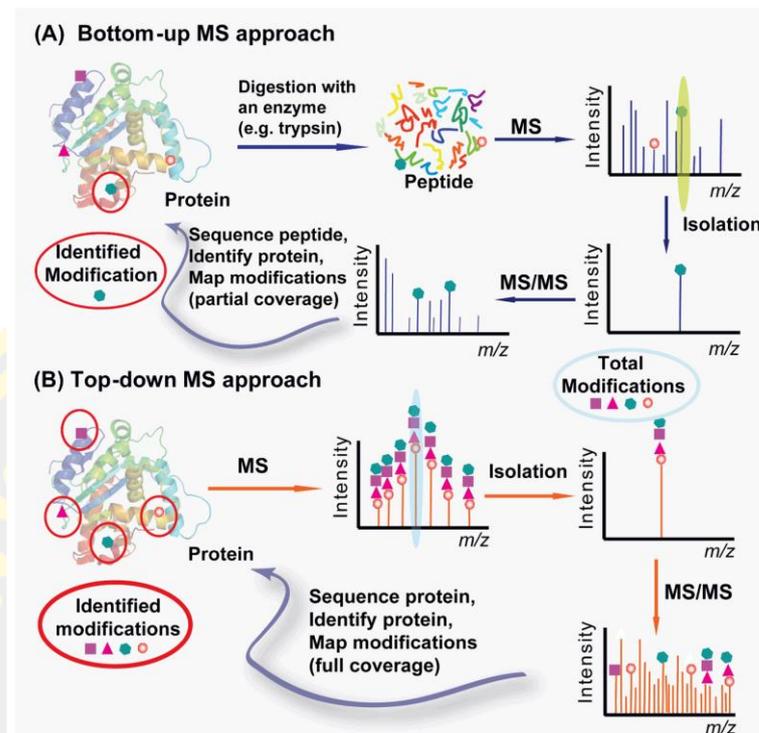


Figure 2-7. Description picture of Bottom-up and top-down proteomics (Zhang & Ge, 2011).

2.4 Sample preparation methods for jellyfish venom proteomics

Since venom proteins are resided in nematocyst, methods for extraction of the venoms should be optimized prior to the proteomic analysis. The sample preparation was started with nematocyst extraction from jellyfish tentacles. Nematocysts can be extracted by various experiments, such as tentacle grinding by using pestle and mortar (Endean, Duchemin, McColm, & Fraser, 1969), autolysis in seawater (Bloom et al., 1998), and osmotic rupture by using cold distilled water (Marino et al., 2007). After nematocysts obtained by extraction, following, venom proteins were extracted from nematocyst. There were several methods for venom protein extraction using chemical or physical forces to disrupt the nematocysts. Jouiaei et al. (2015) and Carneiro et al. (2011) reported that the discharge of nematocysts was induce by using absolute ethanol and freeze-thaw cycles, respectively. In another experiment of venom protein extraction, nematocysts were broke with sound waves vibration by using sonication or ultrasonication (Ayed, Sghaier, Laouini, & Bacha, 2016; So et al., 2016). And

homogenization techniques by using glass beads was performed to extract venom protein from nematocysts (Carrette & Seymour, 2004).

2.5 Types and function of toxins from various jellyfish species

There are various types of jellyfish species which their venoms contain distinct types of proteins as showed on table 2-1. Various functions of toxins were reported, including cytotoxic, neurotoxic, hemolytic, myotoxic, and pore-forming toxins. (Table 2-1). At present, there is no study about types of proteins found in the nematocysts of *Rhopilema hispidum* and *Sanderia malayensis*.

Table 2-1. Toxin protein identified from many jellyfish species.

Jellyfish species	Proteins	Functions	References
<i>Aurelia aurita</i>	metalloproteinases	Cytotoxicity	Lee et al. (2011); Mariottini & Pane (2010); Merquiol, Romano, Ianora, & D'Ambra (2019)
	phospholipase A2	Neurotoxicity, myotoxicity, haemolytic, cytolytic	
	Proteolytic enzymes	Neurotoxic, hemolytic, myotoxic, local skin irritation	
	Tetramine and unidentified protein	Dermotoxic, temporary paralysis, oedema	
	TX-1		
	TX-2		
<i>Chironex fleckeri</i>	Phospholipase A2	Cytolytic, hemolytic	Merquiol et al. (2019); Badré (2014); Brinkman & Burnell (2007); Brinkman et al. (2014); Lee et al. (2016)
	CfTX-1	Pore-forming cnidarian toxin, myotoxic cardiotoxic, cytotoxic, hemolytic	
	CfTX-2	Pore-forming cnidarian toxin, myotoxic cardiotoxic, cytotoxic, hemolytic	
	CfTX-A	Pore-forming cnidarian toxin, cytotoxic, hemolytic	

	CfTX-B	Pore-forming cnidarian toxin, cytotoxic and hemolytic	
	CfTX-Bt	Cardiotoxic, cytotoxic, dermonecrotic, lethal	
<i>Carybdea alata</i>	CaTX-A (CAH1)	Hemolytic	Badré (2014); Brinkman & Burnell (2007); Lassen, Helmholtz, Ruhnau, & Prange (2011); Lee et al. (2016); Merquirol et al. (2019)
	CaTX-B	Hemolytic	
<i>Carybdea rastonii</i>	CrTX-A	Hemolytic	Badré (2014); Lassen et al. (2011)
	CrTX-B	Hemolytic	
<i>Chiropsalmus quadrigatus</i>	CqTX-A	Hemolytic, lethal	Badré (2014); Brinkman & Burnell (2007); Frazão & Antunes (2016); Lee et al. (2016); Mariottini (2014); Merquirol et al. (2019)
<i>Cyanea capillata</i>	CcTX-1	Cytotoxic	Badré (2014); Lassen et al. (2011); Wang et al. (2018)
	CcNT	Neurotoxic	
	Alpha-latrotoxin-Lh1a	Neurotoxic	
	Delta-latroinsectotoxin-L	Neurotoxic	
	T1a	Neurotoxic	
	Cholecystoxin	Neurotoxic	
	Long neurotoxin-1	Neurotoxic	
Ophiophagus venom	Neurotoxic		

	Conotoxin-like toxins	Neurotoxic	
	Cytotoxin-11	Pore-forming toxins	
<i>Cyanea lamarckii</i>	CIGP-1	Cytotoxic	Badré (2014); Frazão & Antunes (2016)
<i>Chiropsalmus quadrumanus</i>	Actinoporin	Pore-forming toxins	
<i>Tamoya haplonema</i>	Actinoporin	Pore-forming toxins	Jaimés-Becerra et al. (2017)
<i>Chrysaora lactea</i>	Latarcin	Pore-forming toxins	
<i>Carukia barnesi</i>	Phospholipase A2	Cytolytic, hemolytic	Merquirol et al. (2019)
	CbTX-I	Neurotoxic	
	CbTX-II	Neurotoxic	
<i>Cyanea nozakii</i>	Metalloproteinases	Cytotoxicity	Lee et al. (2011); Li et al. (2011)
	CnPH	Hemolytic	
<i>Carybdea marsupialis</i>	CmNt	Neurotoxic	Sanchez- Rodriguez et al. (2006)
<i>Malo kingi</i>	MkTX-A	Dermonecrotic, inflammatory	Frazão & Antunes (2016); Merquirol et al. (2019)
	MkTX-B		
<i>Nemopilema nomurai</i>	Metalloprotease	Cytotoxicity gelatinolytic, caseinolytic, fibrinolytic	Lee et al. (2011); Wang et al. (2018); Merquirol et al. (2019)
	Alpha-latrotoxin- Lh1a	Neurotoxic	
	Neurotoxin Nk- 3FTx	Neurotoxic	
	Conotoxin-like toxins	Neurotoxic	
	CqTX-A	Pore-forming toxins	
	CrTX-A	Pore-forming toxins	
	MAC/perforin domain containing	Pore-forming toxins	
	Lysenin	Pore-forming toxins	
<i>Stomolophus</i>	SmP90	Radical scavenging	Li et al. (2012);

<i>meleagris</i>	SmTX	Hemolytic	Li et al. (2013); Mariottini (2014); Merquirol et al. (2019)
	Phospholipase A2	Cytotoxic, cytolytic, hemolytic, local tissue damage	
	C-lectin		
	ShK		
	Kv+ toxin		
	Metalloproteinases		
<i>Physalia physalis</i>	Physalitin	Hemolytic	Badré, (2014); Mariottini (2014); Merquirol et al. (2019)
	P1	Neurotoxic	
	P3	Neurotoxic	
	PpV9.4	Hemolytic	
	PpV19.3	Neurotoxic, cardiotoxic	
	Elastase Histamine	Musculotoxic, cytolytic, hemolytic	
	Collagenase	Cytolytic, hemolytic	
	DNase	Cytolytic, hemolytic	
<i>Rhopilema esculenta</i>	Metalloproteinases	Cytotoxicity	Lee et al. (2011)
<i>Pelagia noctiluca</i>	Proteinaceous macromolecules	Hemolytic, cytotoxic, dermonecrotic, hemolytic, local tissue damage	Merquirol et al. (2019)
<i>Phyllorhiza punctata</i>	Saxitoxin	Neurotoxic	Carneiro et al. (2011); Merquirol et al. (2019)
	Gonyautoxin-4	Neurotoxic	
	Tetrodotoxin	Neurotoxic	
	Brevetoxin-2	Neurotoxic	
	Phospholipase A2	Neurotoxic	
<i>Olindias sambaquiensis</i>	Oshem1	Hemolytic	Badré (2014); Merquirol et al. (2019)
	Oshem2	Hemolytic	
	Metalloproteinases	Cytolytic, neurotoxic	

2.6 Medical applications of venom proteins from other marine animals

Nowadays, toxins from marine animals have been used for various medical treatments, such as severe pain treatment by toxin peptide from cone snail or called conotoxin (McGivern, 2007). The conotoxin comprises of 25 amino acids (Figure 2-8 that were found from *Conus magus*. Ziconotide is the commercial name of this conotoxin (Miljanich, 2004). Prentis, Pavasovic, and Norton (2018) reported that toxin from sea anemone (Figure 2-10), in the phylum of cnidaria, could be developed for autoimmune diseases treatment, because their toxin peptides could block

potassium channel. There were two peptides from sea anemone, including ShK and BgK peptides that were isolated from *Stichodactyla helianthus* and *Bunodosoma granulifera*, respectively (Beeton, 2013). These two peptides are still under developing for use in medical treatment. The ShK peptide contains 35 amino acids and 37 amino acids of BgK peptide (Norton, Pennington, & Wulff, 2004; Rauer, Pennington, Cahalan, & Chandy, 1999) (Figure 2-9).

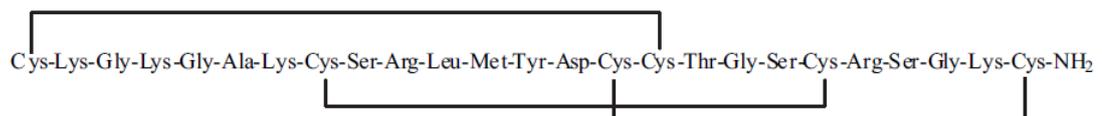


Figure 2-8. A peptide chain of conotoxin from cone snail (Miljanich, 2004)



Figure 2-9. ShK and BgK toxin peptides from sea anemone (Rauer, Pennington, Cahalan, & Chandy, 1999).

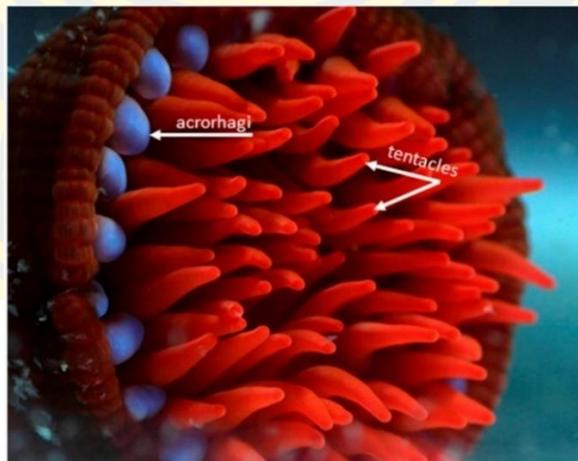


Figure 2-10. Sea anemone (Prentis et al., 2018).

2.7 Biological activity of jellyfish toxins

The jellyfish venom contains a mixture of active proteins with various functions, which could be utilized as the bioactive compounds. Many previous studies reported biological activities of proteins from jellyfish venoms, including, antioxidant,

hemolytic, cytotoxic, cardiotoxic and neurotoxic activities (Table 2-2). The study of biological activities of jellyfish proteins could lead to their future medical utilization. From the literature, there is still a lack of information about some biological activities of proteins found in *Rhopilema hispidum* and *Sanderia malayensis*.

Table 2-2. Previous studied about biological activities from venom of several jellyfish species.

Jellyfish species	Biological activities	Reference
<i>Pelagia noctiluca</i>	Analgesic, antibutyrylcholinestrasic, anti-proliferative and anti-inflammatory activities	Ayed et al. (2012); Ayed et al. (2016)
<i>Phyllorhiza punctata</i>	Neurotoxicity	Carneiro et al. (2011)
<i>Chironex fleckeri</i>	Cardiotoxicity, Cytotoxicity and hemolytic activities	Chaousis et al. (2014); Ramasamy, Isbister, Seymour, & Hodgson (2005); Badré (2014)
<i>Nemopilema nomurai</i>	Cardiotoxicity, cytotoxicity, hemolytic, and anticancer activities	Choudhary et al. (2015); Kang et al. (2009); Choudhary et al. (2018); Lee et al. (2017)
<i>Cyanea nozakii</i>	Hemolytic, cytotoxicity activities	Feng et al. (2010); Li et al. (2011); Lee et al. (2011)
<i>Carybdea marsupialis</i>	Neurotoxicity	Lazcano-Pérez et al. (2017)
<i>Cyanea capillata</i>	Cytotoxicity, hemolytic and cardiovascular toxicities	Lassen et al. (2011); Xiao et al. (2011)
<i>Stomolophus meleagris</i>	Antioxidant, hemolytic, toxicity activities	Li et al. (2012); Li et al. (2013); Li et al. (2014)
<i>Cassiopea andromeda</i>	Acetylcholinesterase inhibitory and cardiotoxicity activities	Mohebbi et al. (2018); Nabipour, Mohebbi, Vatanpour, & Vazirizadeh (2017)

<i>Carukia barnesi</i>	Cardiovascular	Ramasamy et al. (2005)
<i>Rhopilema esculentum</i>	Hemolytic activity	Yu et al. (2007)



CHAPTER 3

RESEARCH METHODOLOGY

3.1 Materials and equipment

3.1.1 Equipment

1. 3M™ Empore™ C18 Extraction Disks (Fisher scientific, USA)
2. Amicon® Ultra – 0.5 ml centrifugal filter units (Merck Millipore Ltd., Carrigtwohill Co. Cork, Ireland)
3. Axio Lab. A1 Laboratory Microscope (Carl Zeiss, Germany)
4. Agilent Cary Eclipse fluorescence spectrophotometer (Agilent, USA)
5. Centrifuge (Z 326 K, HERMLE Labortechnik GmbH, Germany)
6. Diode-Array spectrophotometer (HEWLETT PACKARD, Germany)
7. Incubator (Binder, Germany)
8. Mass spectrometer (Q Exactive™ Hybrid Quadrupole Orbitrap Mass Spectrometer, ThermoFisher Scientific, USA)
9. Maxquant software version 1.6.2.6a
10. Micropipette (Eppendorf, USA)
11. Microplate reader (Versamax, USA.)
12. Parafilm (Pechiney, USA)
13. PEAKS software (Bioinformatics Solutions Inc., Canada)
14. Protein LoBind Tube 1.5 and 2.0 ml (Eppendorf, USA)
15. RunBlue 4-12% Bis-Tris Gel (expedon, UK)
16. SDS-PAGE apparatus (Bio-Rad, USA)
17. Sonicator (VCK 500 Sonics and material, Germany)
18. SpeedVac concentrator (Savant, USA)
19. Thermo Xcalibur 2.2 software (Thermo, Bremen, Germany)

3.1.2 Chemicals

1. Acetonitrile (Fisher Chemical, Belgium)
2. Acetylcholinesterase (Sigma-Aldrich, USA)

3. Acetylthiocholine iodide (Tokyo Chemical Industry, Tokyo, Japan)
4. Angiotensin-converting enzyme (Sigma-Aldrich, USA)
4. Albumin, Bovine Serum (Calbiochem, USA)
6. Ammonium Bicarbonate (Sigma-Aldrich, USA)
7. BCA protein assay kit (Thermo Scientific, USA)
8. 2-Chloroacetamide (Sigma-Aldrich, USA)
9. Captopril (Sigma-Aldrich, USA)
10. Dithiothreitol (Sigma-Aldrich, USA)
11. Di-Sodium hydrogen phosphate (Merck Millipore Ltd., Darmstadt, Germany)
12. Di-Sodium tetraborate decahydrate (Merck Millipore Ltd., Darmstadt, Germany)
13. 5,5'-Dithiobis (2-nitrobenzoic acid) (DTNB) (Tokyo Chemical Industry, Tokyo, Japan)
14. Ethylenediamine tetraacetic acid (EDTA) (Omnipur, India)
15. Phenylmethylsulfonyl fluoride (PMSF) (Omnipur, China)
16. Formic acid (Merck Millipore Ltd., Darmstadt, Germany)
17. Galanthamine hydrobromine (Calbiochem, USA)
18. InstantBlue staining solution (Expedeon, UK)
19. Jupiter® 15 µm C18 300 Å (Phenomenex, USA)
20. LDS Sample 4x concentrate (Expedeon, UK)
21. Molecular weight marker (Bio-rad, USA)
22. MES Run Buffer – 20x (Expedeon, UK)
23. N, N, N', N'-tetramethylethylenediamine (Bio-Rad, USA)
24. N-[3-(2-Furyl) acryloyl]-Phe-Gly-Gly (FAPGG) (Sigma-Aldrich, USA)
25. Pierce™ Quantitative Fluorometric Peptide Assay kit (Thermo Scientific, USA)
26. Potassium chloride (Merck Millipore Ltd., Darmstadt, Germany)
27. Potassium dihydrogen phosphate (Merck Millipore Ltd., Darmstadt, Germany)
28. Sodium dodecyl sulfate (Omnipur, China)

29. Sodium chloride (Chem™, Bangkok, Thailand)
30. Sucrose (Ajax Finechem Pty Ltd, Australia)
31. Triton X-100 (Merck Millipore Ltd., Darmstadt, Germany)
32. Sequencing Grade Modified Trypsin, Porcine (Promega, USA)

3.2 The overview of this research

Venom proteome from edible jellyfish (*Rhopilema hispidum*) and highly venomous jellyfish (*Sanderia malayensis*) were studied in this project. The workflow diagram is shown in figure 3-1.

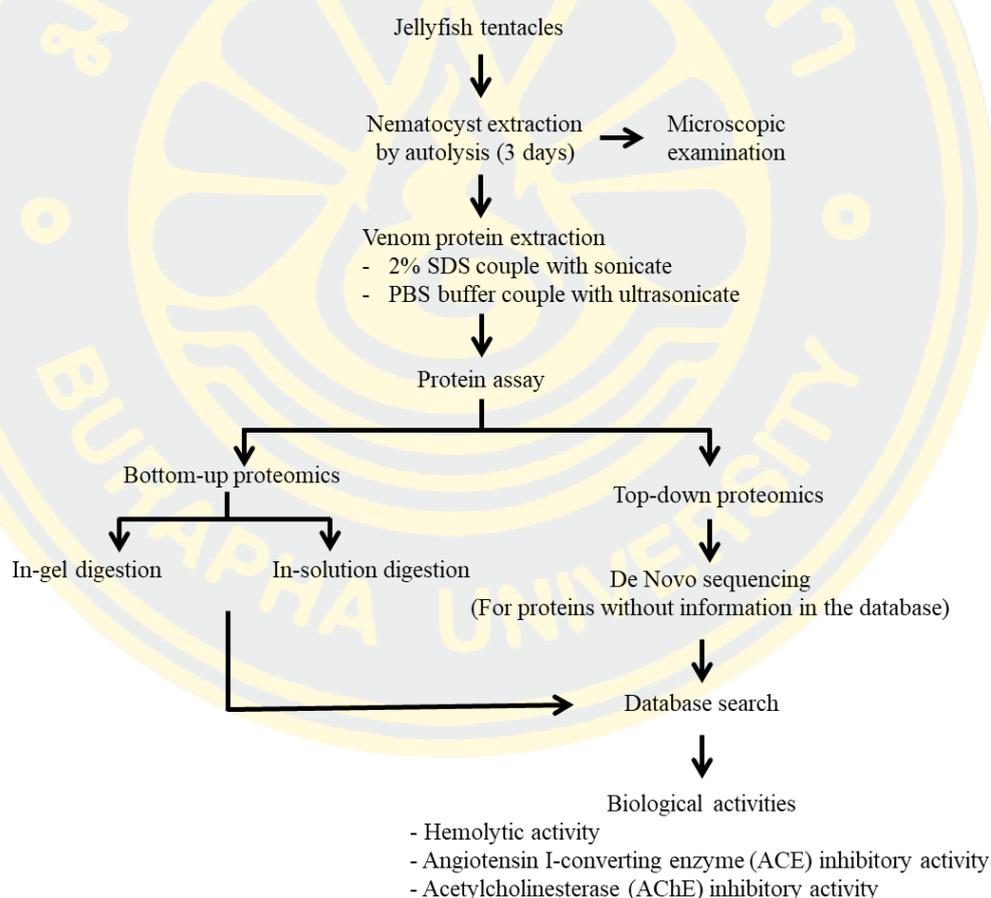


Figure 3-1. Schematic diagram showing the overview of this research.

3.3 Method

3.3.1 Preparation of venom from jellyfish tentacles by autolysis method

Two types of jellyfish were studied, edible jellyfish (*Rhopilema hispidum* Vanhöffen, 1888) and highly venomous jellyfish (*Sanderia malayensis*). Fresh edible jellyfish was collected by fishermen from Angsila or Bangsaen coastal area on 24th July 2019, and 28th August 2019 and kept at -80°C until use. And tentacles of *S. malayensis* was collected from the Institute of Marine Science, Burapha University in February 2019, March 2019, July 2019, September 2019, October 2019, and January 2020 and kept at -80°C until use. The species were confirmed by an expert (Ms. Wilaiwan Phuangsanthia) from the Institute of Marine Science, Burapha University. In this study, tentacles of *S. malayensis* with the age of 3 months or above was used to study. *S. malayensis* was cultured in a glass cabinet with the size of 80 x 160 x 60 cm in the seawater at the temperature of 20 °C and fed by newly hatch *Artemis sp.*. There were 8 *S. malayensis* per one glass cabinet cultured in the whirlpool to mimics nature and ventilation flow.

In this experiment, jellyfish tentacles were dissected prior to separation of nematocyst. Autolysis method was slightly modified from Bloom, Burnett, and Alderslade (1998) in order to extract the nematocyst from jellyfish tentacle. Jellyfish tentacles were cleaned using freshly prepared seawater. After that, the seawater was added to the sample at the ratio of 1g:1ml. The mixture was stirred and incubated at 4 °C to separate nematocysts from the tentacle tissue. The autolysis experiment was carried on for 3 days. Once each day, the tentacle tissue and the seawater solution were collected to monitor the release of nematocysts from the tissue using a light microscope (Axio Lab.A1, Carl Zeiss) connected with canon EOS 800D camera and CANON EOS Utility program. After that the tentacles were separated from the nematocyst by using a mesh filter. Then, the solution was centrifuged at 10,000 x g at 4 °C for 15 minutes to separate the nematocyst. Pellet containing nematocyst was collected. Then two method were performed to extract protein from nematocyst, including 2% of sodium dodecyl sulfate (SDS) couple with sonication, and PBS buffer pH 7.0 couple with ultrasonication. After protein extraction, the solution was centrifuged at 10,000 x g at 4 °C for 15 minutes to separate the protein dissolved in solution from other debris. Supernatant was collected and stored at -20 °C until use.

3.3.2 Measurement of protein concentration by using BCA protein assay

BCA protein assay kit was used for measuring protein concentration. This method was described by Smith et al. (1985). Albumin was used as protein standard at concentration of 0, 25, 125, 250 500, 1000 $\mu\text{g/ml}$. Preparation of working reagent was prepared by mixing reagent A with reagent B (50:1). The working reagent (200 μl) was mixed with the samples (25 μl) and incubated at 37 °C for 30 minutes. In the presence of peptide bonds, Cu^{2+} in working reagent could be reduced to Cu^{+} , and the solution color was changed from green to purple, which can be measured by a microplate reader at 562 nm. The protein concentration of sample can be calculated from protein standard curve.

3.3.3 Proteomics analysis by using bottom-up proteomics approach

3.3.3.1 In-gel digestion

In gel digestion was performed as described by Shevchenko et al. (2006) with slight modifications. Proteins were separated based on molecular weight by using Bis-tris gel electrophoresis. The amount of proteins from *Rhopilema hispidum* and *Sanderia malayensis* were 40 and 10 μg , respectively. Thirteen microliters of samples were mixed with loading buffer (5 μl), and 1 M DTT (2 μl). The solution was heated at 95 °C for 3 minutes and spun down for 30 seconds. After that, the sample solution was loaded to a pre-cast bis-tris gel (4-12% gradient). The proteins were separated by using static voltage at 100 V. After that, the gel was stained by InstantBlue staining solution for 30 minutes to observe size of protein in the gel by comparing with the standard protein marker.

The gel was sliced into 5 fractions and each fraction was cut into small pieces (1x1 cm^2). The gel pieces were incubated and vortexed in 500 μl of a destaining solution containing 100 mM ammonium bicarbonate and acetonitrile (1:1 vol/vol) for 30 minutes. Then the solution was removed and acetonitrile (200 μl) was added to dehydrate the gel. Next, protein in the gel was reduced with 10 mM DTT (200 μl) at 56 °C for 30 minutes. After that, the gel was dehydrated with 200 μl acetonitrile for 10 minutes. The proteins were then alkylated with 55 mM chloroacetamide solution (200 μl) for 20 minutes in the dark. Following another dehydration step, 13 ng/ μl of

trypsin solution (150 μ l) was added to the gel pieces and the mixture was incubated on ice for 90 minutes in order to saturate gel. Excess trypsin solution was removed and 100 μ l of 100 mM ammonium bicarbonate was added to cover the gel pieces. Then proteins were digested by trypsin at 37 °C overnight. After that, peptides were extracted by extraction buffer (5% formic acid and acetonitrile, 1:2 vol/vol) at 37 °C for 15 minutes. Then peptide solution was collected and lyophilized. Then, the peptides were resuspended with 100 μ l of 0.1% formic acid for LC-MS/MS analysis.

3.3.3.2 In-solution digestion

In-solution digestion was slightly modified from Choksawangkarn et al. (2012). For the sample extracted by 2% SDS, a solution containing 50 μ g of venom protein was exchanged with 100 μ l of 50 mM ammonium bicarbonate by using 3 kDa molecular weight cut off filter. For the sample extracted by PBS buffer, 100 μ g of venom protein solution was diluted with 50 mM ammonium bicarbonate. The venom proteins were reduced with 10 mM DTT and incubated at 56 °C for 30 minutes. Then the proteins were alkylated with 20 mM chloroacetamide at room temperature for 30 minutes. After that, venom proteins were digested with trypsin (0.2 μ g/ μ l) and incubated at 37 °C overnight. The reaction was stopped by 0.1% formic acid. After that, the samples were desalted using C18 StageTips (3.3.5).

3.3.3.3 In-solution digestion using PNGaseF and trypsin

This method was slightly modified from Orsini et al. (2018). Sample extracted by PBS buffer was used in this experiment. Venom proteins (50 μ g) were diluted using 50 mM ammonium bicarbonate. Then the proteins were reduced with 10 mM DTT and incubated at 56 °C for 30 minutes. Proteins were alkylated with 20 mM chloroacetamide and incubated at room temperature in the dark for 30 minutes. Then the proteins were digested with 0.5 unit/ μ l of PNGaseF (2 μ l) enzyme for deglycosylation. The reaction was incubated at 37 °C for 3 hours. After PNGaseF digestion, trypsin (0.2 μ g/ μ l) was added to the digest and incubated at 37 °C overnight. The reaction was stopped by adding 0.1% formic acid. Then digested proteins were desalted by C18 StageTips (3.3.5) for analysis by LC-MS/MS.

3.3.4 Proteomics analysis by using top-down approach

Top-down proteomics was performed in order to enhance small protein identification by using LC-MS/MS. Using a bottom-up approach, small proteins could not be digested by trypsin enzyme that lead to no identification. Thus, small proteins without digestion were analyzed in this experiment to increase number of protein identification. This method was described by Yang, Shen, Chen, and Sun (2020) with slightly modification. Proteins (100 µg) in 200 µl of 50 mM ammonium bicarbonate were subjected to ultrafiltration using 3 kDa molecular weight cut off filter to separated small proteins from large proteins. The small proteins were lyophilized and reconstructed by 0.1% formic acid. Later, small venom proteins were loaded on C18 StageTips to desalting sample (3.3.5) for analysis by LC-MS/MS.

3.3.5 Desalting by C18 StageTips

All samples derived from bottom-up (3.3.3) and top-down (3.3.4) proteomics experiments were desalted before analysis by LC-MS/MS by using C18 StageTips. This method was described by Rappsilber, Mann, and Ishihama (2007). C18 StageTips column was prepared by using C18 membrane, C18 silica bead, and pipette tip (200 µl). Firstly, C18 membrane was put into the pipette tip. Secondly, C18 silica bead (2 mg) in acetonitrile (200 µl) was added to the pipette tip. Then, the Stagetips column was centrifuged at 3,000 x g for 3 minutes. After that, 0.1% of formic acid was used to equilibrate column, followed by centrifugation at 3,000 x g for 3 minutes. Later, proteins sample reconstructed by 0.1% formic acid were loaded to the column, which was centrifuged at 3,000 x g for 3 minutes. Then the column was washed with 0.1% formic acid and centrifuged again. After washing, proteins in the column were eluted by an elution buffer containing 70% acetonitrile and 0.1% of formic acid. The sample was lyophilized by speed vacuum and reconstructed by 0.1% formic acid for analysis by LC-MS/MS.

3.3.6 Measurement of peptide concentration by PierceTM Quantitative Fluorometric Peptide Assay

Before LC-MS/MS analysis, peptide concentrations were examined by using quantitative fluorometric peptide assay. Albumin peptides at the concentration of 0,

7.8, 15.6, 31.3, 62.5, 125, 250 500, 1000 $\mu\text{g/ml}$ were used as standard solution. The standard or sample solutions (10 μl) were incubated with 70 μl of fluorometric peptide assay buffer and 20 μl of fluorometric peptide assay reagent for 5 minutes. Fluorescence of sample was measured at excitation wavelengths of 390 nm and emission wavelengths of 475 nm using fluorescence spectrophotometer (Agilent Cary Eclipse fluorescence spectrophotometer, Agilent).

3.3.7 LC-MS/MS analysis

Digested proteins derived from bottom-up proteomic (3.3.3) and small proteins derived from top-down proteomic (3.3.4) were subjected to LC-MS/MS analysis. Venom proteins (400 ng) were injected to C18 analytical column (75 μm x 25 cm, PepMapTM RSLC C18 capillary column, Thermo Scientific), connected with a nano-HPLC (EASY-nLC 1000, Thermo Scientific). The proteins derived from in-gel digestion (3.3.3.1) and top-down proteomic (3.3.4) were separated in the C18 column for 60 minutes using a gradient shown in table 3-1. And the proteins from in-solution digestion (3.3.3.2) was separated in C18 column for 120 min using a gradient shown in table 3-2. Flow rate was set at 300 nanoliter/minutes by using solvent A (0.1% formic acid, 99% Type I distilled water) and solvent B (0.1% formic acid, 99.9% acetonitrile).

Table 3-1. Concentration of solvent A and B were used to elute protein from in-gel digestion and top-down proteomic for 60 minutes.

Time (minutes)	% Solvent A	% Solvent B
0	95	5
43	80	20
53	60	40
55	5	95
60	5	95

Table 3-2. Concentration of solvent A and B were used to elute protein from in-solution digestion for 120 minutes.

Time (minutes)	% Solvent A	% Solvent B
0	97	3
5	92	8
75	80	20
110	60	40
112	5	95
120	5	95

After separation, proteins eluted from the column were ionized by a nano-electrospray ionization before transmitting to the mass spectrometer (Q Exactive™ hybrid quadrupole-Orbitrap mass spectrometer). Precursor ions were detected in a mass range of 350 to 1600 m/z by orbitrap mass analyzer at resolution of 70,000. Maximum injection time was set at 100 milliseconds. ACG target was set at 3×10^6 . Data dependent acquisition was carried out, which 10 most abundant precursor ions were selected for fragmentation. Higher-energy collisional dissociation (HCD) was used for fragmentation with an exclusion of +1 charged ions. The m/z of product ions was recorded at resolution of 17,500. All data were acquired using Thermo Xcalibur 2.2 software.

3.3.8 Data analysis

3.3.8.1 Protein identification using a database search

Proteins were identified from the mass spectra by using Maxquant software version 1.6.2.6a (Cox & Mann, 2008). The group-specific parameters are shown in table 3-3. Dynamic and static modification were set to be oxidation of methionine and carbamidomethylation of cysteine, respectively. Threshold for protein identification was set to 1% false discovery rate. Three databases were created from UniProt database, including (1) taxonomy: Cnidaria (downloaded on 2nd June 2020), (2) keyword: toxin (downloaded on 2nd June 2020) and (3) specified taxonomy: Cnidaria and keyword: toxin (downloaded on 13th August 2020). Proteins from database were used to interpret sequence of a protein by MS/MS spectrum matching.

Table 3-3. Setting of input value to interpret peptide sequence from database.

Input	value
Max. charge	7
Max. missed cleavage sites	2
Min. peptide length	4
Max. peptide mass	4600 Da
First search peptide tolerance	20 ppm
Main search peptide tolerance	4.5 ppm
Max. number of modifications per peptides	5

3.3.8.2 Identification protein from mass spectra by using De Novo sequencing

De Novo sequencing was used for interpretation of protein sequences that are not present in a database. Small proteins derived from top-down proteomics (3.3.4) were identified using PEAKS software (Zhang et al., 2012). Data refinement parameters was shown in the table 3-4.

Table 3-4. Setting of data refinement for De Novo sequencing.

Data	Setting
Instrument	Trap (Orbi-Orbi)
Fragment	CID
Acquisition	DDA
Enzyme	No digestion
Min charge	1
Max charge	6
Precursor mass (using mono isotopic mass)	10 ppm
Fragment ion	0.02 Da
Variable modification	Oxidation (M)
Database	Taxonomy Cnidaria

3.3.8.3 Analysis of amino acids composition and domain of the peptides from De novo sequencing

Domain of peptides sequences identified from De novo sequencing were predicted by using InterPro - EMBL-EBI software (Apweiler et al., 2001). Moreover, amino acids composition of all peptides was analyzed by Protein Information Resource (PIR) (Wu et al., 2006).

3.3.8.4 Biological activity prediction of the peptides from De novo sequencing

Biological activities of novel peptides from edible and highly venomous jellyfish were predicted, including ACE inhibitory and hemolytic activities. In this study, AHTpin software was used to predict ACE inhibitory activity of the peptides (Kumar et al., 2015). And hemolytic activity was predicted about by HemoPred software (Win et al., 2017).

3.3.8.5 Functional analysis

Functions of proteins identified was analyzed by using Protein Information Resource (PIR) (Wu et al., 2002). Biological process, molecular function and cellular component of proteins identified were assessed by using a Gene Ontology Annotation tool on the PIR software.

3.3.9 Hemolytic activity

Hemolytic activity of the jellyfish venom was investigated using an assay modified from Li et al. (2013). Jellyfish venom proteins were extracted by using PBS buffer, pH 7.4 (containing 1mM EDTA and 1 mM PMSF). Erythrocytes were separated from pig bloods (6 ml) by adding 25 ml of PSE buffer, pH 7.4 (0.73 M Sucrose, 0.01 M di-sodium hydrogen phosphate, and 0.001 M EDTA) and centrifugation at 500 rpm for 15 minutes. After centrifugation, pig bloods were separated into three layers, including plasma, erythrocytes, and broken erythrocytes. The middle layer of erythrocytes was collected and diluted with PBSE buffer (PBS buffer containing 1 mM EDTA) at the ratio of 1 vol: 1vol. Then diluted solution (6

ml) was added on PBSE buffer (25 ml) and centrifuged at 1000 rpm for 10 minutes. The pellet of pig erythrocytes was collected and resuspended in 25 ml PBSE buffer before measuring an absorbance at 600 nm. The erythrocyte solution was diluted with PBSE until the absorbance at 600 nm was in a range of 0.3 - 0.4. After that, hemolytic activity was tested by mixing 900 μ l of pig erythrocyte solution and 100 μ l of jellyfish toxins. The mixture was incubated at 37 °C for 30 minutes and centrifuged at 5000 rpm for 15 minutes to separate hemoglobin. Hemoglobin released from lysis of erythrocytes was observed by absorbance measurement at 415 nm. A hundred microliter of 0.1% triton x-100 solution was used as a positive control (100% hemolysis). The equation 1 was used to calculate the percentage of hemolytic activity.

$$\% \text{ Hemolytic activity rate} = [(A_{\text{sample}} - A_0) / (A_{100\%} - A_0)] \times 100 \quad (1)$$

A_{sample} : Absorbance of reaction containing venom protein

$A_{100\%}$: Absorbance of a positive control (100% hemolysis)

A_0 : Absorbance of a blank solution (0% hemolysis)

3.3.10 Angiotensin I-converting enzyme (ACE) inhibitory activity

Antihypertensive activity of toxin proteins extracted by PBS buffer, pH 7 was evaluated. This experiment was slightly modified from Asoodeh, Yazdi, and Chamani (2012). Jellyfish toxins were lyophilized and resuspended with 50 mM sodium borate buffer. Then one hundred microliter of proteins sample (0.125, 0.25, 0.5 and 1 mg/ml) were mixed with 50 mU/ml of ACE enzyme (44 μ l), 0.5 mM of FAPGG substrate (200 μ l) and 50 mM sodium borate buffer (300 μ l). The mixture solution of FAPGG substrate (200 μ l), 50 mU/ml of ACE enzyme (44 μ l), and 50 mM sodium borate buffer (400 μ l) was used as a control. The reaction was incubated at 37 °C for 60 minutes. Then amount of FAPGG substrate were measured at the absorbance of 340 nm. In the absence of ACE inhibitor, FAPGG substrate can be digested with ACE to produce FAP, so the absorbance of FAPGG would be decreased. On the other hand, in the presence of ACE inhibitor, the absorbance of FAPGG should be constant. Equation 2 was used to calculate the percentage of ACE inhibitory activity.

$$\% \text{ ACE inhibition} = [1 - (\Delta A_{\text{sample}} / \Delta A_{\text{control}})] \times 100 \quad (2)$$

ΔA_{sample} : Difference absorbance of sample reaction (all reagent including sample)

$\Delta A_{\text{control}}$: Difference absorbance of control (all reagent without sample)

3.3.11 Acetylcholinesterase (AChE) inhibitory activity

Acetylcholinesterase inhibitory activity of venom proteins was evaluated. This experiment was performed according to the method of Ellman, Courtney, Andres Jr, and Featherstone (1961). A solution of 1 mg/ml galanthamine hydrobromine in ethanol was used as a positive control. Distilled water was used as a negative control. Twenty-five microliters of positive control, negative control, and jellyfish toxin (0.125, 0.25, 0.5, 1, and 2 mg/ml) were mixed with 0.28 U/ml acetylcholinesterase (25 μ l). After that the reaction was pre-incubated at room temperature for 5 minutes. After 5 minutes, 25 μ l of 15 mM acetylthiocholine iodine (ATCI) and 125 μ l of 5,5'-dithiobis (2-nitrobenzoic acid) (DTNB) were added and mixed. In the absence of inhibitor, acetylcholinesterase could digest acetylthiocholine, producing thiocholine and acetate. The reaction product (thiocholine) could further react with DTNB, producing yellow color of TNB. The absorbance at 405 nm was determined. The % AChE inhibition was calculated according to equation 3.

$$\% \text{ AChE inhibition} = \frac{[(A - B) - C]}{A - B} \times 100 \quad (3)$$

A: Absorbance of negative control (distilled water, AChE enzyme, ATCI substrate and DTNB)

B: Absorbance of blank (distilled water and sodium phosphate buffer)

C: Absorbance of sample and positive control (sample or galanthamine hydrobromine, AChE enzyme, ATCI substrate and DTNB)

3.3.12 Statistical analysis

Biological activities results were exhibited as mean \pm standard deviation (SD). Minitab version 17 was used for statistical analysis by using One-way ANOVA with Tukey's post-test. The statistical significance was set at $p < 0.05$.

CHAPTER 4

RESULTS

4.1 Extraction of nematocysts from *Rhopilema hispidum* and *Sanderia malayensis* and determination of their morphology

Jellyfish toxins are contained in the nematocyst capsules, which nematocysts are mostly located in the tentacles. Autolysis method is the process for nematocyst extraction by destroying tentacle tissues. Nematocysts can be released from the tentacles by soaking in the seawater for three days and daily vortex to destroy tentacle tissue. The release of nematocysts from the tissue can be observed under the light microscope. In this experiment, the morphology of nematocysts in the fresh tentacles were observed before extraction by autolysis method. Nematocysts in the tentacles of edible and highly venomous jellyfish were shown in figure 4-1A and 4-2A, respectively. Nematocysts of these two species are distributed along the tentacles of jellyfish. Secondly, nematocysts extracted by autolysis method were observed in the seawater. We found that nematocysts can be extracted from the tentacles of edible and highly venomous jellyfish by using autolysis method for three days. The figure 4-1B, C and D demonstrated that nematocysts of edible jellyfish could be extracted to the seawater in each day. And nematocysts of highly venomous jellyfish could also be released to the seawater as shown in the figure 4-2B, C, and D.

Morphology of nematocysts from edible and highly venomous jellyfish was shown in figure 4-1 and 4-2, respectively. We found that round structure was mostly observed from nematocysts of edible jellyfish, while an oval structure was mostly observed from nematocyst of highly venomous jellyfish. Average diameter of nematocysts of these two species was about 10-20 micrometers. In addition, it was observed that the thread-like tubes discharged from the nematocysts of highly venomous jellyfish was longer than those from the nematocyst of edible jellyfish (Figure 4-1D and 4-2D).

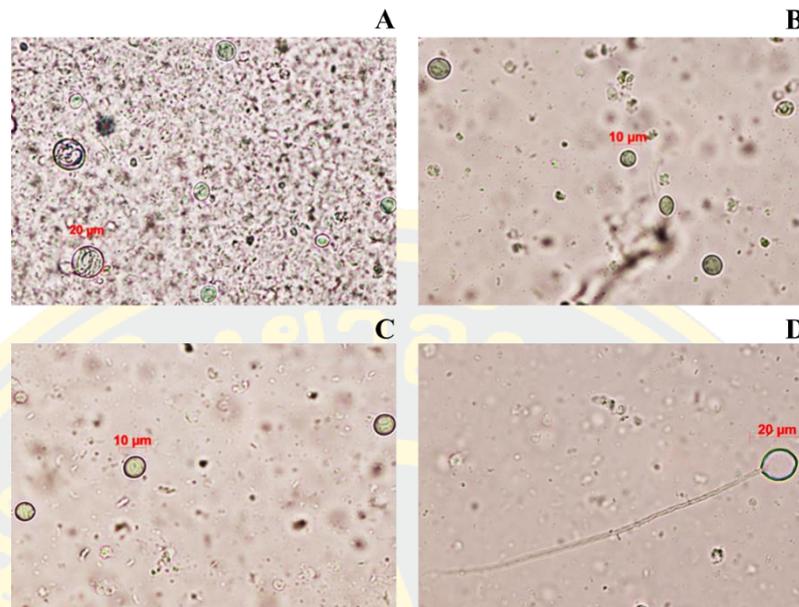


Figure 4-1. Morphology of nematocysts in the tentacle tissue of edible jellyfish (A). During three days of autolysis, nematocysts released to the seawater were observed in each day, day one (B), day two (C), and day three (D).

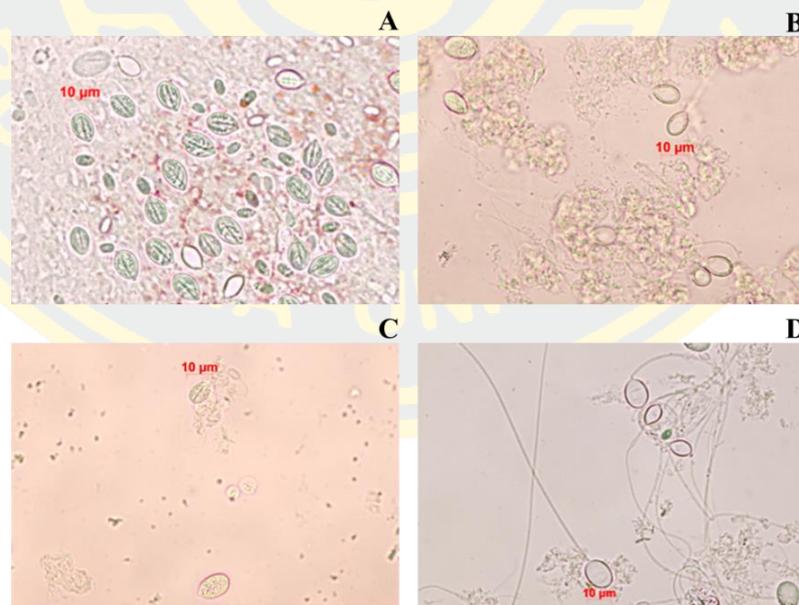


Figure 4-2. Morphology of nematocysts in the tentacle tissue of highly venomous jellyfish (A). During three days of autolysis, nematocysts released to the seawater were observed in each day, day one (B), day two (C), and day three (D).

4.2 Toxin protein extraction from nematocysts of jellyfish

After nematocysts extracted from tentacles by autolysis method, toxin proteins from these two jellyfish species were extracted by using two methods, including (1) 2% SDS coupled with sonication and (2) PBS buffer coupled with ultrasonication. After extraction, toxin proteins were separated from nematocysts by centrifugation and the remaining pellet were examined under light microscope. As a detergent, SDS could destroy the capsule structure of nematocysts and helps releasing the toxin proteins. However, those proteins could be denatured affecting the loss of biological functions. Hence, we attempt to adjust the protein extraction procedure from using SDS to PBS buffer to preserve the structure and functions of proteins. The proteins concentration of extracted proteins and morphology of the pellet were compared.

Based on BCA protein assays, protein concentrations of 2871.388 and 2801.944 $\mu\text{g/ml}$ were obtained from the toxins of edible jellyfish by using SDS and PBS buffer extraction, respectively. And protein concentrations of 349.091 and 525.591 $\mu\text{g/ml}$ were measured from the toxins of highly venomous jellyfish by using SDS and PBS buffer extraction, respectively. The results indicated that using both procedures of SDS and PBS extractions can extract toxin proteins from nematocysts. The protein concentration of edible jellyfish was higher than that of highly venomous jellyfish. Since edible jellyfish are a larger than the highly venomous jellyfish, higher number of nematocysts can be extracted from tentacles, resulting in higher protein concentration in the edible jellyfish as compared to the highly venomous jellyfish. The remaining pellets after protein extraction by SDS solution and PBS buffer were represented in figure 4-3 and 4-4, respectively. We found that the discharged nematocysts were observed in the pellet after protein extraction by SDS and PBS buffer. However, some of the intact nematocyst were also found in the pellet of these two species.

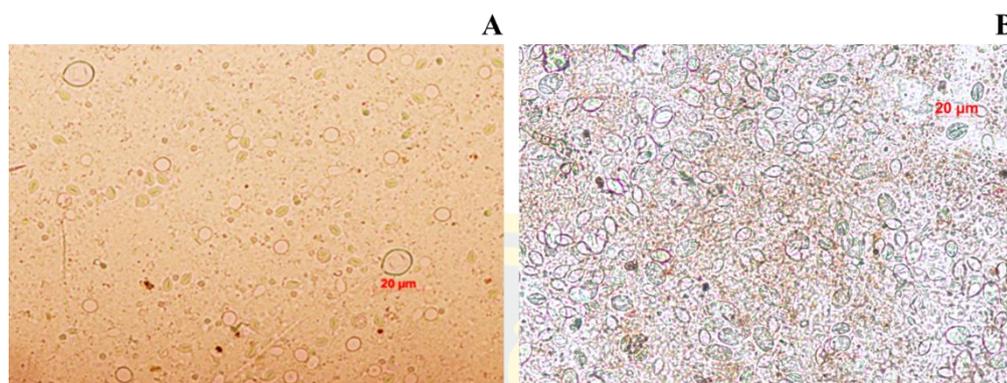


Figure 4-3. Nematocysts in the pellet after protein extraction by SDS coupled with sonication from edible jellyfish (A) and highly venomous jellyfish (B).

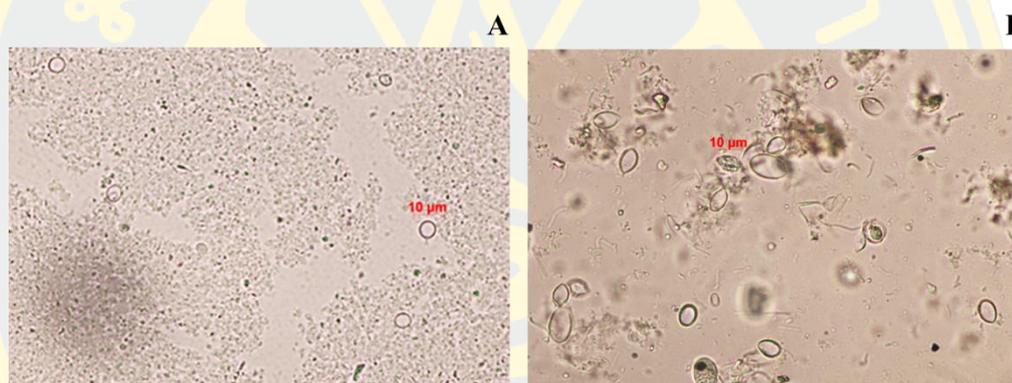


Figure 4-4. Nematocysts in the pellet after protein extraction by PBS buffer coupled with ultrasonication from edible jellyfish (A) and highly venomous (B) jellyfish.

4.3 Analysis of protein profile using bis-tris gel electrophoresis

Gel electrophoresis profile of crude tentacle proteins and nematocyst proteins from edible and highly venomous jellyfish were shown in figure 4-5 and 4-6. Molecular weight of proteins from these two species were in a range of 10 to 250 kDa with distinct profile. High intensity of the protein bands in the molecular weight range of 75 to 150 kDa was observed in the edible jellyfish samples; while darker bands at the molecular weight of 37 kDa was shown in the highly venomous jellyfish samples.

Using different methods of extraction slightly affected the gel electrophoresis profile as observed from figure 4-6. High intensity band at the molecular weight of 250 kDa was appeared in the highly venomous jellyfish sample extracted by SDS solution; while it was not observed in the PBS extracted samples (Figure 4-6).

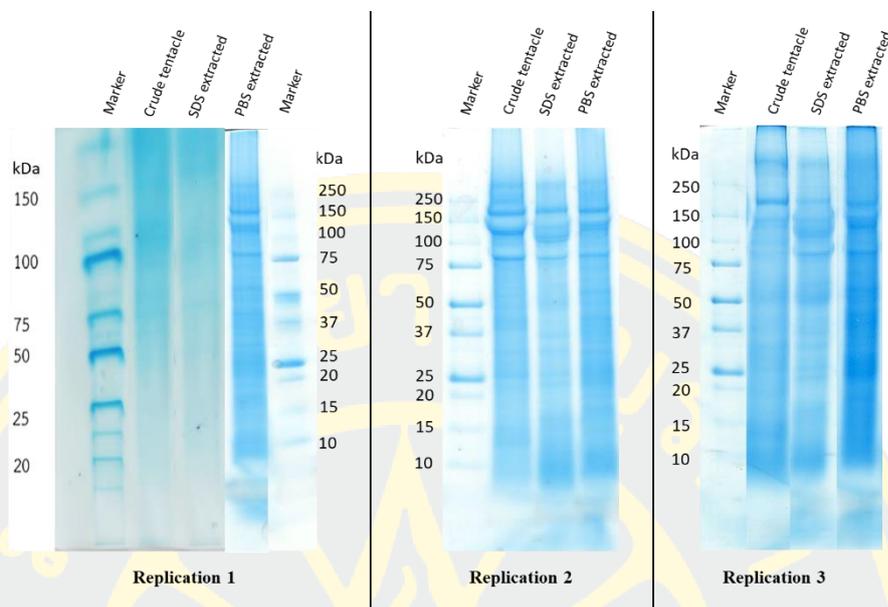


Figure 4-5. Bis-tris gel electrophoresis profiles of proteins from crude tentacle, proteins extracted by SDS solution, and proteins extracted by PBS buffer from edible jellyfish.

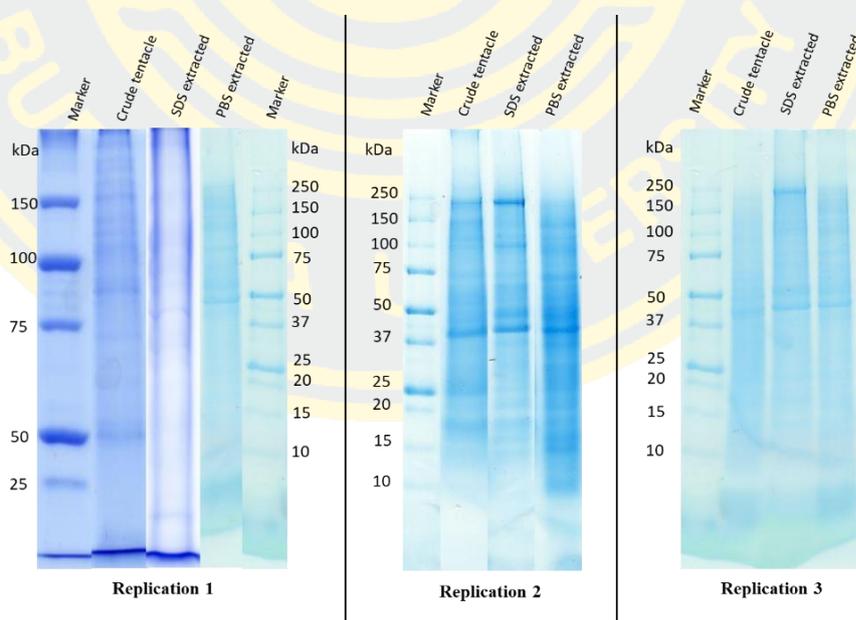


Figure 4-6. Bis-tris gel electrophoresis profiles of proteins from crude tentacle, proteins extracted by SDS solution, and proteins extracted by PBS buffer from highly venomous jellyfish.

4.4 Bottom-up proteomics

To develop an effective treatment for jellyfish stinging, it is necessary to evaluate the composition of toxin proteins from edible and highly venomous jellyfish. There was no information published about the toxin protein component from these two species. Thus, the component of these two jellyfish species was analyzed using bottom-up proteomics experiment. There were two strategies used to prepare sample, including in-solution and in-gel digestions. In this experiment, complex protein mixtures were digested with trypsin. Proteins were identified from digested peptides by searching MS/MS spectra against three databases retrieved from UniProtKB including, (A) taxonomy: Cnidaria, (B) taxonomy: Cnidaria and keyword: toxin, (C) keyword: toxin.

4.4.1 In-solution digestion

4.4.1.1 Identification of proteins obtained from different extraction methods (SDS and PBS buffer) by using the database A (taxonomy: Cnidaria) and B (taxonomy: Cnidaria and keyword: toxin)

Two different procedures for protein extraction were compared including SDS and PBS buffer extraction methods. Figure 4-7A shows that there were 261 proteins and 169 proteins identified from edible jellyfish by using SDS and PBS buffer extraction methods, respectively (Appendix D, table D-4 and D-5). Of these, 64 proteins were shared between these two extractions. In contrast, higher number of proteins identified from nematocysts of highly venomous jellyfish were observed using PBS buffer extraction (313 proteins), as compared to SDS (283 proteins) as shown in figure 4-7B (Appendix G, table G-4 and G-5). There were 134 proteins of highly venomous jellyfish shared between two different extraction procedures.

Considering only toxin proteins identified from these two species, using PBS extraction provided higher number of toxins identified than SDS extraction. There were 11 and 18 toxins identified from edible and highly venomous jellyfish by using PBS extraction, respectively (Appendix E and H, table E-5 and H-5). And there were 8 and 12 toxin proteins identified from edible and highly venomous jellyfish by using SDS extraction, respectively (Appendix E and H, table E-4 and H-4). Moreover, using PBS extraction, we found higher number of neurotoxins and metalloproteases

identified from these two jellyfish than those from SDS extraction. Furthermore, higher number of toxins proteins were identified from highly venomous jellyfish, as compared to edible jellyfish. Based on in-solution digestion, using PBS buffer with ultrasonication was a better method for proteins extraction than SDS extraction, due to larger number of toxin proteins identified and preservation of the protein functions. These toxin proteins identified could be beneficial for treatment of jellyfish envenomation.

To enhance identification of glycosylated proteins, PNGaseF enzyme was used for digestion prior to tryptic digestion. Glycoprotein contains glycan groups with many negative charges, which could interfere in the process of ionization. Thus, using PNGaseF enzyme digestion, followed by trypsin digestion could increase the number of protein identification. The results indicated that 62 more proteins from edible jellyfish could be identified in addition to the list from only trypsin digestion (Figure 4-7A) (Appendix D, table D-6). Figure 4-7B showed that using PNGaseF digestion can further identify 133 proteins of highly venomous jellyfish in addition to the procedure of trypsin digestion (Appendix G, table G-6). Moreover, we found that using PNGasesF digestion could increase the number of toxins identified from edible jellyfish, which proteins were involved with the function of metalloproteases, hydrolase, and neurotoxins (Appendix E, table E-6). For toxin proteins identified from highly venomous jellyfish, pore-forming proteins was the new proteins found after using PNGaseF digestion. And other groups of toxins were also found, including metalloproteases, and neurotoxin (Appendix H, table H-6). The pore-forming toxins were solely found in *S. malayensis* that could cause more serious toxic effect of the venom from this species than the edible jellyfish.

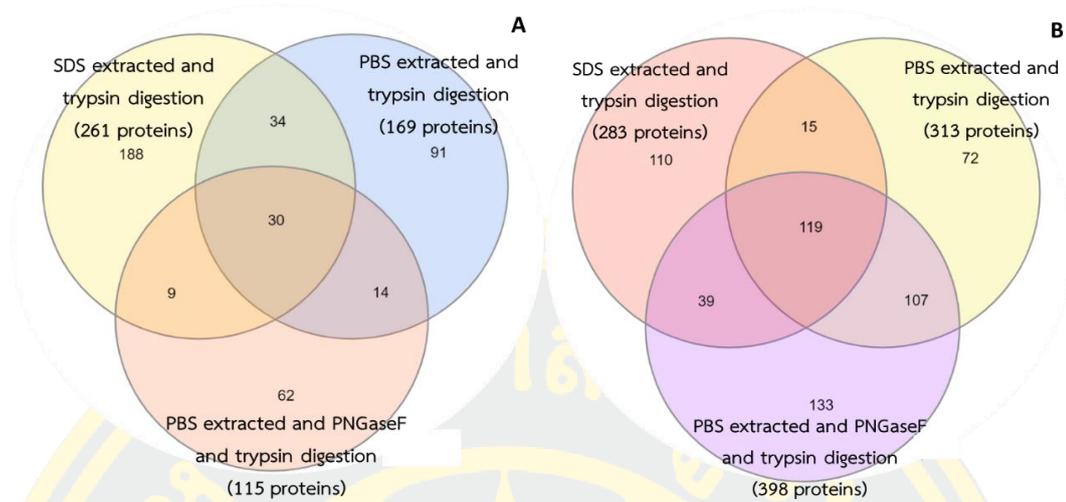


Figure 4-7. Venn diagram of protein identified from nematocysts of edible jellyfish (A) and highly venomous jellyfish (B) by using in-solution digestion experiment.

4.4.1.2 Analysis of all nematocyst proteins identified from in-solution digestion of edible and highly venomous jellyfish by using the database A (taxonomy: Cnidaria database) and B (taxonomy: Cnidaria and keyword: toxin)

All proteins identified from in-solution digestion with different extraction and digestion procedures were combined and analyzed. The results indicated that we could identify 429 proteins from edible jellyfish and 595 proteins identified from highly venomous jellyfish. It is noticeable that highly toxic jellyfish contained higher number of proteins identified than the edible jellyfish. There were 149 proteins shared between these two species, which structural proteins were mostly found, such as non-muscle actin II, histone H2B, and tubulin beta chain.

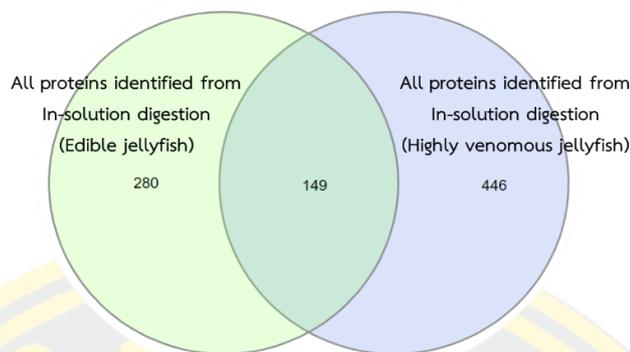


Figure 4-8. Comparison of all proteins identified from nematocyst of edible and highly venomous jellyfish by using in-solution digestion.

4.4.1.3 Identification of proteins from the in-solution digestion experiments by using the database C (keyword: toxin)

Jellyfish toxin proteins were further identified from the database with specified keyword “toxin” from all species, in order to identify possible toxin proteins in the same family as other venomous animals. There were three important functions of the toxin proteins identified from edible jellyfish, including hydrolase, neurotoxic, and hemolysis functions (Appendix F, table F-4, F-5, and F-6). And there were five important functions of the proteins identified from highly venomous jellyfish, including hydrolase, neurotoxic, metalloprotease, hemolysis, and cytolysis functions (Appendix I, table I-4, I-5, and I-6). However, hydrolase is the majority group of toxin proteins identified from both edible and highly venomous jellyfish, which were different from proteins identified using Cnidaria database. As mentioned earlier, metalloprotease was the main group of toxin protein identified from the Cnidaria database.

4.4.2 In-gel digestion

In-gel digestion was performed in addition to in-solution digestion for a pre-fractionation. Based on data dependent acquisition, the high abundant proteins in the proteins complex were selected to analyze. Thus, less abundant proteins would be suppressed from high abundant proteins, that could lead to less abundant proteins unidentified. In this experiment, proteins with a different molecular weight were separated using gel electrophoresis and the gel was divided into five fractions

according to their molecular weight, as shown example in figure 4-9. Then, each piece of the gel was cut into small pieces for digestion with trypsin enzyme. Peptides were extracted from gel and analyzed by LC-MS/MS. In this study, three databases were used for the MS/MS ion search as shown in the in-solution digestion experiment.

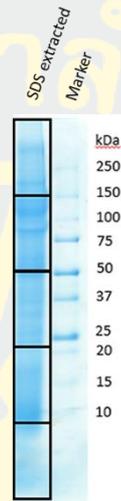


Figure 4-9. Fractionation of proteins for analysis in the in-gel digestion experiment.

4.4.2.1 Identification of proteins obtained from crude tentacles and nematocysts proteins with different extraction (SDS and PBS buffer) by using the database A (taxonomy: Cnidaria database) and B (taxonomy: Cnidaria and keyword: toxin)

After protein profile was analyzed using gel electrophoresis (4.3), the proteins were subjected to in-gel digestion. Number of proteins identified from these two species were demonstrated in figure 4-10. There were 375 and 395 proteins identified from crude tentacle of edible and highly venomous jellyfish, respectively (Appendix D and G, table D-1 and G-1). And the number of proteins identified from nematocysts with two different extraction methods were analyzed. There were 261 and 433 proteins identified from edible jellyfish by using SDS and PBS extraction, respectively (Figure 4-10A) (Appendix D, table D-2 and D-3). Comparing these two extraction procedures, there were 147 proteins shared between SDS and PBS extraction of edible jellyfish. For highly venomous jellyfish, using PBS extraction also provided larger number of proteins identified than SDS extraction. There were

462, and 481 proteins identified from highly venomous jellyfish using SDS and PBS buffer extraction, respectively (Figure 4-10B) (Appendix G, table G-2 and G-3). Of those, 321 proteins were shared between these two extractions.

Considering toxin proteins identified from these two jellyfish species, there were 9, 9, and 8 toxins identified from crude tentacle, nematocyst proteins extracted by SDS, and nematocyst proteins extracted by PBS of edible jellyfish, respectively (Appendix E, table E-1, E-2, and E-3). For highly venomous jellyfish, there were 11, 11, and 8 toxin proteins identified from crude tentacle, proteins extracted by SDS, and proteins extracted by PBS, respectively (Appendix H, table H-1, H-2, and H-3). Metalloprotease, hydrolase, neurotoxic, and hemolysis functions were found from toxins of edible jellyfish; whereas metalloprotease, hydrolase, neurotoxic, and pore-forming functions were found from highly venomous jellyfish. However, metalloproteases were the major group of protein found from these two species.

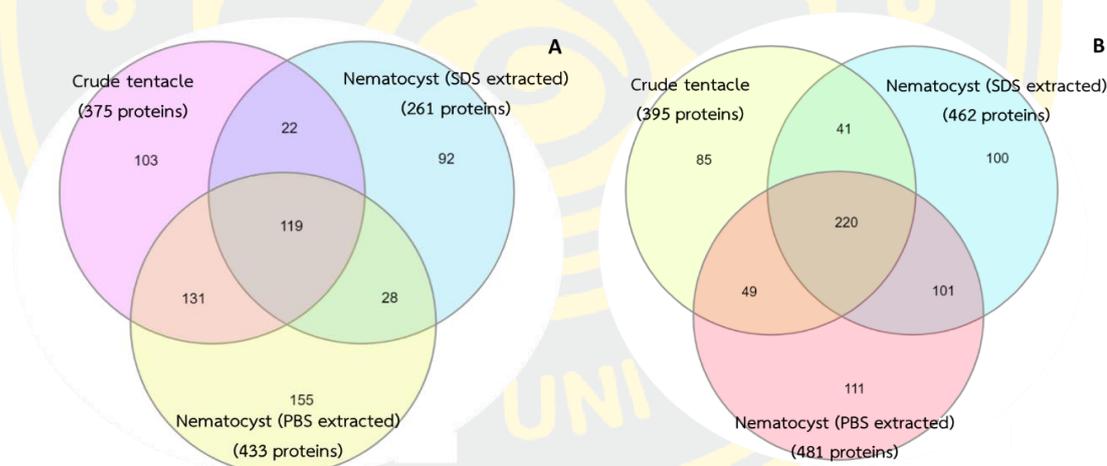


Figure 4-10. Venn diagram of protein identified from crude tentacle and nematocyst of edible jellyfish (A) and highly venomous jellyfish (B) using in-gel digestion experiment.

4.4.2.2 Analysis of all nematocyst proteins identified from in-solution and in-gel digestion of edible and highly venomous jellyfish by using the database A (taxonomy: Cnidaria database) and B (taxonomy: Cnidaria and keyword: toxin)

All nematocyst proteins identified from edible and highly venomous jellyfish were compared between in-solution and in-gel digestion. Figure 4-11 showed that higher nematocyst proteins identified from in-gel digestion than the in-solution digestion of these two species. There were 429 and 548 proteins identified from edible jellyfish by using in-solution and in-gel digestion experiments, respectively (Figure 4-11A).

And there were 595 and 623 proteins identified from highly venomous jellyfish by using in-solution and in-gel digestion experiments, respectively (Figure 4-11B). However, there were 168 and 335 proteins shared between these two experiments of edible and highly venomous jellyfish, respectively. Structural proteins were mostly found from shared proteins. Higher number of proteins identified from in-gel digestion was observed since the separation by gel electrophoresis could enhance identification of less abundant proteins. Furthermore, higher number of proteins were identified from highly venomous jellyfish (883 proteins) than the edible jellyfish (809 proteins).

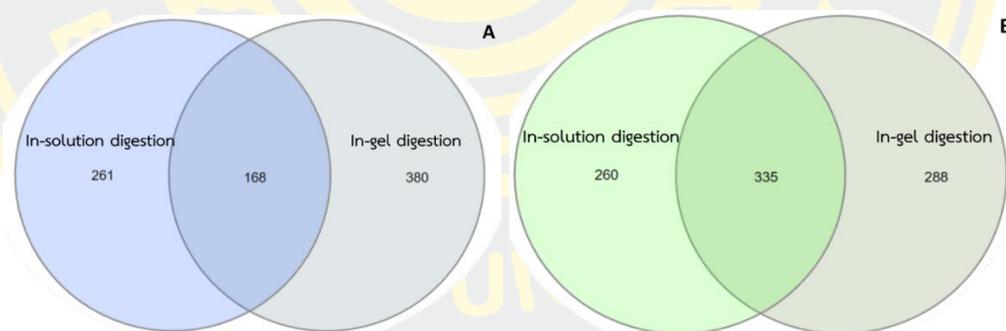


Figure 4-11. Comparison of nematocyst proteins identified from in-solution and in-gel digestion of edible jellyfish (A) and highly venomous jellyfish (B).

4.4.2.3 Identification of proteins from the in-gel digestion experiment by using the database C (keyword: toxin)

Jellyfish toxin proteins were also identified using specific database of proteins with keyword “toxin” from all venomous species. Three important classes of toxins were shown from the edible jellyfish sample, including hydrolase, neurotoxin, and cytolysis proteins (Appendix F, table F-1, F-2, and F-3). Almost all toxins identified

from highly venomous jellyfish by using in-gel digestion were in a group of hydrolases (Appendix I, table I-1, I-2, and I-3). Moreover, hydrolase was considered as a major group of toxin proteins identified from in-gel digestion experiment from both edible and highly venomous jellyfish, which were similar to those identified from in-solution digestion experiment (4.4.1.3).

4.5 Top-down proteomics

4.5.1 Identification of small proteins from top-down proteomic experiment by using the database A (taxonomy: Cnidaria database) and B (taxonomy: Cnidaria and keyword: toxin)

Intact small proteins could be identified from both edible and highly venomous jellyfish using SDS extraction, as shown in figure 4-12A and B. In contrast, using PBS buffer extraction, only small proteins from edible jellyfish could be identified (Figure 4-12A). Moreover, a toxin protein (nephrotoxin PsTX-115 (Fragments)) was identified from highly venomous jellyfish by using SDS extraction (Appendix H, table H-7); while there was no toxin protein identified from the edible jellyfish.

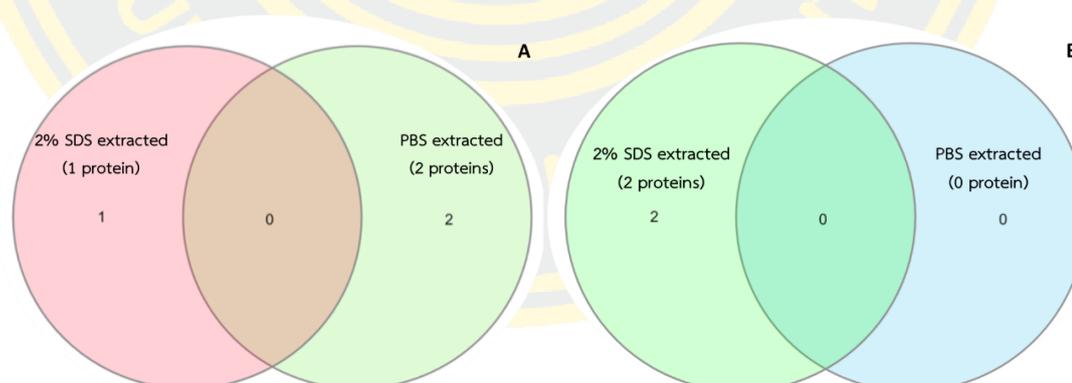


Figure 4-12. Venn diagram of intact proteins identified from nematocyst of edible jellyfish (A) and highly venomous jellyfish (B) by using top-down proteomic experiment.

4.5.2 Identification of proteins from top-down proteomic experiment by using the database C (keyword: toxin)

The results indicated that neurotoxin and metalloprotease inhibitors were identified from edible jellyfish (Appendix F, table F-7). For toxins identified from highly venomous jellyfish, the toxins were related to the functions of neurotoxic, metalloproteases, and metalloproteases inhibitor (Appendix I, table I-7 and I-8). Using this database, major function of the toxin proteins identified were different from those found from in-solution (4.4.1.3) and in-gel digestion (4.4.2.3) experiments, which proteins identified using the specific keyword “toxin” were involved with hydrolase function.

4.5.3 Novel peptides identification using De Novo sequencing

De Novo sequencing was used to interpret novel sequences of the proteins that are not presented in the Cnidaria database. Small proteins from top-down proteomics were analyzed. The results showed that there were 112 and 49 peptides identified from nematocysts of edible jellyfish by using SDS and PBS extractions, respectively (Figure 4-13A) (Appendix J, table J-1 and J-2). It is noticeable that using SDS extraction provide higher number of the proteins identified from edible jellyfish than using PBS extraction. Considering proteins identified from highly venomous jellyfish, PBS extraction provided higher number of proteins identified than SDS extraction. There were 16 and 185 peptides identified from nematocysts of highly venomous jellyfish by using SDS and PBS extractions, respectively (Figure 4-13B) (Appendix J, table J-3 and J-4). Furthermore, almost all novel peptides identified from edible jellyfish were different from the highly venomous jellyfish (Figure 4-13C). Moreover, we found that the length of peptides from edible jellyfish were in the range of 4-16 residues with molecular weight ranging from 350 to 1700 Da. And the length of peptides from highly venomous jellyfish were in the range of 4-26 residues with molecular weight ranging from 360 to 2000 Da. In this study, charges of the novel peptides were mostly +1 and +2. The novel proteins identified from these two species could be important species with significant functions. In addition, small peptides have been of interest for development of new drug, because they are able to be synthesized and easy to penetrate to cell membrane.

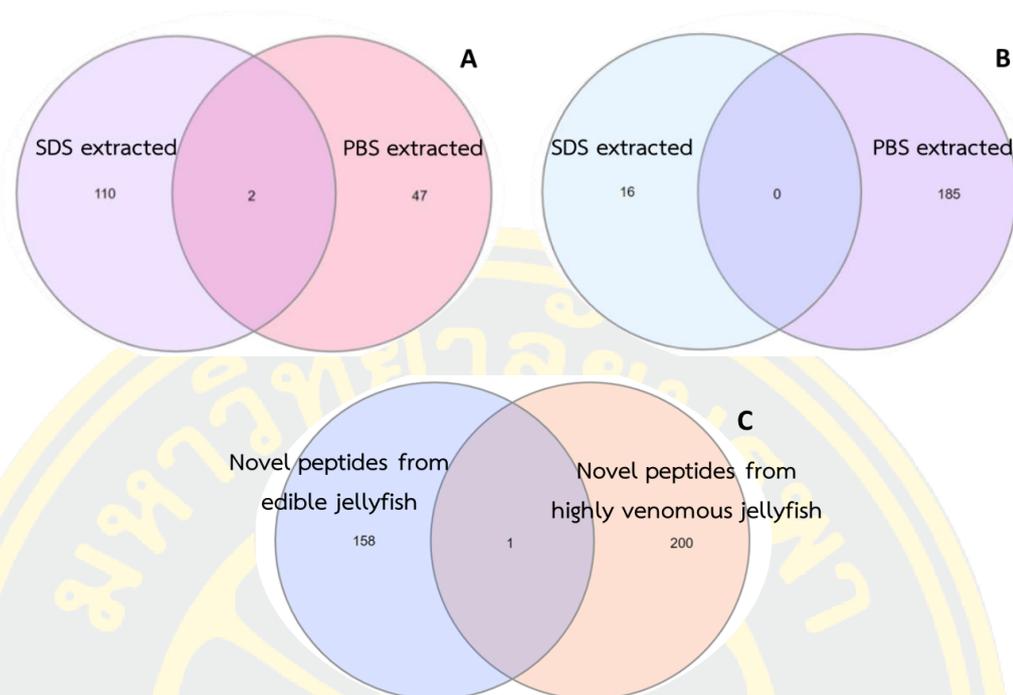


Figure 4-13. Comparison of novel protein identified from nematocyst of edible jellyfish (A) and highly venomous jellyfish (B) by using two different extractions of SDS and PBS. All novel peptides identified were compared between edible and highly venomous jellyfish (C).

4.5.3.1 Analysis of amino acids composition of the novel peptides

Various novel peptides were identified from edible and highly venomous jellyfish. To observe their amino acids composition, the peptides was analyzed by Protein Information Resource. The results in the figure 4-14 showed that leucine, glycine, and proline were the major amino acids found from the novel peptides of edible jellyfish. And figure 4-15 indicated that glutamate and proline were highly found from the novel peptides of highly venomous jellyfish.

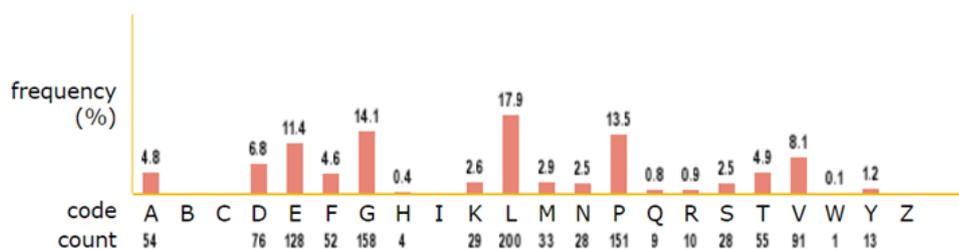


Figure 4-14. Amino acid composition analysis of all novel peptides identified from edible jellyfish.



Figure 4-15. Amino acid composition analysis of all novel peptides identified from highly venomous jellyfish.

4.5.3.2 Prediction of protein domain from the novel peptides

In this experiment, we evaluated the protein domain that could be match with the novel peptides, especially toxin protein domain by using InterPro - EMBL-EBI software. After analysis, there was no toxin proteins domain matching to these novel peptides of edible and highly venomous jellyfish. There was only one peptide (LGEYGFQNALLVR) from edible jellyfish that could match with the domain of serum albumin (IPR014760, PS51438).

4.5.3.3 Biological activity prediction from the novel peptides

In this work, hemolytic, angiotensin I-converting enzyme (ACE) inhibitory, and acetylcholinesterase (AChE) inhibitory activities of the venom from edible and highly venomous jellyfish were studied. The results of these biological activities were demonstrated in the topic 4.7. Therefore, we attempted to predict biological activity of the novel peptides from edible and highly venomous jellyfish. Thus, three biological activity including hemolytic, ACE inhibitory, and AChE inhibitory activities of the novel peptides were selected for prediction. In this study, the peptides with hemolytic and ACE inhibitory activities were predicted by AHTpin and HemoPred software, respectively. Unfortunately, there is no software available for prediction of peptide with AChE inhibitory activity at the present. Therefore, the results of hemolytic and ACE inhibitory activities prediction were indicated. Table 4-1 and 4-2 showed that 55 and 34 novel peptides from edible jellyfish could possibly have ACE inhibitory and

hemolytic activities, respectively. Table 4-3 and 4-4 showed that 82 and 9 novel peptides from highly venomous jellyfish could possibly have ACE inhibitory and hemolytic activities, respectively.

Table 4-1. List of novel peptides derived from edible jellyfish that were predicted to possess ACE inhibitory activity.

Sample extraction	Peptide Sequences	SVM Score	Molecular weight
SDS extraction	LGALGEAGPGAGPVG	0.41	1221.6353
	AGGPGPLGPPGGP	1.26	1183.5984
	LVGKAGMEGEVGRGP	0.02	1471.7454
	LVTSHPLYVPVSHPDE	1.12	1788.9045
	LLETLPK	0.31	812.5007
	LGPPGPP	0.3	633.3486
	LTAGPMP	0.67	701.3418
	LTGVPGP	1.49	639.3591
	GPTGPLG	0.75	597.3122
	PGGPGFP	0.59	627.3016
	LEPTVVDE	1.47	900.444
	LGPSGSAP	1.53	684.3442
	YLADKPEL	0.49	947.4963
	PGGPGGPGP	0.08	691.3289
	PGGPGGGPP	0.08	691.3289
	SFGGGTGSG	0.05	725.298
	LGPPGGP	0.13	747.3915
	PGGGPGGPP	0.08	691.3289
	TLLQFGKTP	0.34	1003.5702
	VVYLPEGQGV	0.53	1059.5601
	LLSKLPDGGP	0.59	995.5651
	LDEYLADKEP	1.07	1191.5659
	NLGGVKKGPTGP	0.3	1123.635
	LGAAGRPGPLGN	0.22	1078.5884
	PGGPGP	0.95	480.2332
	VGPPPP	1.04	562.3115
	LGPPGP	0.96	536.2958
	VVEPYN	0.3	719.349
	VGPLNN	0.52	612.3231
	LLAPPE	1	638.3639

	LLNEPT	0.76	685.3646
	PGGLP	0.57	439.243
	LLNPP	1.09	552.3271
	LEPLP	1.13	567.3268
	LDPTP	0.38	541.2748
	LLAPP	0.99	509.3213
	LGPPP	1.38	479.2744
	LLPP	2.23	438.2842
	VVMP	1.07	460.2356
	LAPP	2.26	396.2372
	PLYE	1.6	520.2533
	LMEP	0.73	504.2254
	LAGP	0.86	356.2059
PBS extraction	TSVKEPML	0.43	919.4684
	VAPEEHPVL	1.37	989.5181
	ELEETGRVL	0.28	1044.5452
	EAEKPKVVL	0.52	1011.5964
	EETYPPEPA	0.35	1031.4447
	YDESGKNPPP	0.36	1102.4932
	EEEAPPPVNP	1.01	1077.4978
	EEEAPPVPGGP	1.84	1077.4978
	LTPELL	0.54	684.4058
	LEEDLL	0.09	730.3749
	LPLEDV	0.15	684.3694
	LPLL	0.86	454.3155

Table 4-2. List of novel peptides derived from edible jellyfish that were predicted to possess hemolytic activity.

Sample Extraction	Peptide Sequences	Molecular weight	Charge
SDS extraction	LGALGEAGPGAGPVG	1221.6353	+1
	VLGANAPAVEAELKKN	1622.8992	+1
	TGFGLKV	720.417	+2
	TLSNGGV	646.3286	+1
	LTGVPGP	639.3591	+1
	LTLGGGE	645.3333	+1
	NFGGGGF	654.2761	+1
	FGGGTGSG	725.298	+1
	TLLQFGKTP	1003.5702	+1

	VVYLPEGQGV	1059.5601	+1
	VGPLNN	612.3231	+1
	LLEGL	543.3268	+1
	LLFDD	621.301	+1
	LLANN	543.3016	+1
	LGGSL	445.2536	+1
	LAVDL	529.3112	+1
	LYGFN	612.2907	+1
	LLEML	633.3408	+1
	LDVDL	573.301	+1
	LGGAV	415.2431	+1
	LLPP	438.2842	+1
	LLEM	520.2567	+1
	LLEE	502.2639	+1
	LLFM	538.2825	+1
PBS extraction	DDLDF	623.2438	+1
	VVDLL	557.3425	+1
	VLGF	434.2529	+1
	LVEL	472.2897	+1
	VGLF	434.2529	+1
	LPLL	454.3155	+1
	LGLL	414.2842	+1
	VLDF	492.2584	+1
	TFAL	450.2478	+1
	FDDF	542.2012	+1

Table 4-3. List of novel peptides derived from highly venomous jellyfish that were predicted to possess ACE inhibitory activity.

Sample extraction	Peptide Sequences	SVM Score	Molecular weight
SDS extraction	FYPGGDTLFGK	0.02	1200.5815
	GPPGP	0.84	423.2118
	VAPEE	0.14	543.254
	PGGPP	0.84	423.2118
	PVVET	0.19	543.2904
	APVEE	0.14	543.254
	LDEP	0.37	472.2169
	YPPP	3.57	472.2321
	PGPP	2.93	366.1903
	EEVP	0.24	472.2169

PBS extraction	EEPANVEETAKSE	0.74	1431.6365
	EDEAKNNEEEAPR	0.16	1529.6594
	EGASDKPKDEAENKTE	0.69	1746.7908
	NSGGGGGGSSGGRGSGGGSSGGSLNR	0.58	2078.9072
	DPEDVLR	1.22	842.4134
	PGGPGPP	0.37	577.2859
	EEVPVKE	0.48	828.4229
	EDPEPVR	1.81	840.3977
	PAVEEPAK	0.17	839.4388
	FAGDDAPR	0.23	847.3824
	PEEEVVTR	0.75	957.4767
	PEEEVVTH	0.85	938.4345
	LDEDAPER	1.91	943.4246
	VEEPAKVE	0.23	899.46
	GPPGGPGP	0.22	691.3289
	VLSGGTTM	0.1	780.3688
	LVDKVTDE	0.28	917.4705
	EEVPVKEE	0.14	957.4655
	PGPGGPGP	0.22	634.3074
	GDDPTLEK	0.5	873.408
	PAKVEEPA	0.17	839.4388
	DEELRSPN	0.77	958.4355
	DDVPEVQK	1.09	928.4501
	ESGPSLVH	1.03	824.4028
	GPPGGGPP	0.22	634.3074
	EPATEEPVK	0.19	998.492
	EPEEEVLVK	0.35	1070.5496
	EPEEEVVTH	0.46	1067.4771
	EPEEEVVTR	0.43	1086.5193
	EPEEELVTR	0.35	1100.5349
	ALDEDAPER	1.45	1014.4617
	MPDDAKEPT	0.13	1002.4328
	EDLDLTESK	0.11	1048.4924
	GPPGGPGPG	0.08	691.3289
	KEVVPKEPE	0.84	1053.5706
	TPGDELEGS	1.1	903.3821
	KEVVPKEEP	0.84	1053.5706
	YDESGPSLVH	0.49	1102.4932
	TESDELTRP	0.53	1147.5356
	EEPEEEVLVK	0.11	1199.592
TEEPEEELVTR	0.15	1330.6252	
TEEPEEEVVTR	0.15	1316.6096	
EETPAKVDEPAN	0.05	1197.5513	
ETEPEEEVVTR	0.15	1316.6096	

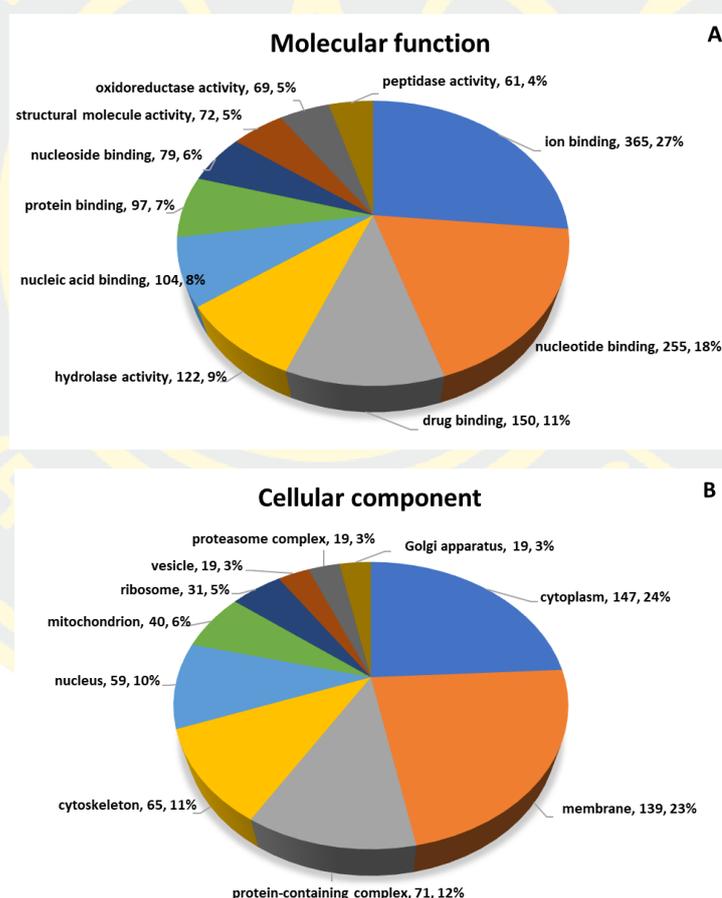
ETEPEEEVLVK	0.08	1300.6399
EEDPDALAETGR	0.51	1301.5735
PPALDE	0.38	640.3068
APTPEM	0.25	644.2839
PSAPEP	0.4	596.2806
LDPGNP	0.27	611.2914
TPYGGP	1.33	590.27
LLDTDN	1	689.3232
PPGPP	1.3	463.243
EEVVP	0.3	571.2853
EELAP	0.16	557.2697
PPENF	0.82	602.27
LEEP	0.22	486.2325
VVGY	0.59	436.2322
PPPL	3.11	422.2529
SPAF	0.65	420.2009
YPTE	1.18	508.2169
PSYP	2.7	462.2114
LVSP	0.99	414.2478
PVSY	1.77	464.2271
PFSL	0.86	462.2478
PEVP	1.95	440.2271
PELP	1.97	454.2427
LLAP	0.9	412.2686
PVFE	0.8	490.2427
VVVP	0.87	412.2686
DVMP	0.74	476.1941
SPVY	1.77	464.2271

Table 4-4. List of novel peptides derived from highly venomous jellyfish that were predicted to possess hemolytic activity.

Sample Extraction	Peptide Sequences	Molecular weight	Charge
PBS extraction	VLSGGTT	633.3334	+1
	VLSGGTMM	780.3688	+1
	LGGGF	449.2274	+1
	LGGGL	415.2431	+1
	LAGGL	429.2587	+1
	LAGF	406.2216	+1
	LLEE	502.2639	+1
	LLAP	412.2686	+1
	VVVP	412.2686	+1

4.6 Gene ontology annotation

Molecular function, cellular component, and biological process of proteins identified were analyzed using a gene ontology annotation tool. Figure 4-16A and 4-17A indicated that binding function was the major molecular function annotated from the proteins of edible and highly venomous jellyfish. Cytoplasm was the main cellular component of the proteins identified from these two jellyfish species (Figure 4-16B, and 4-17B). Regulation of biological process was the main biological process of the proteins identified from both edible and highly venomous jellyfish (Figure 4-16C, and 4-17C).



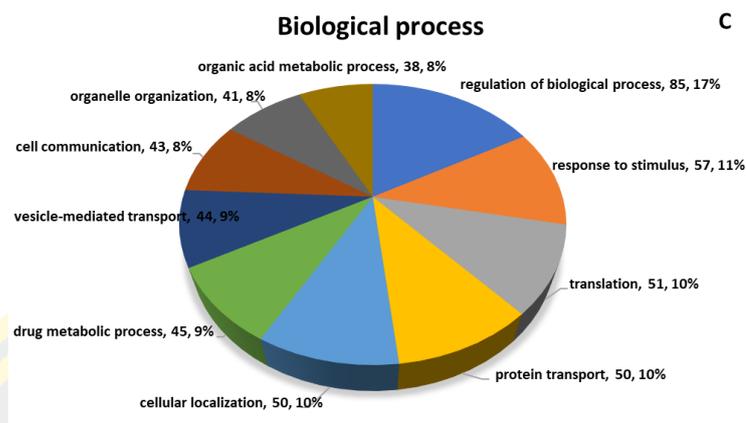
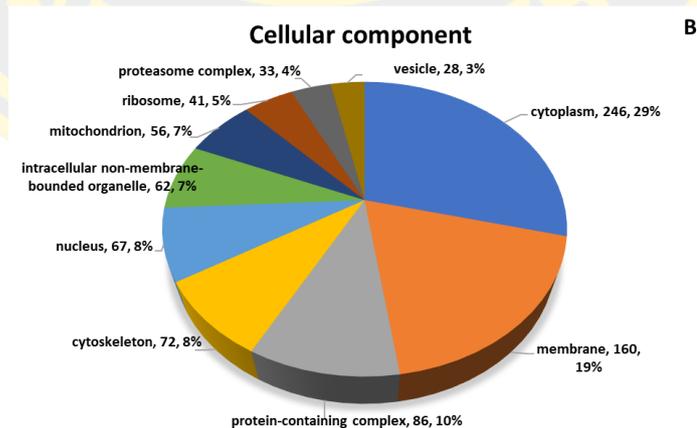
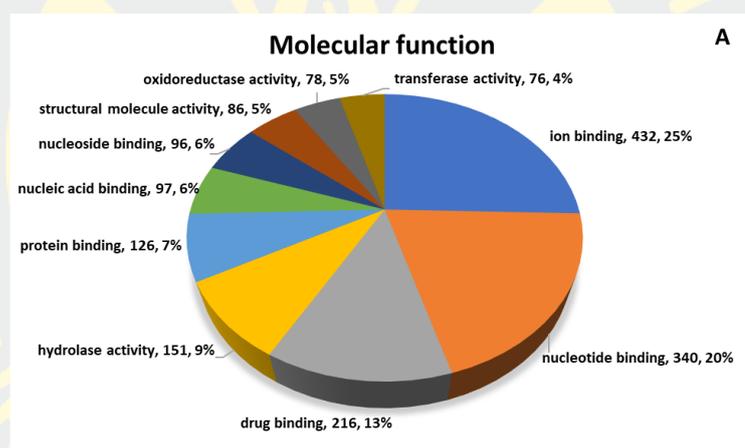


Figure 4-16. Gene ontology annotation of protein identified from edible jellyfish, including molecular function (A), cellular component (B), and biological process (C).



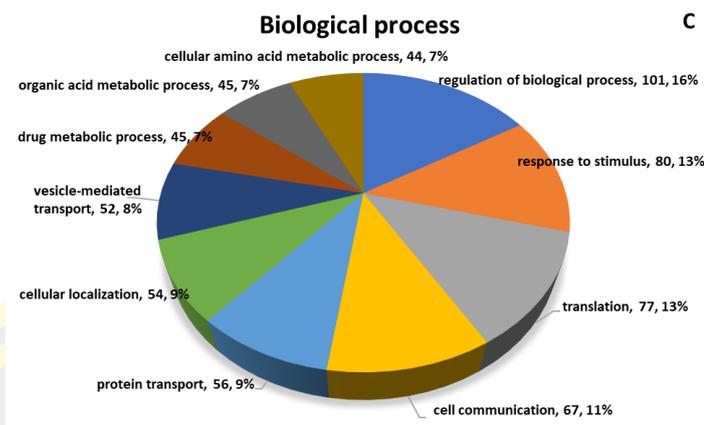


Figure 4-17. Gene ontology annotation of protein identified from highly venomous jellyfish, including molecular function (A), cellular component (B), and biological process (C).

4.7 Biological activity

4.7.1 Hemolytic activity

Hemolytic activity of the venom proteins was evaluated using pig red blood cells. The % hemolysis was calculated by comparing to the positive control (0.1% triton x-100). The results demonstrated that toxin proteins from *R. Hispidum* had hemolytic activity against pig red blood cells (Figure 4-18). The EC₅₀ value of the edible jellyfish toxins was as 0.243 ± 0.032 mg/ml (Table 4-5). For the proteins extracted from nematocyst of *S. malayensis*, no hemolytic effect was observed.

There was hemolysis protein of toxin CaTX-A that was identified from edible jellyfish. The hemolytic effect against the red blood cells of edible jellyfish toxin in this study could be resulted from this protein. However, pore-forming proteins, including DELTA-actitoxin-Aas1a, DELTA-sagatoxin-Srs1a, and DELTA-actitoxin-Aeq1c were identified from highly venomous jellyfish. These pore-forming toxins could cause hemolysis effect as well, but there was no hemolytic effect found in this study. It could cause from low amount of these toxins extracted from nematocysts that was not enough to study for this activity. In further study, purification of these pore-forming proteins prior to determination of hemolytic activity might be necessary for studying the hemolytic effect of these toxins.

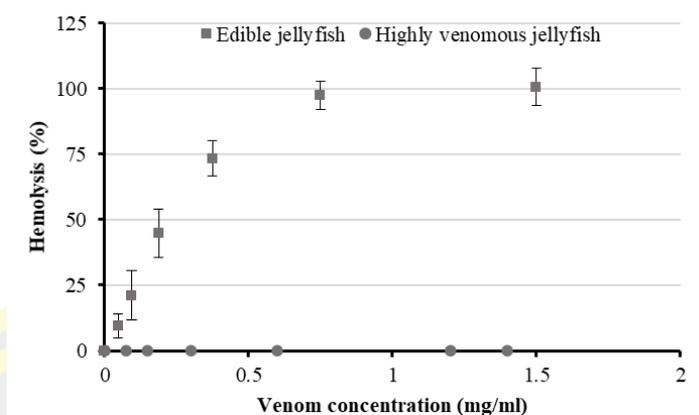


Figure 4-18. Determination of hemolytic activity of the toxins from edible and highly venomous jellyfish at various concentrations.

* The triplicates were measured and represented as means \pm S.D.

Table 4-5. EC₅₀ values of hemolysis ability of the jellyfish venom proteins.

Jellyfish toxins	EC ₅₀ (mg/ml)
Edible jellyfish	0.243 \pm 0.032
Highly venomous jellyfish	N.D.

4.7.2 Angiotensin I-converting enzyme (ACE) inhibitory activity

ACE is an enzyme that converts angiotensin I to angiotensin II in the liver. Production of angiotensin II causes hypertension. Many commercial inhibitors for ACE are short peptides; therefore, ACE inhibitory activity of the jellyfish venom proteins was evaluated. It could be useful for a medical application for the treatment of hypertension disease. The results in figure 4-19 indicated that jellyfish toxins from edible and highly venomous jellyfish cannot inhibit ACE. Besides, we found that ACE was also identified from the nematocyst of edible jellyfish (Appendix D, table D-2), which could lead to negative anti-ACE activity of the toxin from the edible jellyfish (Figure 4-19A).

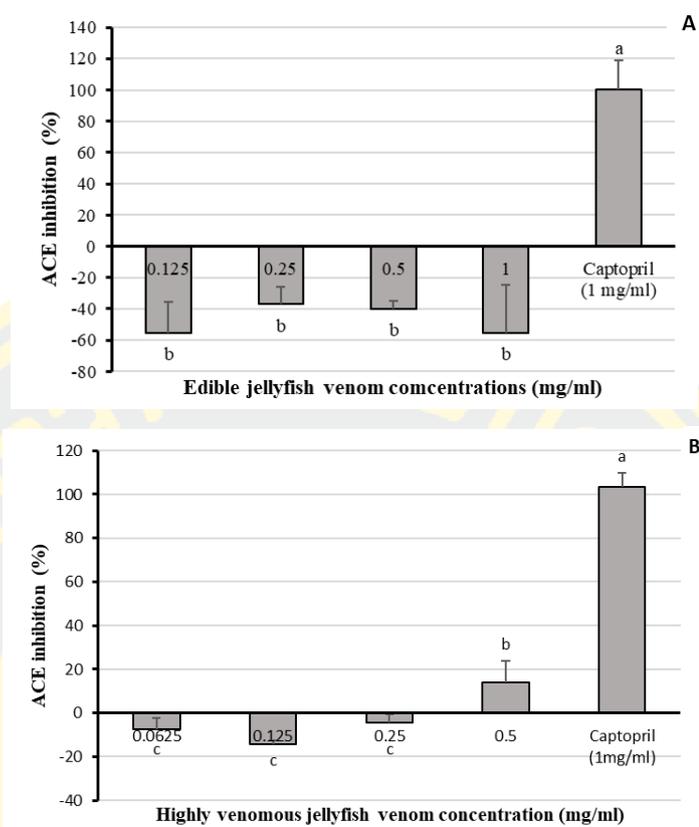


Figure 4-19. Measurement of angiotensin I-converting enzyme inhibitory activity of the toxin proteins from edible jellyfish (A) and highly venomous jellyfish (B) at different concentrations.

* All data in this study was demonstrated in the form of means \pm S.D. The different letters indicated significant difference ($p < 0.05$).

4.7.3 Acetylcholinesterase (AChE) inhibitory activity

AChE is one of the main causes of the Alzheimer's disease. The neurotransmitter, acetylcholine, can be hydrolyzed by this enzyme. Decreasing of acetylcholine can lead to the brain problems, such as memory impairment. Thus, acetylcholinesterase inhibitory activity of both jellyfish venoms was evaluated. The result showed that proteins from the edible jellyfish could inhibit AChE, which the protein concentration of 2 mg/ml showed 21 percent inhibition (Figure 4-20A). But, toxin proteins from highly venomous jellyfish showed no AChE inhibitory activity (Figure 4-20B). Inhibition of AChE by the venom from edible jellyfish could be developed into new drug for Alzheimer's disease.

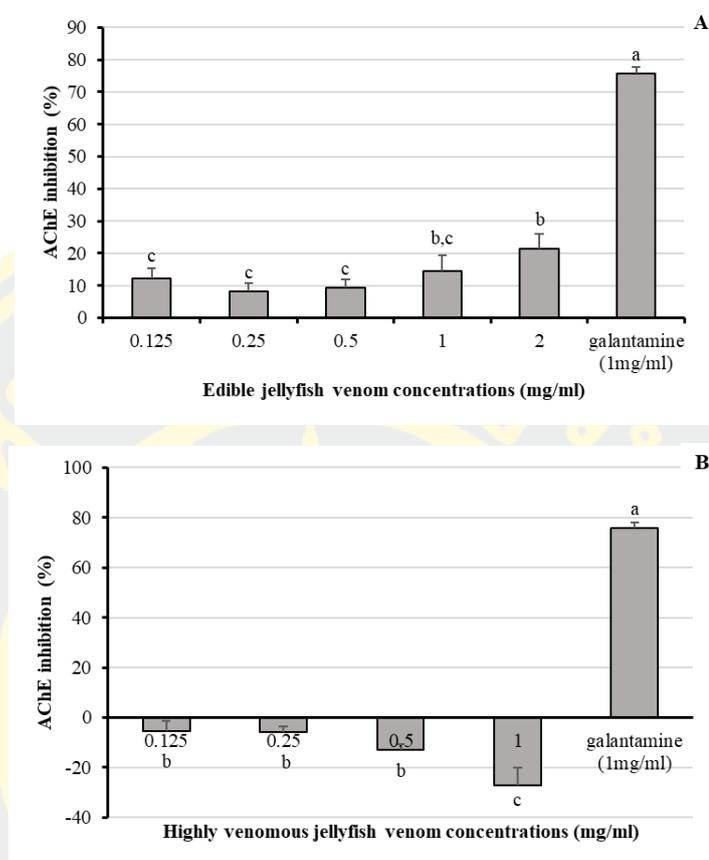


Figure 4-20. Determination of acetylcholinesterase inhibitory activity of the toxin proteins from edible jellyfish (A) and highly venomous jellyfish (B) at different concentrations.

*The results were exhibited as means \pm S.D, which different letters indicated significant difference ($p < 0.05$).

CHAPTER 5

DISCUSSIONS AND CONCLUSIONS

5.1 Discussions

Envenomation of jellyfish affects human health with different symptoms. Some jellyfish, such as box jellyfish (*Chironex fleckeri*) and Portuguese man-of-war (*Physalia physalis*) can be lethal within minutes (Lumbley et al., 1988; Burnett, & Gable, 1989). Less toxic jellyfish was also reported to cause injury, such as pruritus, eruption, painful, and burning skin (Kawahara et al., 2006). *Rhopilema hispidum* is distributed along the Gulf of Thailand, including bangsae coastal area. Jellyfish venoms are contained in specialized organelle called nematocysts, which were densely located in the tentacle (Beckmann & Özbek, 2012). At the present, there is no antivenom for jellyfish envenomation available in Thailand. In this project, the aims of this study were to identify proteins from nematocysts of edible (*R. hispidum*) and highly venomous jellyfish (*S. malayensis*) to investigate toxins component for the development of antivenom in the future. In addition, biological activities of both jellyfish venoms were evaluated including hemolytic, angiotensin I-converting enzyme (ACE) inhibitory, and acetylcholinesterase (AChE) inhibitory activities.

To analyze nematocyst protein components of edible and highly venomous jellyfish, proteins were extracted from nematocysts of jellyfish tentacles by autolysis method (Bloom et al., 1998). Morphology of nematocysts released from the jellyfish tentacles were observed using a light microscope. Round structure was mostly observed from nematocysts of edible jellyfish, whereas oval structure was mostly observed from highly venomous jellyfish. Various size of nematocysts can be observed from these two species. Nematocysts of both species had an average diameter of 10-20 micrometers. In other jellyfish species, nematocysts with multiple sizes were also found (Doyle et al., 2017). Analysis of nematocysts types from edible jellyfish was previously reported. Four types of nematocysts were classified from *R. hispidum*, including small ellipsoid isorhiza, medium round isorhiza, large round isorhiza, and rhopaloid (Kondo et al., 2020). It is noticeable that round isorhiza was mostly observed from nematocyst of edible jellyfish similar to this study. However,

there is no information about nematocyst structures of the highly venomous jellyfish. *Pelagia noctiluca* is in the same family as *S. malayensis*. There was previous reports that about 5 types of nematocyst found from *P. noctiluca*, including heterotrichous microbasic euryteles, heterotrichous isorhizas, holotrichous O-isorhizas, atrichous a-isorhizas, and undescribed type (Avian, Del Negro, & Sandrini, 1991). From the previous work of Avian et al. (1991), three types of nematocysts with oval structure were observed from *P. noctiluca*, including heterotrichous microbasic euryteles, heterotrichous isorhizas, atrichous a-isorhizas. It was similar to nematocyst structure of *S. malayensis*. Moreover, thread-like tubes discharged of these two species was incidentally observed. We noticed that thread-like tubes discharged from nematocyst of highly venomous jellyfish were longer than edible jellyfish. It was in agreement with previous reports of Kondo et al. (2020) and Avian et al. (1991), which stated that the length of thread-like tubes discharged from edible jellyfish was about 313 micrometers. And length of thread-like tubes discharged from nematocyst of *P. noctiluca*, which was in the same family as highly venomous jellyfish was reported up to 570 micrometers. One factor that cause higher toxicity could be the longer thread-like tubes discharged from the highly venomous jellyfish, which could penetrate through the human skin.

After nematocyst releasing from the tissue, two different procedures were used to extract toxin proteins from nematocysts, including (1) 2% SDS coupled with sonication, and (2) PBS buffer coupled with ultrasonication. Using sonication and ultrasonication for proteins extraction was performed according to the previous reported of Ayed et al. (2016) and So et al. (2016). Based on property of detergent, SDS was used to destroy nematocyst membrane to release the toxin. However, function of the proteins was not preserved after using SDS. Thus, to maintain the function of the proteins, PBS buffer was alternatively used to extract proteins. Protein concentrations from nematocyst of edible jellyfish were 2871.388 and 2801.944 $\mu\text{g/ml}$, using SDS and PBS extraction, respectively. And concentrations of the proteins from nematocysts of highly venomous jellyfish were 349.091 and 525.591 $\mu\text{g/ml}$, using SDS and PBS extraction, respectively. We found that both different extraction method could release proteins from edible and highly venomous jellyfish. Higher proteins concentration was observed from edible jellyfish than highly

venomous jellyfish could be resulted from the larger number of nematocysts extracted from edible jellyfish than the highly venomous jellyfish, due to larger size of the jellyfish. Bell diameter of edible jellyfish was reported to be about 30 to 60 cm, while the bell diameter of highly venomous jellyfish was previously reported to be about 1 to 13.5 cm (Gul & Morandini, 2015; Morandini & Gul, 2016). After protein extraction, the morphology of the remaining pellets was observed. Using both of SDS and PBS extraction, there were both discharged and undischarged nematocysts in the remaining pellet.

Proteins from these two species had similar molecular weight range, between 10 to 250 kDa. However, there was different band intensity between edible and highly venomous jellyfish. High intensity of protein bands was shown at the molecular weight range of 75 to 150 kDa from edible jellyfish sample and 37 kDa from highly venomous jellyfish sample. Furthermore, using different procedure for protein extraction provided different band intensity; SDS extraction provided high intensity of the protein band at the molecular weight of 250 kDa from highly venomous jellyfish sample, which was not observed in the PBS extracted sample.

Nowadays, studies of jellyfish venom from various species are increasingly of interest. The venoms component was investigated to find the cause of clinical symptoms from jellyfish sting and to develop new drugs for therapeutics. Proteomic analysis of the box jellyfish (*Chironex fleckeri*) venoms was reported. Sixty-one proteins were identified, which were related to the cytolytic, sensation of pain, inflammatory, and lethal properties (Brinkman et al., 2012). Moreover, there were 163 proteins identified from the venom of *Chrysaora fuscescens*, which 27 of those proteins were found to be toxins, such as venom allergens and pore-forming toxins (Ponce, Brinkman, Potriquet, & Mulvenna, 2016). In this study, bottom-up proteomic, including in-solution and in-gel digestion was used to analyze proteins composition of edible and highly venomous jellyfish. MS/MS spectrum derived from these two jellyfish species were search against the Uniprot databases of (A) taxonomy: Cnidaria, (B) taxonomy: Cnidaria and keyword: toxin, and (C) keyword: toxin.

In the in-solution digestion analysis, using database A and B for protein identification, we found that PBS extraction provided higher number of toxin proteins identified than SDS extraction. PBS buffer was used to extract proteins coupled with

ultrasonication. The ultrasonication was previously reported to be more effective method for disruption of yeast cells than using sonication bath, due to the direct contact between the ultrasonication probe and the sample solution. So, the sample directly received shear force for disruption the cells. Using a sonication bath, the sample received lower shear force for disruption (Liu, Zeng, Sun, & Han, 2013). Therefore, in our experiment, using PBS coupled with ultrasonication provided higher number of toxin proteins identified than using SDS extraction method. Moreover, in this study, the number of toxins identified from highly venomous jellyfish were higher than edible jellyfish. Major toxins identified from these two species were involved with metalloproteases and neurotoxins. Metalloprotease was also majorly found from toxins of other jellyfish species, such as *Nemopilema nomurai*, *Rhopilema esculenta*, *Cyanea nozakii*, *Aurelia aurita*, and *Pelagia noctiluca*. Effects of metalloprotease were related to toxicity, hemolysis, lethality, and inflammation (Yu et al., 2020; Lee et al., 2011; Li, Yu, Yue, & Li, 2018). The metalloproteases were known to be significance factor for clinical symptoms of jellyfish sting (Lee et al., 2011). In addition to metalloproteases, neurotoxins were also identified from edible and highly venomous jellyfish. There was previous report about neurotoxins from jellyfish *Cyanea nozakii* that was related to pain and itch symptoms (Li et al., 2016). Therefore, information of jellyfish toxins identified in this study could be beneficial for treatment of symptoms from *R. hispidum* and *S. malayensis* envenomation. *R. hispidum* envenomation causes eruption, dermatitis, and oedema symptoms (Kawahara et al., 2006; Kondo et al., 2020). There was no report about clinical symptom from *S. malayensis*; however, toxins from *P. noctiluca* (close family of *S. malayensis*) can cause pigmentary lesions or whip-like scar at the area contact sting (Del Pozo et al., 2016; Frazão et al., 2017).

Brinkman et al. (2012) reported that glycosylation of the proteins was commonly found from toxin of *Chironex fleckeri*. Thus, we attempted to enhance number of glycosylated proteins identification from edible and highly venomous jellyfish. PNGaseF enzyme was used for deglycosylation, followed by trypsin digestion (Orsini et al., 2018). PNGase F enzyme provided cleavage site at the amide bond between glycan group and asparagine (Suzuki, Kitajima, Inoue, & Inoue, 1995). The results indicated that 62 and 133 proteins were further identified from edible and

highly venomous jellyfish, respectively, in addition to the proteins from only trypsin digestion. Toxin proteins in the groups of metalloproteases, neurotoxins, and hydrolase were identified from edible jellyfish; whereas metalloproteases, neurotoxins, and pore-forming proteins were identified from highly venomous jellyfish. We noticed that pore-forming proteins were identified from highly venomous jellyfish after using PNGaseF digestion. Pore-forming protein was only found from highly venomous jellyfish, and not observed in the edible jellyfish sample. Membrane-bound pore-forming proteins can insert through lipid bilayer and generate pore in the bilayer. As example, forming of oligomeric transmembrane pores could be caused by actinoporins, which affected osmotic imbalance and cell death (Podobnik & Anderluh, 2017). It is possible that stronger toxic effect in the highly venomous jellyfish, as compared to edible jellyfish, could be resulted from these pore-forming proteins. Moreover, the nematocyst proteins identified from highly venomous jellyfish in the in-solution digestion were higher than those from edible jellyfish. The results showed that 429 and 595 proteins identified from edible and highly venomous jellyfish, respectively.

Based on previous work of Choksawangarn et al. (2012), comparison of three methods (in-gel digestion, in-solution digestion, and on-filter proteolysis) was used to remove detergent. They found that the highest number of proteins identified was from using in-gel digestion, which could increase the number of low abundant proteins identified. In this project, proteins from crude tentacle and nematocyst proteins were also compared using the in-gel digestion protocol, followed by searching with database A and B. A number of 375 and 395 proteins were identified from crude tentacle of edible and highly venomous jellyfish, respectively. In this study, using PBS extraction provided higher number of proteins identified from both types of jellyfish than using SDS extraction. Metalloproteases, hydrolases, and neurotoxins proteins were found from both edible and highly venomous jellyfish. The metalloproteases were also major protein found from these two species similar to in-solution digestion. In addition, proteins with hemolytic and pore-forming functions were found from edible and highly venomous jellyfish, respectively. The pore-forming protein was also only observed in the toxin of highly venomous jellyfish by analysis in the in-gel digestion. However, hemolytic function of the toxin CaTX-A

was identified from the edible jellyfish. The CaTX-A toxin was isolated from the box jellyfish *Carybdea alata* that showed strong hemolytic activity (Nagai et al., 2000). There were previous reports about 13 toxins proteins identified from *Nemopilema nomurai*, which thrombin-like toxin and hemolysins were found to involve with lethality (Li, Yu, Li, & Li, 2020). For toxins identified from edible and highly venomous jellyfish, these toxins could be the key to clinical treatment of these two species.

In addition, all nematocyst proteins identified from these two jellyfish species were compared between in-solution and in-gel digestion. Larger number of nematocyst proteins were identified from in-gel digestion than in-solution digestion of both edible and highly venomous jellyfish. This was in agreement with the previous work that less abundant proteins could be identified by using in-gel digestion experiment (Choksawangkar et al., 2012). Combining all proteins identified from both procedures (in-gel and in-solution digestion), larger number of proteins were identified from highly venomous jellyfish (883 proteins), as compared to edible jellyfish (809 proteins). Our result showed superior number of proteins identified from edible and highly venomous jellyfish, comparing to the other studies. There were 150 proteins identified from venom of *Nemopilema nomurai* by using proteomic analysis (Choudhary et al., 2019). A total of 181 proteins were identified from nematocyst of *Stomolophus meleagris* (Li et al., 2012). Moreover, there were 163 proteins identified from jellyfish *Chrysaora fuscescens* (Ponce et al., 2016).

Intact small proteins from nematocyst of edible and highly venomous jellyfish could be underrepresented in the bottom-up studies, due to limitation of the sample preparation methods and bioinformatics constrains. Therefore, top-down proteomics was employed to analyze this group of small proteins. The importance of small proteins from venomous animals have been reported to use for medical therapeutics. For example, ziconotide, a small toxin from the cone snail *Conus magus*, is the commercial drug for treatment of severe chronic pain (McGivern, 2007). Peptides from scorpion venom, such as chlorotoxin (ClTx) from *Leiurus quinquestriatus*, and margatoxin (MgTx) from *Centruroides margaritatus* could be developed for anticancer therapeutic (Ortiz, Gurrola, Schwartz, & Possani, 2015). Therefore, small proteins from these two jellyfish were also analyzed to seek for potential proteins with

significant functions. In the top-down proteomics, using two different extraction methods, the results were in contrast with the results from in-solution and in-gel digestion experiments. Using SDS for protein extraction were better than using PBS extraction, because SDS extraction provided a list of proteins identified from both edible and highly venomous jellyfish. But using PBS extraction only provided proteins identified from edible jellyfish. Nephrotoxin PsTX-115 (Fragments) toxin was identified from highly venomous jellyfish by using SDS extraction.

In addition to the Cnidaria database, alternative database containing toxin proteins from all venomous animals were used (database (C) with keyword: toxin). It was reported that some of the jellyfish venoms were homologous to other venomous animals, such as spider, scorpion, and snake (Weston et al., 2013). In this study, toxins identified from all venomous animals were majorly involved with the hydrolase function that was found from both edible and highly venomous jellyfish. There were previous reports about hydrolase protein (glycoside hydrolase) identified from jellyfish *Chrysaora fuscescens*, which this toxin was involved with chitin degradation. Normally, chitin is the composition of exoskeletons that was found in the creatures of arthropods and insects (Ponce et al., 2016). Other functions, including neurotoxic, cytolysis, hemolysis, and metalloprotease inhibitor functions were also found from toxins of these two jellyfish species. Besides, metalloprotease was found in the toxins of highly venomous jellyfish by using database C.

For proteins without in the database, de novo sequencing was performed to identify novel peptides from edible and highly venomous jellyfish. Small proteins filtered through 3 kDa cut off filter were analyzed by PEAK software (Zhang et al., 2012). There were 159 and 201 peptides identified from edible and highly venomous jellyfish, respectively. Almost all peptides identified from edible jellyfish were distinct from highly venomous jellyfish. These novel peptides had molecular weight range from 350 to 2000 Da. Protein Information Resource software was used to analyze amino acid composition of all novel peptides identified. We found that leucine, glycine, and proline were mostly found in the peptides sequence of edible jellyfish. And glutamate, and proline were the major amino acid found from the peptides of highly venomous jellyfish. In addition, protein domain was predicted from

these novel peptides in order to find toxin domain match with the peptide. However, there was no toxin domain matched to the novel peptides in this study.

Many biological activities of the novel peptides from other species were reported. For example, novel peptide (SmP90) from the venom of *Stomolophus meleagris* showed antioxidant activity (Li et al., 2012). Novel three kunitz-like peptides identified from the toxin of *Palythoa caribaeorum* (Anthozoa) could be developed for neurodegenerative disease therapeutics (Liao et al., 2018). In this study, we observed biological activity of these novel peptides by using bioinformatic tools for prediction. AHTpin and HemoPred software were used to predict ACE inhibitory and hemolytic activities of the peptides, respectively (Kumar et al., 2015; Win et al., 2017). The results showed that 55 peptides from edible jellyfish and 82 peptides from highly venomous jellyfish could have ACE inhibitory activity. And 34 and 9 peptides were predicted to have hemolytic activity from edible and highly venomous jellyfish, respectively. These novel peptides could be beneficial for disease treatment in the future. Because the small peptides are increasingly of interest to develop as drug, due to their ease of synthesis, high specificity, and infiltrate into the cell membrane (Marqus, Pirogova, & Piva, 2017; Gupta et al., 2013).

Molecular function, cellular component, and biological process were analyzed from all proteins identified from edible and highly venomous jellyfish. For the proteins identified from both jellyfish, it was found that binding function was a major molecular function annotated from these two species. Cytoplasm and regulation of biological process were annotated to be the most frequently found cellular component, and biological process, respectively. From the previous study, functions of the protein were found to be distinctive in each jellyfish species. Function of the proteins identified from *Chrysaora fuscescens* were classified, which binding function was the main molecular function annotated from proteins identified. Cell and cellular process were annotated as major cellular component and biological process of the proteins identified from this species (Ponce et al., 2016). Moreover, molecular function, cellular component, and biological process of the proteins identified from *Nemopilema nomurai* were involved with translation regulator activity, cell junction, and cellular process, respectively (Choudhary et al., 2019).

There were several reports about biological activity of the jellyfish venoms, including cytotoxic, hemolytic, neurotoxic, and cardiotoxic activities. In this work, hemolytic activity was determined. The hemolysis effect was evaluated by using porcine red blood cells. The results indicated that hemolysis effect was only found from toxins of edible jellyfish at the EC_{50} of 0.243 ± 0.032 mg/ml. As compared to same genus of edible jellyfish species, venoms of jellyfish *Rhopilema spp.* had 50% hemolysis effect against the erythrocytes of mice, humans, and sheep at concentrations of 250, 300 and 400 μ g/ml (Jafari, Honari, Zargan, & Jahromi, 2019). We found that hemolytic activity of the toxins from *R. hispidum* was similar to the toxins from *Rhopilema spp.*. Moreover, highly toxic jellyfish was reported to possess higher EC_{50} value than the edible jellyfish. As example, CnPH toxin isolated from jellyfish *Cyanea nozakii* showed 50% hemolysis of chicken erythrocyte at the concentration of 5 μ g/ml (Li et al., 2011). And SmTx toxin from *Stomolophus meleagris* could cause 50% hemolysis at concentration of 70 μ g/ml (Li et al., 2013). It was possible that hemolytic activity observed from edible jellyfish toxins could be resulted from CaTX-A protein identified. Hemolytic activity of CaTX-A toxin from *Carybdea alata* was previously reported (Nagai et al., 2000).

In our study, pore-forming proteins (DELTA-actitoxin-Aas1a, DELTA-sagatoxin-Srs1a, and DELTA-actitoxin-Aeq1c) were identified from highly venomous jellyfish. Normally, hemolysis effect could be resulted from pore-forming proteins, such as actionoporins, CFTX toxin, and hydralysins proteins (Podobnik & Anderluh, 2017). But, in this study, hemolytic activity was not observed from toxins of highly venomous jellyfish. It could be caused by several factors. Firstly, highly venomous jellyfish sample was obtained from the aquarium of the Institute of Marine Science at Burapha University. It was not collected from nature. Therefore, toxins component of the cultured jellyfish could be less toxic than those from the nature. Secondly, the amount of toxin proteins extracted from highly venomous jellyfish was possibly not enough to study their hemolytic activity. It was observed that thread-like tubes discharged from highly venomous jellyfish were longer than those from edible jellyfish. That could lead to high efficiency of toxin injection to the human skins during envenomation. Therefore, after highly venomous jellyfish envenomation, higher amount of toxins could be penetrated into the human skin than the amount of

extracted toxins performed in this study. However, there was no report about serious symptoms of hemolytic effect from the edible jellyfish envenomation; while we observed this activity in our study. It is possible that toxins from edible jellyfish cannot penetrate to the human blood vessel due to short thread-like tubes discharged of nematocyst. Lastly, it could be caused by less abundance of hemolysins extracted from the nematocyst of highly venomous jellyfish. To confirm about hemolytic activity in the venom of highly venomous jellyfish, these hemolysins should be purified prior to determination of the hemolytic activity in the future study.

In addition, jellyfish venom could be applied in medical treatment. Hence, angiotensin I-converting enzyme (ACE) and acetylcholinesterase (AChE) inhibitory activities of the toxins from edible and highly venomous jellyfish were investigated. The results demonstrated that venom proteins of these two species could not inhibit the activity of ACE. We found that ACE was also identified in edible jellyfish venom. That could enhance negative anti-ACE activity from the edible jellyfish venom. However, another study indicated that the proteins hydrolysate from *R.hispidum* showed the ability to inhibit ACE (Sun et al., 2018). Furthermore, there were previous reports that ACE could be inhibited by venom hydrolysate from the box jellyfish (*Chiropsalmus quadrigatus*) (So et al., 2016).

At present, aging population has been increasing, which this population has a high risk to become Alzheimer's disease. One of the main causes of the Alzheimer's disease was the reduction of acetylcholine, an important neurotransmitter, due to over-function of acetylcholinesterase enzyme (AChE). Enhancement of acetylcholine by inhibiting AChE could be used as a treatment for Alzheimer's disease (Orhan, Şener, Choudhary, & Khalid, 2004). Therefore, AChE inhibitory activity of the venoms from edible and highly venomous jellyfish was also evaluated. Edible jellyfish venom showed AChE inhibitory activity. The venom concentration of 2 mg/ml showed about 21% inhibition. However, for the other reports about Alzheimer's disease treatment, there were previous reports about neurosteroidal alkaloid from venom of *Cassiopea andromeda*. It was found that neurosteroidal alkaloid exhibited acetylcholinesterase inhibitory activity with IC_{50} value of 2.24 μ M (Mohebbi et al., 2018). In addition to acetylcholinesterase, butyrylcholinesterase (BChE) is another enzyme which plays a similar role to acetylcholinesterase (Orhan et

al., 2004). Antibutyrylcholinesterase activities was evaluated from crude venom of *Pelagia noctiluca*. There were two fractions that contained anti-BuChE activity with the IC₅₀ values of 58 and 75.5 µg/ml (Ayed et al., 2012). Moreover, there was a previous report about altering the swimming pattern of zebrafish, that was correlated with the downregulation of acetylcholinesterase activity in the brain tissue after treatment with the venoms from *Nemopilema nomurai* (Prakash et al., 2020).

5.2 Conclusions

After nematocysts extraction from jellyfish tentacle tissue, we found that nematocyst morphology from edible (*Rhopilema hispidum*) and highly venomous (*Sanderia malayensis*) jellyfish were distinct. Round structure and oval structure were mostly observed from the nematocysts of edible jellyfish and highly venomous jellyfish, respectively. The length of thread-like tubes discharged from the nematocyst might be one of the factors affecting the severity of the jellyfish envenomation. We found that the tubes discharged from nematocyst of highly venomous jellyfish were longer than those from edible jellyfish. In this work, proteins were extracted from nematocysts by using two methods, including (1) 2% SDS coupled with sonication, and (2) PBS buffer coupled with ultrasonication. It was found that these two procedures provided similar protein concentration and nematocyst morphology. In addition, identification of proteins by using different extraction was examined. We found that using PBS extraction was better than SDS extraction, due to higher number of toxins identified from the in-solution digestion and the in-gel digestion experiments. Based of LC-MS/MS analysis, followed by a search against the Cnidaria database ((A) taxonomy: Cnidaria database, (B) taxonomy: Cnidaria and keyword: toxin), toxin proteins identified from edible and highly venomous jellyfish were mostly in the group of metalloproteases. Functions of the toxin proteins identified from these two species were mostly similar, such as neurotoxic, hemolytic, hydrolase, and metalloprotease functions. Although the functions of proteins identified were similar, but types of the proteins from these two species were mostly different. Pore-forming proteins were only identified from highly venomous jellyfish. These pore-forming proteins could lead to more serious toxic effect than edible jellyfish. Moreover, we found that the number of nematocyst proteins identified from highly

venomous jellyfish were larger than that from edible jellyfish. In addition, hydrolase function was a major function of the proteins identified in the alternative database of the toxins from all venomous animals. The data about toxins identified in this study could be used for development of drugs for treatment of jellyfish envenomation.

Three biological activities, including hemolytic, angiotensin I-converting enzyme (ACE) inhibitory, and acetylcholinesterase (AChE) inhibitory activities were investigated from the venoms of both jellyfish. Hemolytic and AChE inhibitory activities were solely exhibited from the toxins of edible jellyfish. Furthermore, pore-forming proteins were identified from highly venomous jellyfish. But there was no hemolytic activity from the toxins of highly venomous jellyfish. For ACE inhibitory activity, toxins from both edible and highly venomous jellyfish could not inhibit ACE, which this enzyme was also identified from edible jellyfish. The information about venom biological activities from these two jellyfish species could be useful to develop as novel drugs for medical treatment in the future.

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APPENDIX



APPENDIX A
Preparing solutions

1. Preparation of 2% (w/v) SDS	Total volume	10 ml
1.1 SDS		0.2 g
1.2 Distilled water (Type II)		10 ml
2. Preparation of 1x PBS buffer, pH 7.0	Total volume	1 L
2.1 Sodium chloride (NaCl)		8 g
2.2 Potassium chloride (KCl)		200 mg
2.3 di-Sodium hydrogen phosphate (Na ₂ HPO ₄)		1.44 g
2.4 Potassium dihydrogen phosphate (KH ₂ PO ₄)		240 mg
2.5 Distilled water (Type II)		1 L
3. BCA protein assay		
3.1 Preparation of albumin solution	Total volume	1 ml
3.1.1 Albumin		2 mg
3.1.2 Distilled water (Type II)		1 ml
3.2 Preparation of working reagent (50:1 vol/vol)	Total volume	5.508 ml
3.2.1 Reagent A		5400 µl
3.2.2 Reagent B		108 µl
4. In-gel digestion		
4.1 100 mM Ammonium bicarbonate	Total volume	100 ml
4.1.1 Ammonium bicarbonate		0.79 g
4.1.2 Distilled water (Type I)		100 ml
4.2 10 mM DTT	Total volume	20 ml
4.2.1 DTT		0.031 g
4.2.2 100 mM Ammonium bicarbonate solution		20 ml
4.3 55 mM Chloroacetamide	Total volume	20 ml
4.3.1 2-Chloroacetamide		0.103 g
4.3.2 100 mM Ammonium bicarbonate solution		20 ml
4.4 10% Acetonitrile	Total volume	5 ml
4.4.1 100% Acetonitrile		500 µl
4.4.2 Distilled water (Type I)		4500 µl
4.5 100 mM Ammonium bicarbonate in 10% acetonitrile	Total volume	2 ml
4.5.1 Ammonium bicarbonate		0.016 g

4.5.2 10% acetonitrile	2 ml
4.6 13 ng/ μ l of Trypsin enzyme	Total volume 1539 μ l
4.6.1 Trypsin	20 μ g
4.6.2 10 mM Ammonium bicarbonate in 10% acetonitrile	1539 μ l
4.7 Extraction buffer	Total volume 3 ml
4.7.1 5% Formic acid	1 ml
4.7.2 100% Acetonitrile	2 ml

5. In-solution digestion

5.1 50 mM Ammonium bicarbonate	Total volume 50 ml
5.1.1 Ammonium bicarbonate	0.197 g
5.1.2 Distilled water (Type I)	50 ml
5.2 1 M DTT	Total volume 100 μ l
5.2.1 DTT	0.0154 g
5.2.2 50 mM Ammonium bicarbonate solution	100 μ l
5.3 1 M Chloroacetamide	Total volume 100 μ l
5.3.1 2-Chloroacetamide	0.009 g
5.3.2 50 mM Ammonium bicarbonate solution	100 μ l
5.4 0.2 μ g/ μ l of Trypsin enzyme solution	Total volume 100 μ l
5.4.1 Trypsin	20 μ g
5.4.2 50 mM Ammonium bicarbonate solution	100 μ l
5.5 10% Formic acid	Total volume 10 ml
4.8.1 100% Formic acid	1 ml
4.8.2 Distilled water (Type I)	9 ml

6. Hemolytic activity

6.1 PBSE buffer, pH 7.4	Total volume 1 L
6.1.1 Sodium chloride (NaCl)	8 g
6.1.2 Potassium chloride (KCl)	200 mg
6.1.3 di-Sodium hydrogen phosphate (Na_2HPO_4)	1.44 g
6.1.4 Potassium dihydrogen phosphate (KH_2PO_4)	240 mg
6.1.5 EDTA	0.37 g

6.1.6 Distilled water (Type II)	1 L
6.2 PSE buffer, pH 7.4	Total volume 1 L
6.2.1 Sucrose	250 g
6.2.2 di-Sodium hydrogen phosphate (Na_2HPO_4)	1.44 g
6.2.3 EDTA	0.37 g
6.3 0.1% Triton X-100	Total volume 10 ml
6.3.1 100% Triton X-100	0.01 ml
6.3.2 Distilled water (Type II)	9.99 ml

7. Angiotensin I-converting enzyme (ACE) inhibitory activity

7.1 50 mM Sodium borate buffer, pH 8.3	Total volume 200 ml
7.1.1 di-Sodium tetraborate decahydrate	3.81 g
7.1.2 Sodium chloride	5.84 g
7.1.3 Distilled water (Type II)	200 ml
7.2 0.5 mM N-[3-(2-Furyl) acryloyl]-Phe-Gly-Gly (FAPGG)	Total volume 5 ml
7.2.1 N-[3-(2-Furyl) acryloyl]-Phe-Gly-Gly (FAPGG)	0.001 g
7.2.2 50 mM Sodium borate buffer, pH 8.3	5 ml
7.3 Captopril	Total volume 1 ml
7.3.1 Captopril	1 mg
7.3.2 50 mM Sodium borate buffer, pH 8.3	1 ml
7.4 2.5 U/ml Angiotensin converting enzyme	Total volume 100 μl
7.4.1 Angiotensin converting enzyme	0.25 Unit
7.4.2 50 mM Sodium borate buffer, pH 8.3	100 μl

8. Acetylcholinesterase (AChE) inhibitory activity

8.1 0.02 M Sodium phosphate buffer, pH 7	Total volume 500 ml
8.1.1 Sodium dihydrogen phosphate ($\text{NaH}_2\text{PO}_4 \cdot \text{H}_2\text{O}$)	0.583 g
8.1.2 di-Sodium hydrogen phosphate (Na_2HPO_4)	0.823 g
8.1.3 Distilled water (Type II)	500 ml
8.2 100 mM Galantamine	Total volume 0.5 ml
8.2.1 Galantamine	0.02 g
8.2.2 Absolute ethanol	0.5 ml
8.3 3 mM 5,5'-Dithiobis (2-nitrobenzoic acid) (DTNB)	Total volume 10 ml

8.3.1 5,5'-Dithiobis (2-nitrobenzoic acid) (DTNB)	0.012 g
8.3.2 0.02 M Sodium phosphate buffer, pH 7	10 ml
8.4 Acetylcholinesterase	Total volume 1 ml
8.4.1 Acetylcholinesterase	500 unit
8.4.2 0.02 M Sodium phosphate buffer, pH 7	1 ml





APPENDIX B

Measurement of protein concentration by BCA protein assay

1. Determination of protein concentration of the jellyfish toxins

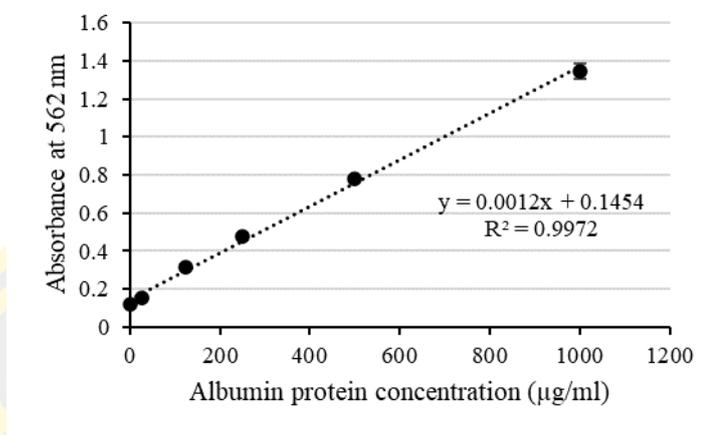


Figure B-1. Standard curve of the albumin protein

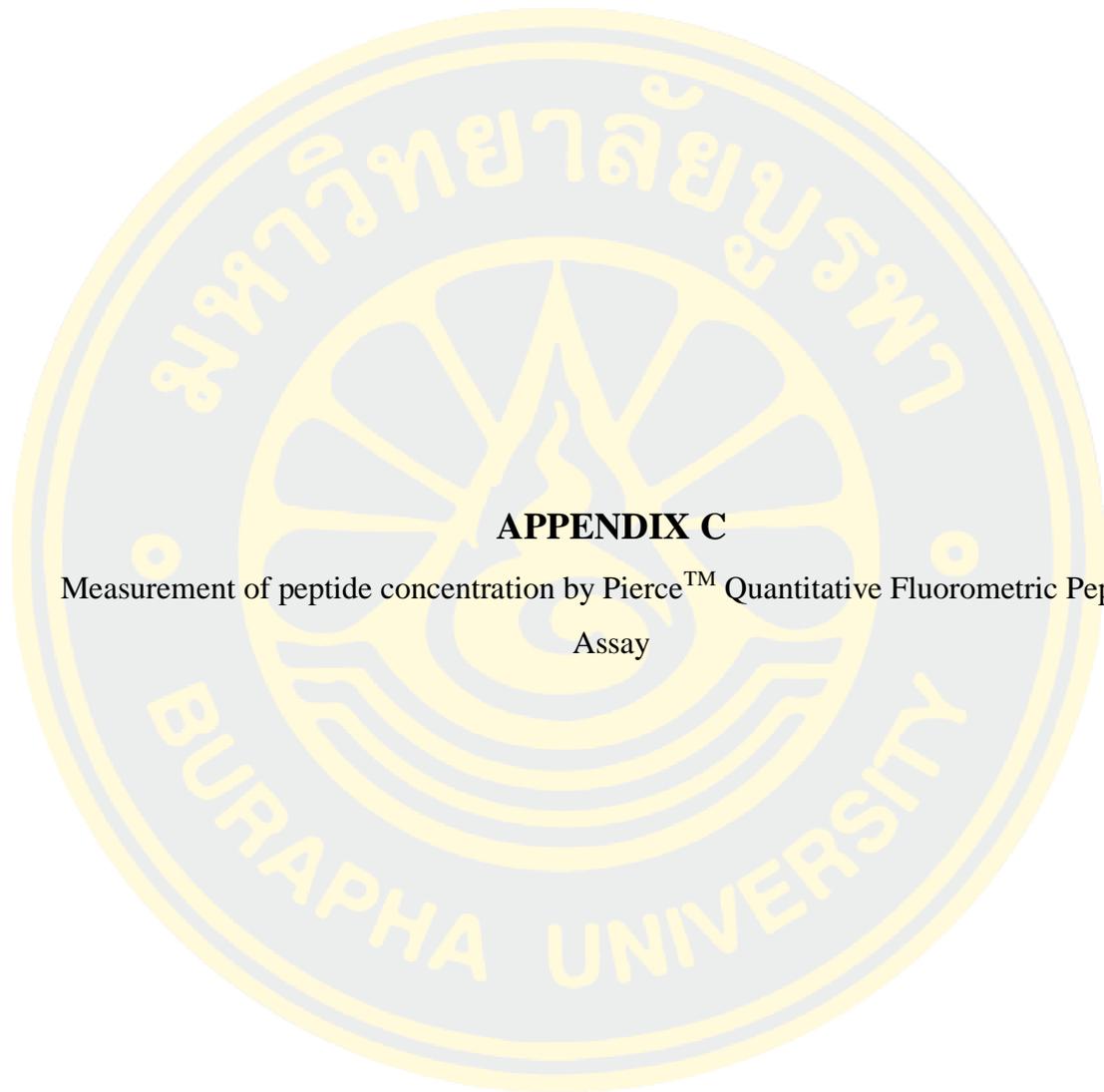
Calculation of the protein concentration of edible jellyfish toxins that was used equation (1).

$$y = 0.0012x + 0.1454 \quad (1)$$

where, y = absorbance at 562 nm
 x = protein concentration (µg/ml)

Table B-1. Protein concentration of the jellyfish venom samples

Sample	Protein extraction	Protein concentration (µg/ml)
Crude tentacle of edible jellyfish	Dissolved in SDS	2702.222
Edible jellyfish	SDS extraction	2871.388
Edible jellyfish	PBS extraction	2801.944
Crude tentacle of highly venomous jellyfish	Dissolved in SDS	1166.667
Highly venomous jellyfish	SDS extraction	349.091
Highly venomous jellyfish	PBS extraction	525.591



APPENDIX C

Measurement of peptide concentration by PierceTM Quantitative Fluorometric Peptide Assay

1. Peptide concentration of edible and highly venomous jellyfish toxin from in-gel digestion proteomic experiment

Table C-1. Peptide concentration of edible jellyfish toxin from in-gel digestion proteomic experiment

Edible jellyfish toxin sample	Wavelength of Ex 390 nm/ Em 475 nm	Peptide concentration (µg/ml)
Crude tentacle protein 1 (replication 1)	11.683	-26.688
Crude tentacle protein 2 (replication 1)	12.277	-23.916
Crude tentacle protein 3 (replication 1)	12.173	-24.402
Crude tentacle protein 4 (replication 1)	12.636	-8.245
Crude tentacle protein 5 (replication 1)	15.635	-8.254
Crude tentacle protein 1 (replication 2)	21.680	0.173
Crude tentacle protein 2 (replication 2)	20.135	-7.945
Crude tentacle protein 3 (replication 2)	25.344	19.427
Crude tentacle protein 4 (replication 2)	25.119	18.245
Crude tentacle protein 5 (replication 2)	19.820	-9.601
Crude tentacle protein 1 (replication 3)	21.060	-3.084
Crude tentacle protein 2 (replication 3)	28.081	33.809
Crude tentacle protein 3 (replication 3)	18.557	-16.237
Crude tentacle protein 4 (replication 3)	18.191	-18.161
Crude tentacle protein 5 (replication 3)	29.639	41.996
Nematocyst extracted by 2% SDS (1) (replication 1)	16.9784	-1.9897
Nematocyst extracted by 2% SDS (2) (replication 1)	17.4412	0.1688
Nematocyst extracted by 2% SDS (3) (replication 1)	19.0011	7.4448
Nematocyst extracted by 2% SDS (4) (replication 1)	15.5483	-8.6589
Nematocyst extracted by 2% SDS (5) (replication 1)	14.3536	-14.2323
Nematocyst extracted by 2% SDS (1) (replication 2)	13.855	-45.352
Nematocyst extracted by 2% SDS (2) (replication 2)	15.731	-34.601
Nematocyst extracted by 2% SDS (3) (replication 2)	25.657	22.281
Nematocyst extracted by 2% SDS (4) (replication 2)	14.075	-44.092
Nematocyst extracted by 2% SDS (5) (replication 2)	24.432	15.261
Nematocyst extracted by 2% SDS (1) (replication 3)	17.687	-20.809
Nematocyst extracted by 2% SDS (2) (replication 3)	25.227	18.812
Nematocyst extracted by 2% SDS (3) (replication 3)	20.762	-4.650
Nematocyst extracted by 2% SDS (4) (replication 3)	25.158	18.449
Nematocyst extracted by 2% SDS (5) (replication 3)	20.376	-6.679
Nematocyst extracted by PBS buffer (1) (replication 1)	13.523	-47.255
Nematocyst extracted by PBS buffer (2) (replication 1)	13.449	-47.679

Nematocyst extracted by PBS buffer (3) (replication 1)	26.238	25.610
Nematocyst extracted by PBS buffer (4) (replication 1)	10.080	-66.985
Nematocyst extracted by PBS buffer (5) (replication 1)	11.486	-58.928
Nematocyst extracted by PBS buffer (1) (replication 2)	39.734	95.045
Nematocyst extracted by PBS buffer (2) (replication 2)	22.107	2.417
Nematocyst extracted by PBS buffer (3) (replication 2)	25.303	19.212
Nematocyst extracted by PBS buffer (4) (replication 2)	20.829	-4.298
Nematocyst extracted by PBS buffer (5) (replication 2)	20.071	-8.282
Nematocyst extracted by PBS buffer (1) (replication 3)	30.018	43.988
Nematocyst extracted by PBS buffer (2) (replication 3)	28.72	37.167
Nematocyst extracted by PBS buffer (3) (replication 3)	27.188	29.117
Nematocyst extracted by PBS buffer (4) (replication 3)	20.784	-4.534
Nematocyst extracted by PBS buffer (5) (replication 3)	17.667	-20.914

Table C-2. Peptide concentration of highly venomous jellyfish toxin from in-gel digestion proteomic experiment

Highly venomous jellyfish toxin sample	Wavelength of Ex 390 nm/ Em 475 nm	Peptide concentration (µg/ml)
Crude tentacle protein 1 (replication 1)	2.582	11.209
Crude tentacle protein 2 (replication 1)	2.009	9.258
Crude tentacle protein 3 (replication 1)	1.751	8.383
Crude tentacle protein 4 (replication 1)	1.149	6.347
Crude tentacle protein 5 (replication 1)	0.959	5.707
Crude tentacle protein 1 (replication 2)	30.309	45.517
Crude tentacle protein 2 (replication 2)	22.411	4.014
Crude tentacle protein 3 (replication 2)	26.982	28.035
Crude tentacle protein 4 (replication 2)	20.968	-3.568
Crude tentacle protein 5 (replication 2)	24.247	13.663
Crude tentacle protein 1 (replication 3)	24.789	18.799
Crude tentacle protein 2 (replication 3)	24.675	18.211
Crude tentacle protein 3 (replication 3)	24.138	15.443
Crude tentacle protein 4 (replication 3)	24.557	17.603
Crude tentacle protein 5 (replication 3)	17.041	-21.139
Nematocyst extracted by 2% SDS (1) (replication 1)	3.360	13.873
Nematocyst extracted by 2% SDS (2) (replication 1)	3.237	13.451
Nematocyst extracted by 2% SDS (3) (replication 1)	2.054	9.411
Nematocyst extracted by 2% SDS (4) (replication 1)	1.916	8.942
Nematocyst extracted by 2% SDS (5) (replication 1)	1.934	9.003

Nematocyst extracted by 2% SDS (1) (replication 2)	16.278	-31.467
Nematocyst extracted by 2% SDS (2) (replication 2)	20.730	-5.954
Nematocyst extracted by 2% SDS (3) (replication 2)	24.086	13.278
Nematocyst extracted by 2% SDS (4) (replication 2)	15.911	-33.570
Nematocyst extracted by 2% SDS (5) (replication 2)	18.93	-16.269
Nematocyst extracted by 2% SDS (1) (replication 3)	27.541	32.984
Nematocyst extracted by 2% SDS (2) (replication 3)	26.119	25.655
Nematocyst extracted by 2% SDS (3) (replication 3)	26.928	29.825
Nematocyst extracted by 2% SDS (4) (replication 3)	20.616	-2.711
Nematocyst extracted by 2% SDS (5) (replication 3)	22.025	4.551
Nematocyst extracted by PBS buffer (1) (replication 1)	22.880	6.366
Nematocyst extracted by PBS buffer (2) (replication 1)	28.054	36.017
Nematocyst extracted by PBS buffer (3) (replication 1)	26.652	27.983
Nematocyst extracted by PBS buffer (4) (replication 1)	17.330	-25.438
Nematocyst extracted by PBS buffer (5) (replication 1)	23.743	11.312
Nematocyst extracted by PBS buffer (1) (replication 2)	19.251	-9.747
Nematocyst extracted by PBS buffer (2) (replication 2)	27.533	32.943
Nematocyst extracted by PBS buffer (3) (replication 2)	26.183	25.984
Nematocyst extracted by PBS buffer (4) (replication 2)	23.753	13.459
Nematocyst extracted by PBS buffer (5) (replication 2)	15.551	-28.819
Nematocyst extracted by PBS buffer (1) (replication 3)	26.610	28.185
Nematocyst extracted by PBS buffer (2) (replication 3)	22.307	6.005
Nematocyst extracted by PBS buffer (3) (replication 3)	26.564	27.948
Nematocyst extracted by PBS buffer (4) (replication 3)	28.255	36.665
Nematocyst extracted by PBS buffer (5) (replication 3)	26.12	25.659

2. Peptide concentration of edible and highly venomous jellyfish toxin from in-solution digestion proteomic experiment

Table C-3. Peptide concentration of edible jellyfish toxin from in-solution digestion proteomic experiment

Edible jellyfish toxin sample	Wavelength of Ex 390 nm/ Em 475 nm	Peptide concentration ($\mu\text{g/ml}$)
Nematocyst extracted by 2% SDS (large 3 kDa) replication 1	102.748	39.0550
Nematocyst extracted by 2% SDS (large 3 kDa) replication 2	N/A	N/A
Nematocyst extracted by 2% SDS (large 3 kDa) replication 3	N/A	N/A
Nematocyst extracted by PBS buffer	52.423	175.667

replication 1		
Nematocyst extracted by PBS buffer replication 2	70.634	38.692
Nematocyst extracted by PBS buffer replication 3	43.275	123.243
Nematocyst extracted by PBS buffer replication 1 (PNGase and trypsin digest)	42.583	94.712
Nematocyst extracted by PBS buffer replication 2 (PNGase and trypsin digest)	62.427	201.306
Nematocyst extracted by PBS buffer replication 3 (PNGase and trypsin digest)	43.545	96.348

Table C-4. Peptide concentration of highly venomous jellyfish toxin from in-solution digestion proteomic experiment

Highly venomous jellyfish toxin sample	Wavelength of Ex 390 nm/ Em 475 nm	Peptide concentration (µg/ml)
Nematocyst extracted by 2% SDS (large 3 kDa) replication 1	N/A	N/A
Nematocyst extracted by 2% SDS (large 3 kDa) replication 2	60.677	126.349
Nematocyst extracted by PBS buffer replication 1	43.275	123.243
Nematocyst extracted by PBS buffer replication 2	41.433	104.593
Nematocyst extracted by PBS buffer replication 3	40.767	101.159
Nematocyst extracted by PBS buffer replication 1 (PNGase and trypsin digest)	40.068	97.557
Nematocyst extracted by PBS buffer replication 2 (PNGase and trypsin digest)	41.412	104.484
Nematocyst extracted by PBS buffer replication 3 (PNGase and trypsin digest)	49.891	148.191

3. Peptide concentration of edible and highly venomous jellyfish toxin from top-down proteomic experiment

Table C-5. Peptide concentration of edible jellyfish toxin from top-down proteomic experiment

Edible jellyfish toxin sample	Wavelength of Ex 390 nm/ Em 475 nm	Peptide concentration ($\mu\text{g/ml}$)
Nematocyst extracted by 2% SDS (less 3 kDa) replication 1	19.561	10.0559
Nematocyst extracted by 2% SDS (less 3 kDa) replication 2	N/A	N/A
Nematocyst extracted by 2% SDS (less 3 kDa) replication 3	N/A	N/A
Nematocyst extracted by PBS buffer (less 3 kDa) replication 1	24.158	11.623
Nematocyst extracted by PBS buffer (less 3 kDa) replication 2	23.182	6.610
Nematocyst extracted by PBS buffer (less 3 kDa) replication 3	25.34	17.694

Table C-6. Peptide concentration of highly venomous jellyfish toxin from top-down proteomic experiment

Highly venomous jellyfish toxin sample	Wavelength of Ex 390 nm/ Em 475 nm	Peptide concentration ($\mu\text{g/ml}$)
Nematocyst extracted by 2% SDS (less 3 kDa) replication 1	N/A	N/A
Nematocyst extracted by 2% SDS (less 3 kDa) replication 2	14.820	-35.861
Nematocyst extracted by PBS buffer (less 3 kDa) replication 1	27.850	33.791
Nematocyst extracted by PBS buffer (less 3 kDa) replication 2	20.995	-6.6273
Nematocyst extracted by PBS buffer (less 3 kDa) replication 3	17.812	-25.395

4. Calculation of peptide concentration

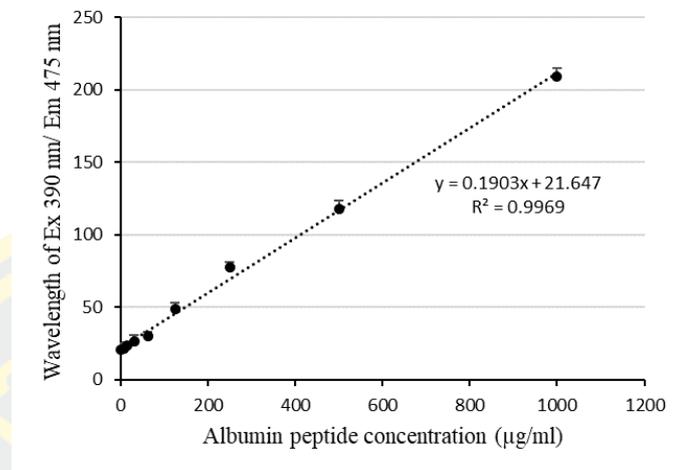


Figure C-1. Albumin peptide standard curve for calculation of peptide concentration

Peptide concentration of edible and highly venomous jellyfish toxins that were used equation (1) to calculate.

$$y = 0.1903x + 21.647 \quad (1)$$

where, y = wavelength of Ex 390 nm/ Em 475 nm of sample peptide
 x = peptide concentration (µg/ml)



APPENDIX D

Protein identified from edible jellyfish toxin using Cnidaria database search

1. In-gel digestion

1.1 Identification of protein from crude of tentacle

Table D-1. List of proteins identified (366 proteins) from crude tentacles of edible jellyfish, which these proteins identified were derived from in-gel digestion experiment. Database of taxonomy Cnidaria (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
A7RKS5	40S ribosomal protein SA OS=Nematostella vectensis	3.5	1
T2MGY6	Sodium/potassium-transporting ATPase subunit alpha OS=Hydra vulgaris	1.7	1
T2MGR0	60S ribosomal protein L17 OS=Hydra vulgaris	8.7	1
P38984	40S ribosomal protein SA OS=Hydra viridissima	4.1	1
P51539	Ras-like protein RAS1 OS=Hydra vulgaris	13.4	2
P62184	Calmodulin OS=Renilla reniformis	40.9	4
B3EZK6	Ribosomal protein S5 (Fragment) OS=Cyanea capillata	13.5	2
B1PM92	Calmodulin OS=Acropora muricata	65.8	5
A0A068FU94	Frizzled 1 OS=Rhopilema esculentum	2.9	1
A0A069DNI2	Secreted tripeptidyl peptidase (Fragment) OS=Clytia hemisphaerica	2.7	1
A0A0A6Z4X6	Cytochrome c oxidase subunit 2 OS=Dendrophyllia cribrosa	8.1	1
A0A1V0IGH5	Histone H2B OS=Hydra vulgaris	11.2	1
A0A0C2IXY6	Putative ATP-dependent RNA helicase DDX5 OS=Thelohanellus kitauei	4	2
A0A0C2IZS4	Outer membrane protein TolC OS=Thelohanellus kitauei	3.8	1
T2MF79	Transforming protein RhoA OS=Hydra vulgaris	8.9	1
A0A0C2JEY5	6-phosphogluconate dehydrogenase, decarboxylating OS=Thelohanellus kitauei	5	2
A0A0C2JMN8	Uncharacterized protein OS=Thelohanellus kitauei	13.8	1
A0A0C2JSW9	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 OS=Thelohanellus kitauei	1.9	1
A0A0C2M5P0	Outer membrane protein A OS=Thelohanellus kitauei	5.6	2
A0A0C2M9V2	Arginine--tRNA ligase, cytoplasmic OS=Thelohanellus kitauei	1.8	1
C1IJE5	Smooth muscle myosin heavy chain 11 isoform-like protein (Fragment) OS=Myxobolus cerebralis	5.5	1
A0A0C2MUS2	60 kDa chaperonin OS=Thelohanellus kitauei	4.7	1
A0A0C2N354	ATP synthase subunit beta OS=Thelohanellus kitauei	15.4	5
A0A0C2N442	Ras-related protein Rab-11A OS=Thelohanellus kitauei	5.3	1
A0A0C2N916	Casein kinase I isoform gamma-1 OS=Thelohanellus kitauei	3.9	1
A0A0C4VZ14	78 kDa glycose-regulated protein (Fragment) OS=Capnella imbricata	7.1	2
A0A181ZLN7	Heat shock protein 70 (Fragment) OS=Sinularia cf. cruciata GS-2016	11.5	3
A0A4Y6KM02	Cytochrome c oxidase subunit 2 (Fragment) OS=Montipora flabellata	8.9	1
A0A0N7F1C5	MAC/Perforin domain containing protein OS=Rhopilema esculentum	3	1
A0A0U2E1U9	Cytochrome c oxidase subunit 2 OS=Sagartia ornata	8.1	1
A0A169Q0T5	Glyceraldehyde-3-phosphate dehydrogenase OS=Aurelia sp. SETO	12.8	3
A0A2Z5WH77	Actin-1 OS=Aurelia sp. 2017-HT	57.7	17
A0A1B3IQV6	Histone H2B OS=Hydractinia echinata	10.1	1
A0A1B3IQX8	Histone H2A OS=Hydractinia echinata	29	2

A0A1L2A726	Superoxide dismutase [Cu-Zn] OS=Cyanea capillata	8.4	1
A0A1U9XQR0	Fructose-bisphosphate aldolase OS=Aurelia sp. 1 GW-2014	20.2	7
A0A1U9XQR2	Prolyl 4-hydroxylase subunit alpha-1 OS=Aurelia sp. 1 GW-2014	3.3	1
A0A288W1V0	Mitogen-activated protein kinase OS=Aurelia aurita	13.3	3
A0A3M6TX36	Protein kinase domain-containing protein OS=Pocillopora damicornis	5.2	1
A0A2B4R2I0	Fumarylacetoacetase (Fragment) OS=Stylophora pistillata	5.1	1
A0A2B4R9G5	Histone H2B OS=Stylophora pistillata	7.3	2
A0A2B4R9Q9	Histone H4 OS=Stylophora pistillata	29.7	11
A0A2B4R9T9	Chaperone protein DnaK OS=Stylophora pistillata	2.3	1
A7RQD8	Predicted protein OS=Nematostella vectensis	39.8	3
A0A2B4RB68	Transmembrane 9 superfamily member (Fragment) OS=Stylophora pistillata	7.6	1
A0A3M6T6K2	Uncharacterized protein OS=Pocillopora damicornis	3.1	1
T2MHV0	Aldehyde dehydrogenase,mitochondrial OS=Hydra vulgaris	2.3	1
A0A2B4RCT7	4-hydroxyphenylpyruvate dioxygenase OS=Stylophora pistillata	4.9	1
T2MEZ1	dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial (Fragment) OS=Hydra vulgaris	3.2	1
A7S0B1	Predicted protein OS=Nematostella vectensis	8.1	1
A0A3M6UM75	HATPase_c domain-containing protein OS=Pocillopora damicornis	7.6	4
A0A2B4RHG2	V-type proton ATPase catalytic subunit A OS=Stylophora pistillata	8.8	3
A0A2B4RHH4	Heat shock protein 70 B2 OS=Stylophora pistillata	10.8	3
A0A2B4RHH5	Enoyl-CoA hydratase, mitochondrial OS=Stylophora pistillata	6	1
A0A2B4RI23	GTP-binding protein SAR1 OS=Stylophora pistillata	6.8	1
A0A2B4RIA2	Polyadenylate-binding protein 4 OS=Stylophora pistillata	2.4	1
A0A2B4RIF3	Retrovirus-related Pol polyprotein OS=Stylophora pistillata	3.2	1
A0A2B4RJH1	Tubulin beta chain OS=Stylophora pistillata	59.5	23
A0A3M6TIL0	Uncharacterized protein OS=Pocillopora damicornis	6.5	1
A7STE6	Predicted protein OS=Nematostella vectensis	6.5	1
A0A2B4RPA9	Clathrin heavy chain OS=Stylophora pistillata	9.5	12
A0A3M6V4M9	Uncharacterized protein OS=Pocillopora damicornis	9.5	2
A0A2B4RQY2	Ubiquitin-conjugating enzyme E2 L3 OS=Stylophora pistillata	21.4	2
Q93116	Ub52 OS=Acropora millepora	41.1	5
T2M6W3	Mothers against decapentaplegic homolog (Fragment) OS=Hydra vulgaris	3.2	1
A0A2B4RU80	Coatomer subunit beta OS=Stylophora pistillata	4.6	3
Q2F6G0	Prohibitin (Fragment) OS=Anthopleura elegantissima	10	1
T2M3D0	Nucleolar protein 58 OS=Hydra vulgaris	2.6	1
A0A3M6U1C8	NAC-A/B domain-containing protein OS=Pocillopora damicornis	6.2	1
A0A3M6U3P0	Uncharacterized protein OS=Pocillopora damicornis	1.5	1
A0A3M6UGY3	UBIQUITIN_CONJUGAT_2 domain-containing protein OS=Pocillopora damicornis	16.4	2
A0A2B4RXI4	Ras-related protein Rab-5B OS=Stylophora pistillata	10.6	2
A7S494	40S ribosomal protein S27 OS=Nematostella vectensis	15.5	1
T2M648	AP-1 complex subunit mu-1 OS=Hydra vulgaris	3.3	1
A0A2B4S029	Aminoamidase OS=Stylophora pistillata	2.7	1
A0A3M6TYB3	Uncharacterized protein OS=Pocillopora damicornis	10.8	1
L0AUB3	Alpha q G protein OS=Acropora palmata	10.2	3

A0A2B4S129	Peroxiredoxin-1 OS=Stylophora pistillata	8.4	2
T2MJH6	rRNA/tRNA 2-O-methyltransferase fibrillar-like protein 1 OS=Hydra vulgaris	7.3	1
A0A2B4S1K1	La-related protein 1 OS=Stylophora pistillata	1.3	1
A0A2B4S1U8	Gamma-glutamyltranspeptidase 1 OS=Stylophora pistillata	3.4	1
A0A2B4S2W7	Major vault protein OS=Stylophora pistillata	4.8	3
A7SWV8	Predicted protein OS=Nematostella vectensis	3.9	1
A0A2B4S3I9	Non-specific serine/threonine protein kinase OS=Stylophora pistillata	4.9	3
A0A3M6TR43	AA_TRNA_LIGASE_II domain-containing protein OS=Pocillopora damicornis	1.7	1
A7SFJ3	Predicted protein OS=Nematostella vectensis	4.4	1
T2MEG1	Cell division control protein 42 homolog OS=Hydra vulgaris	11	2
Q8WRT4	Beta-catenin (Fragment) OS=Nematostella vectensis	6.3	2
A0A3M6UUZ3	Uncharacterized protein OS=Pocillopora damicornis	6.1	1
A0A2B4S5A3	S-adenosylmethionine synthase OS=Stylophora pistillata	3.3	3
A0A3M6UGG9	Uncharacterized protein OS=Pocillopora damicornis	8.7	5
A7T5I4	6-phosphogluconate dehydrogenase, decarboxylating (Fragment) OS=Nematostella vectensis	3.6	1
A0A2B4S643	Doublesex-and mab-3-related transcription factor A2 OS=Stylophora pistillata	3.3	2
A0A2B4S6M0	Tubulin alpha-1D chain OS=Stylophora pistillata	39.9	16
A0A2B4S736	Vacuolar proton pump subunit B OS=Stylophora pistillata	5.8	2
A0A2B4S7H9	Serine/arginine-rich splicing factor 12 OS=Stylophora pistillata	5	1
A7TCR2	Predicted protein (Fragment) OS=Nematostella vectensis	12.5	1
T2MEK8	Ras-related protein Rab-1A OS=Hydra vulgaris	23.3	3
A0A2B4SC49	Actin-related protein 3 OS=Stylophora pistillata	14.8	3
A0A2B4SCP3	Peptidylprolyl isomerase OS=Stylophora pistillata	10.6	2
T2M856	Dynein light chain OS=Hydra vulgaris	12.4	1
T2MF62	Small nuclear ribonucleoprotein Sm D2 OS=Hydra vulgaris	8.5	1
A7SS49	Predicted protein OS=Nematostella vectensis	11.1	4
A0A2B4SFU3	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Stylophora pistillata	5.1	1
A0A2B4SGD6	Centrosome and spindle pole-associated protein 1 OS=Stylophora pistillata	1.1	1
A7RRK9	Predicted protein (Fragment) OS=Nematostella vectensis	3.7	1
A0A3M6U381	Uncharacterized protein OS=Pocillopora damicornis	7	1
T2MF68	Small nuclear ribonucleoprotein E OS=Hydra vulgaris	12.6	1
T2ME66	Ras-related protein Rab-11A OS=Hydra vulgaris	9.6	2
A0A3M6TKN8	Transaldolase OS=Pocillopora damicornis	10.6	4
A0A2B4SIW6	Serine/threonine-protein phosphatase OS=Stylophora pistillata	6.1	1
A7SPP0	ATP synthase subunit beta OS=Nematostella vectensis	27.9	8
A0A2B4SJQ6	Rab GDP dissociation inhibitor OS=Stylophora pistillata	7.2	2
A0A3M6UYR9	Sm domain-containing protein OS=Pocillopora damicornis	15.5	1
A0A3M6V0P1	RPN2_C domain-containing protein (Fragment) OS=Pocillopora damicornis	2.2	1
A0A2B4SLL2	SEC23-interacting protein OS=Stylophora pistillata	1.6	2
A0A3M6VAC5	Uncharacterized protein OS=Pocillopora damicornis	2.8	1
A0A2B4SMR1	Proteasome subunit beta OS=Stylophora pistillata	7.2	1
A0A3M6V678	Protein kinase domain-containing protein OS=Pocillopora damicornis	3.9	1
A0A3M6TT70	V-type proton ATPase proteolipid subunit OS=Pocillopora damicornis	11.7	1

A7RV73	Vacuolar protein sorting-associated protein 29 OS=Nematostella vectensis	12.6	2
A7SKL5	Predicted protein (Fragment) OS=Nematostella vectensis	3	1
A7SHU3	Predicted protein OS=Nematostella vectensis	32.1	6
A0A3M6TRH7	Uncharacterized protein OS=Pocillopora damicornis	0.9	3
A0A2B4SQT0	Unconventional myosin-Ie OS=Stylophora pistillata	1	2
A7T0V9	Predicted protein OS=Nematostella vectensis	10.5	1
T2MF57	Coatomer subunit alpha OS=Hydra vulgaris	2.7	3
A0A3M6UDV1	WD_REPEATS_REGION domain-containing protein OS=Pocillopora damicornis	3.8	1
A0A2B4SSB1	NudC domain-containing protein 1 OS=Stylophora pistillata	3.1	1
A7T2Q5	Serine/threonine-protein phosphatase OS=Nematostella vectensis	14.2	3
A0A2B4STP6	Kinesin-like protein KIF28P OS=Stylophora pistillata	1.4	1
A0A2B4STW2	Tetrapeptide repeat protein 28 OS=Stylophora pistillata	0.9	1
A0A3M6UQ20	PCI domain-containing protein OS=Pocillopora damicornis	2.4	1
A0A2B4SUW9	Isocitrate dehydrogenase [NADP] OS=Stylophora pistillata	5.3	2
A0A2B4SV07	Tubulin beta chain OS=Stylophora pistillata	57.4	23
A7SQP1	Predicted protein OS=Nematostella vectensis	15.9	3
A0A3M6TU98	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	9.9	1
A7RID7	Predicted protein OS=Nematostella vectensis	5.9	1
A0A2B4SWI5	TIR domain-containing protein OS=Stylophora pistillata	10.4	2
A0A3M6UTM8	Uncharacterized protein OS=Pocillopora damicornis	2.6	2
A7SAY0	Predicted protein OS=Nematostella vectensis	6.4	1
A0A3M6TP56	DUF667 domain-containing protein (Fragment) OS=Pocillopora damicornis	12.6	2
A0A2B4SYS5	Sodium/potassium-transporting ATPase subunit alpha OS=Stylophora pistillata	2.5	1
A0A2B4SYV9	Small nuclear ribonucleoprotein Sm D1 OS=Stylophora pistillata	9.2	1
A0A2B4SZL5	Radixin OS=Stylophora pistillata	3.4	1
A0A2B4SZV5	Ras GTPase-activating-like protein IQGAP1 OS=Stylophora pistillata	1.6	2
A0A2B4T1C4	ATP synthase subunit alpha OS=Stylophora pistillata	16.5	6
A7SBR9	Predicted protein OS=Nematostella vectensis	3	1
A7T1M0	RNA-binding protein 8A (Fragment) OS=Nematostella vectensis	12.5	1
Q7YZL5	Tubulin alpha chain (Fragment) OS=Aurelia aurita	56	16
A0A2Z5WH73	Myosin heavy chain OS=Aurelia sp. 2017-HT	5.3	8
A0A2Z5WH78	Ser-Thr kinase OS=Aurelia sp. 2017-HT	2.3	1
A0A2Z5WH80	Myosin regulatory light chain OS=Aurelia sp. 2017-HT	22.2	3
A0A2Z5WH81	Myosin essential light chain OS=Aurelia sp. 2017-HT	7.3	1
A0A3M6T8X3	Calcium-transporting ATPase OS=Pocillopora damicornis	5.1	3
A7SIT2	Predicted protein OS=Nematostella vectensis	5.5	2
A0A3M6T9K8	Thioredoxin domain-containing protein OS=Pocillopora damicornis	9.5	2
T2MD57	Calcium-transporting ATPase OS=Hydra vulgaris	1.7	1
A7SXV0	Predicted protein OS=Nematostella vectensis	3	1
A0A3M6TLD9	Uncharacterized protein OS=Pocillopora damicornis	22.1	4
A0A3M6TLH9	Uncharacterized protein OS=Pocillopora damicornis	7.7	4
A0A3M6TMJ8	A2M_recep domain-containing protein OS=Pocillopora damicornis	1.5	1
A0A3M6TST2	Uncharacterized protein OS=Pocillopora damicornis	5.4	1

A7SNV4	Peptidyl-prolyl cis-trans isomerase OS=Nematostella vectensis	6.3	1
A0A3M6TVV7	Hcy-binding domain-containing protein OS=Pocillopora damicornis	4.4	1
A0A3M6TYE7	Uncharacterized protein OS=Pocillopora damicornis	11.4	2
A0A3M6U1Z2	Uncharacterized protein OS=Pocillopora damicornis	5	2
A0A3M6U454	Histone H2A OS=Pocillopora damicornis	17.4	2
A0A3M6U7U8	Uncharacterized protein OS=Pocillopora damicornis	5	2
A0A3M6U8F9	PHB domain-containing protein OS=Pocillopora damicornis	2.9	1
A0A3M6U8Y8	Proteasome subunit alpha type OS=Pocillopora damicornis	6.3	1
A0A3M6UCJ5	Transcription elongation factor SPT5 OS=Pocillopora damicornis	1.5	1
A0A3M6UEA3	Uncharacterized protein OS=Pocillopora damicornis	3.7	3
A7RMA8	Predicted protein OS=Nematostella vectensis	4.5	1
A0A3M6UGM1	V-type proton ATPase subunit a OS=Pocillopora damicornis	4.4	1
A0A3M6UHG1	Uncharacterized protein OS=Pocillopora damicornis	1.9	1
A0A3M6UN42	DUF4709 domain-containing protein OS=Pocillopora damicornis	2.1	1
A0A3M6UP81	Uncharacterized protein OS=Pocillopora damicornis	47.9	13
A0A3M6UPZ4	Uncharacterized protein OS=Pocillopora damicornis	4.3	2
A7RL80	Predicted protein OS=Nematostella vectensis	13.2	2
A0A3M6UYC1	cGMP-dependent protein kinase OS=Pocillopora damicornis	1.7	1
A0A3M6UZ63	Annexin OS=Pocillopora damicornis	7.2	4
A0A3M6V263	Isochorismatase domain-containing protein OS=Pocillopora damicornis	5.6	1
A0A3M6V2N5	Adenosylhomocysteinase OS=Pocillopora damicornis	8.3	3
A0A4V1H7U6	Cytochrome c oxidase subunit 2 OS=Stomolophus sp. CG-2019	23.4	3
A3F9E8	Histone H2B (Fragment) OS=Anacropora matthai	17.9	2
A7RGP8	Predicted protein OS=Nematostella vectensis	2.2	1
A7RGV0	Predicted protein OS=Nematostella vectensis	3.5	1
A7RHF7	Eukaryotic translation initiation factor 6 OS=Nematostella vectensis	10.2	1
T2M9F1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Hydra vulgaris	1.5	1
A7RHS7	Predicted protein OS=Nematostella vectensis	4.1	2
A7RIF0	T-complex protein 1 subunit eta OS=Nematostella vectensis	6.6	3
Q5U9S0	Ubiquitin/ribosomal L40 fusion protein OS=Scleronephthya gracillimum	41.4	5
A7RL59	Predicted protein OS=Nematostella vectensis	5.2	1
A7RL77	Coatomer subunit beta OS=Nematostella vectensis	2.3	2
A7RM97	Predicted protein OS=Nematostella vectensis	13.6	2
A7RME1	Adenosylhomocysteinase OS=Nematostella vectensis	8.5	2
A7RNT1	Succinyl-CoA:3-ketoacid-coenzyme A transferase OS=Nematostella vectensis	2.3	1
A7RPG9	Predicted protein OS=Nematostella vectensis	4.4	1
A7RQR3	10-formyltetrahydrofolate dehydrogenase OS=Nematostella vectensis	1.4	1
A7RRG9	Predicted protein OS=Nematostella vectensis	14.9	1
A7T836	Predicted protein (Fragment) OS=Nematostella vectensis	2.7	1
A7RT97	Predicted protein OS=Nematostella vectensis	2.8	2
A7T8K2	Predicted protein OS=Nematostella vectensis	12.8	1
A7RUF9	Predicted protein (Fragment) OS=Nematostella vectensis	8.9	1
A7RVC0	Clathrin heavy chain OS=Nematostella vectensis	7.3	9

A7RVD9	Tubulin alpha chain OS=Nematostella vectensis	41.3	13
E7BTP8	Rab14 OS=Aiptasia pulchella	12.9	3
A7S0U6	Predicted protein OS=Nematostella vectensis	1	1
A7S1I1	Predicted protein OS=Nematostella vectensis	1.6	1
A7S1I9	Predicted protein OS=Nematostella vectensis	11.8	2
A7S214	Predicted protein OS=Nematostella vectensis	33.1	5
A7S289	Predicted protein OS=Nematostella vectensis	17.9	1
A7S335	Predicted protein OS=Nematostella vectensis	2.6	4
A7S378	Isocitrate dehydrogenase [NADP] OS=Nematostella vectensis	6.6	2
A7S4X0	Predicted protein OS=Nematostella vectensis	4.5	4
A7S5L3	Predicted protein (Fragment) OS=Nematostella vectensis	3.6	3
A7S5Z0	Predicted protein OS=Nematostella vectensis	15	4
A7S616	Predicted protein OS=Nematostella vectensis	24	3
A7S690	Predicted protein (Fragment) OS=Nematostella vectensis	20.4	2
A7S7K4	Predicted protein OS=Nematostella vectensis	7.9	2
A7SB00	Protein transport protein SEC23 OS=Nematostella vectensis	1.6	1
A7SC77	Predicted protein OS=Nematostella vectensis	21.5	5
A7SDY3	Tubulin alpha chain OS=Nematostella vectensis	44.3	16
A7SF39	Predicted protein OS=Nematostella vectensis	3.3	1
A7SG05	GTP-binding nuclear protein OS=Nematostella vectensis	16.1	3
A7SJR5	Predicted protein OS=Nematostella vectensis	1.2	1
A7SNP7	Predicted protein OS=Nematostella vectensis	3.1	1
A7SPM9	Predicted protein (Fragment) OS=Nematostella vectensis	2.3	1
A7SPQ4	Predicted protein OS=Nematostella vectensis	16.5	4
A7SQ60	Predicted protein OS=Nematostella vectensis	11	3
A7SQS1	Malate dehydrogenase OS=Nematostella vectensis	9.4	2
A7SQV3	Proteasome subunit beta OS=Nematostella vectensis	10	3
A7SRK8	Adenosylhomocysteinase OS=Nematostella vectensis	2.9	1
A7SRV8	40S ribosomal protein S4 OS=Nematostella vectensis	7.6	2
A7SSL5	Predicted protein OS=Nematostella vectensis	4.6	3
A7SSV8	Polyadenylate-binding protein OS=Nematostella vectensis	2.6	1
A7SX44	Predicted protein (Fragment) OS=Nematostella vectensis	4.3	1
A7SX99	Predicted protein OS=Nematostella vectensis	13.6	1
A7SZN8	Predicted protein OS=Nematostella vectensis	3.1	1
A7T352	Predicted protein OS=Nematostella vectensis	3.2	1
A7T6F7	Predicted protein (Fragment) OS=Nematostella vectensis	24.1	1
A8DRV3	Vacuolar ATP synthase subunit B (Fragment) OS=Urticina eques	9.9	1
A8DX89	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Urticina eques	3.7	1
C0JP85	Ribosomal protein S2 (Fragment) OS=Carybdea marsupialis	24.1	2
C1IS27	Clathrin heavy chain (Fragment) OS=Carukia barnesi	16.4	2
C1IS28	Clathrin heavy chain (Fragment) OS=Carukia barnesi	30.9	6
T2ME96	Striatin-3 OS=Hydra vulgaris	1.8	1
I2G9E9	Myosin II heavy chain, smooth/non-muscle-type (Fragment) OS=Clytia hemisphaerica	3.4	1

K0A063	Beta-actin (Fragment) OS=Chrysaora quinquecirrha	58.9	16
M1E2A8	Calmodulin (Fragment) OS=Rhizostoma octopus	42.6	3
Q0H8V3	Heat shock protein 70 (Fragment) OS=Cnidaria environmental sample	6.3	1
Q56GW1	60S ribosomal protein L12 (Fragment) OS=Hydractinia echinata	16.5	1
Q56GW5	40S ribosomal protein S4 (Fragment) OS=Hydractinia echinata	14.3	1
Q5EN86	S-adenosylhomocysteine hydrolase (Fragment) OS=Aurelia aurita	19.3	2
Q5EN87	Putative tyrosine-rich heat shock protein (Fragment) OS=Aurelia aurita	5.8	1
Q5EN91	Putative 3-hydroxyacyl-Coenzyme A dehydrogenase (Fragment) OS=Aurelia aurita	13.7	2
Q5WR13	Non-muscle actin (Fragment) OS=Hydra viridissima	43.6	6
Q6PTK3	Triosephosphate isomerase (Fragment) OS=Obelia sp. KJP-2004	13.3	2
Q6YCH0	Ribosomal protein S3 (Fragment) OS=Hydra vulgaris	18.5	4
Q7YZI4	90-kDa heat-shock protein (Fragment) OS=Aurelia aurita	16.7	5
Q7YZJ5	Elongation factor 2 (Fragment) OS=Aurelia aurita	15.5	2
Q7YZK4	Tubulin beta chain (Fragment) OS=Aurelia aurita	64.1	22
Q9NDL6	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Sandieria malayensis	30	1
Q9NFW1	60S ribosomal protein L12 OS=Hydra vulgaris	9.7	1
R9S1E9	Bone morphogenetic protein (Fragment) OS=Aurelia aurita	3.3	1
R9S2H2	Uncharacterized protein (Fragment) OS=Aurelia aurita	0.5	1
R9S2M2	Elongation factor 1-alpha OS=Aurelia aurita	15.6	5
T2M2P0	Coatmer subunit gamma (Fragment) OS=Hydra vulgaris	2.7	2
T2M2T1	Putative deoxyribose-phosphate aldolase OS=Hydra vulgaris	4.3	1
T2M2W2	Talin-2 OS=Hydra vulgaris	1.1	2
T2M338	Stomatin-like protein 2 OS=Hydra vulgaris	2.7	1
T2M388	Calcium/calmodulin-dependent protein kinase type II subunit alpha OS=Hydra vulgaris	4.8	2
T2M3I0	Microtubule-associated protein RP/EB family member 3 (Fragment) OS=Hydra vulgaris	3.2	1
T2M3I7	RuvB-like helicase OS=Hydra vulgaris	6.6	2
T2M4D5	Leucyl-tRNA synthetase,cytoplasmic (Fragment) OS=Hydra vulgaris	1.5	1
T2M4N6	Guanine nucleotide-binding protein subunit beta-4 (Fragment) OS=Hydra vulgaris	10	3
T2M5A4	GrpE protein homolog (Fragment) OS=Hydra vulgaris	4.8	1
T2M5D3	Protein transport protein Sec61 subunit alpha isoform 2 OS=Hydra vulgaris	14.1	4
T2M5K6	Transmembrane 9 superfamily member OS=Hydra vulgaris	1.7	1
T2M644	Microtubule-associated proteins 1A/1B light chain 3C OS=Hydra vulgaris	26.4	2
T2M694	Prohibitin OS=Hydra vulgaris	12.3	3
T2M6Q7	Transmembrane emp24 domain-containing protein 9 OS=Hydra vulgaris	9.3	2
T2M6Z7	26S proteasome non-ATPase regulatory subunit 1 (Fragment) OS=Hydra vulgaris	1.5	1
T2M7H4	Transcription factor BTF3 OS=Hydra vulgaris	8.9	1
T2M7J1	Vacuolar protein sorting-associated protein 35 (Fragment) OS=Hydra vulgaris	8.7	5
T2M7N8	Ras-related protein Rab-8B OS=Hydra vulgaris	11.1	2
T2M866	Phosphomannomutase (Fragment) OS=Hydra vulgaris	4.2	1
T2M8F7	Actin-related protein 2/3 complex subunit 1A (Fragment) OS=Hydra vulgaris	3.8	1
T2M8J0	Sec1 family domain-containing protein 1 (Fragment) OS=Hydra vulgaris	2.2	1
T2M8M9	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Hydra vulgaris	4.1	1

T2M8Q9	Probable aminopeptidase NPEPL1 OS=Hydra vulgaris	2.8	2
T2M9A6	SH3 domain-containing RING finger protein 3 OS=Hydra vulgaris	1.7	1
T2M9Q3	Sorting nexin OS=Hydra vulgaris	3.5	1
T2MCX5	Vacuolar protein sorting-associated protein 26B (Fragment) OS=Hydra vulgaris	4	1
T2MD44	Major vault protein OS=Hydra vulgaris	4.3	3
T2MDB0	Eukaryotic initiation factor 4A-II OS=Hydra vulgaris	5.9	2
T2MDG4	Flotillin-2 OS=Hydra vulgaris	3.5	2
T2MDK8	Spliceosome RNA helicase DDX39B OS=Hydra vulgaris	5.3	2
T2MDL8	26S proteasome non-ATPase regulatory subunit 2 OS=Hydra vulgaris	2.9	2
T2MDQ1	NAD(P) transhydrogenase,mitochondrial OS=Hydra vulgaris	2.3	2
T2MDT0	Cytoplasmic dynein 1 heavy chain 1 OS=Hydra vulgaris	1	3
T2ME03	Quinone oxidoreductase OS=Hydra vulgaris	3.7	1
T2MEB5	ADP-ribosylation factor 1 OS=Hydra vulgaris	33.1	4
T2MEH3	Casein kinase II subunit alpha OS=Hydra vulgaris	10.6	3
T2MEH6	Dynein light chain Tctex-type 1 OS=Hydra vulgaris	14.2	1
T2MEI1	AP-2 complex subunit beta (Fragment) OS=Hydra vulgaris	6.1	4
T2MEJ9	Eukaryotic translation initiation factor 6 (Fragment) OS=Hydra vulgaris	7.2	1
T2MEK4	60S ribosomal protein L8 OS=Hydra vulgaris	5.4	2
T2MEN5	Clathrin heavy chain OS=Hydra vulgaris	6.9	9
T2MEP0	26S protease regulatory subunit 10B OS=Hydra vulgaris	10.5	3
T2MEP2	40S ribosomal protein S18 OS=Hydra vulgaris	7.1	1
T2MEQ7	26S protease regulatory subunit 4 OS=Hydra vulgaris	6.1	2
T2MET8	WD repeat-containing protein 5 OS=Hydra vulgaris	9.1	2
T2MEV0	Ras-related protein Rab-4B (Fragment) OS=Hydra vulgaris	12	2
T2MEV1	Tubulin beta chain (Fragment) OS=Hydra vulgaris	31.8	15
T2MEY1	60S ribosomal protein L11 (Fragment) OS=Hydra vulgaris	7.2	1
T2MEY3	T-complex protein 1 subunit beta (Fragment) OS=Hydra vulgaris	6.1	2
T2MF15	Eukaryotic peptide chain release factor subunit 1 OS=Hydra vulgaris	4.7	2
T2MF54	60S ribosomal protein L7a (Fragment) OS=Hydra vulgaris	8.2	2
T2MF63	Serine/threonine-protein phosphatase OS=Hydra vulgaris	21.8	6
T2MF93	Ras-related protein Rab-14 (Fragment) OS=Hydra vulgaris	21.9	3
T2MFG0	Transmembrane emp24 domain-containing protein 10 (Fragment) OS=Hydra vulgaris	11.5	2
T2MFH7	Poly(RC)-binding protein 3 (Fragment) OS=Hydra vulgaris	4.1	1
T2MFJ1	Stress-70 protein, mitochondrial (Fragment) OS=Hydra vulgaris	2.3	1
T2MFK0	Isocitrate dehydrogenase [NADP],mitochondrial (Fragment) OS=Hydra vulgaris	9.6	4
T2MFM1	Transitional endoplasmic reticulum ATPase (Fragment) OS=Hydra vulgaris	8.3	4
T2MFM6	Ribonuclease UK114 OS=Hydra vulgaris	14.8	2
T2MFQ3	Coatomer subunit beta (Fragment) OS=Hydra vulgaris	4.1	3
T2MFR8	Ras-related protein Rab-7a OS=Hydra vulgaris	34	7
T2MFV4	Isoleucyl-tRNA synthetase,cytoplasmic (Fragment) OS=Hydra vulgaris	1.7	2
T2MFY6	Hippocalcin-like protein 1 OS=Hydra vulgaris	22	4
T2MG07	Proteasome subunit alpha type OS=Hydra vulgaris	14.5	2
T2MG36	Myosin-10 OS=Hydra vulgaris	0.7	1

T2MG47	Radixin OS=Hydra vulgaris	2.7	1
T2MG74	Serine hydroxymethyltransferase,mitochondrial OS=Hydra vulgaris	2.2	1
T2MGH4	Proteasome subunit alpha type OS=Hydra vulgaris	3.6	1
T2MGI7	ADP/ATP translocase 3 (Fragment) OS=Hydra vulgaris	4.3	2
T2MGJ0	Polyadenylate-binding protein OS=Hydra vulgaris	2.7	1
T2MGL9	40S ribosomal protein S17-like OS=Hydra vulgaris	7.5	1
T2MGN9	Fructose-1,6-bisphosphatase 1 (Fragment) OS=Hydra vulgaris	6.3	2
T2MGQ4	ER lumen protein retaining receptor 2 OS=Hydra vulgaris	8.3	1
T2MGS3	cAMP-dependent protein kinase catalytic subunit alpha OS=Hydra vulgaris	8.3	2
T2MGX7	60S ribosomal protein L13 (Fragment) OS=Hydra vulgaris	4.7	1
T2MGY7	40S ribosomal protein S12 OS=Hydra vulgaris	10.2	1
T2MH18	Adenosylhomocysteinase OS=Hydra vulgaris	5.7	2
T2MH23	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial (Fragment) OS=Hydra vulgaris	2.5	1
T2MH25	Peptidyl-prolyl cis-trans isomerase OS=Hydra vulgaris	7.9	1
T2MH41	78 kDa glucose-regulated protein OS=Hydra vulgaris	6.6	5
T2MH46	Filamin-A OS=Hydra vulgaris	0.6	1
T2MHA3	Histone H1.0 OS=Hydra vulgaris	5.2	1
T2MHI3	Flotillin-1 (Fragment) OS=Hydra vulgaris	6.3	2
T2MHI5	Alpha-actinin-1 OS=Hydra vulgaris	2.6	2
T2MHJ0	Non-specific serine/threonine protein kinase OS=Hydra vulgaris	5.8	2
T2MHJ7	60 kDa heat shock protein,mitochondrial (Fragment) OS=Hydra vulgaris	2	1
T2MHT5	Heat shock protein HSP 90-alpha OS=Hydra vulgaris	11.4	10
T2MHY4	Argininosuccinate synthase (Fragment) OS=Hydra vulgaris	2.9	1
T2MI35	Splicing factor 3B subunit 1 (Fragment) OS=Hydra vulgaris	1.2	1
T2MI99	ATP-binding cassette sub-family B member 7, mitochondrial OS=Hydra vulgaris	1.7	1
T2MIB9	AP-2 complex subunit alpha OS=Hydra vulgaris	2.9	2
T2MIC5	Sorting nexin-2 (Fragment) OS=Hydra vulgaris	2.4	1
T2MIK0	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Hydra vulgaris	1.3	2
T2MIU1	Nucleolar protein 56 (Fragment) OS=Hydra vulgaris	5	2
T2MIV7	Endothelial differentiation-related factor 1 OS=Hydra vulgaris	10.1	1
T2MJ22	Calumenin OS=Hydra vulgaris	5.4	1
T2MJJ5	Myosin regulatory light chain 12B OS=Hydra vulgaris	22.9	3

1.2 Identification of protein from nematocyst

Table D-2. List of proteins identified (252 proteins) from nematocyst of edible jellyfish by using extraction of SDS coupled with sonication. The proteins were derived from in-gel digestion experiment. Database of taxonomy Cnidaria (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
A7SGU1	Glucose-6-phosphate isomerase OS=Nematostella vectensis	2.7	1

A7RKS5	40S ribosomal protein SA OS=Nematostella vectensis	3.5	1
T2MCI6	Transmembrane emp24 domain-containing protein 2 OS=Hydra vulgaris	4.6	1
E5F7D0	Non-muscle actin II OS=Hydractinia echinata	29.8	8
T2MGY6	Sodium/potassium-transporting ATPase subunit alpha OS=Hydra vulgaris	1.7	1
P38984	40S ribosomal protein SA OS=Hydra viridissima	4.1	1
B3EZK5	Ribosomal protein S5 (Fragment) OS=Hydra vulgaris	10.7	1
B1PM92	Calmodulin OS=Acropora muricata	33.6	3
A0A069DMJ2	Glutamate deshydrogenase (Fragment) OS=Clytia hemisphaerica	2.1	1
A0A069DNI2	Secreted tripeptidyl peptidase (Fragment) OS=Clytia hemisphaerica	2.7	1
A0A0C2IH62	26S protease regulatory subunit 10B OS=Thelohanellus kitauei	15.5	1
A0A1V0IGH5	Histone H2B OS=Hydra vulgaris	11.2	1
A0A0C2JEY5	6-phosphogluconate dehydrogenase, decarboxylating OS=Thelohanellus kitauei	5	2
A0A0C2JHL7	Uncharacterized protein OS=Thelohanellus kitauei	11.4	1
A0A0C2M5P0	Outer membrane protein A OS=Thelohanellus kitauei	2.5	1
A0A0C2M876	Eukaryotic translation initiation factor 3 subunit A OS=Thelohanellus kitauei	1.9	1
A0A0C2MJH4	Sortilin-related receptor OS=Thelohanellus kitauei	10.9	1
C1IJE5	Smooth muscle myosin heavy chain 11 isoform-like protein (Fragment) OS=Myxobolus cerebralis	5.5	1
A0A0C2MSM4	USP6 N-terminal-like protein OS=Thelohanellus kitauei	3.4	1
A7RVW7	Predicted protein (Fragment) OS=Nematostella vectensis	6.2	1
A0A0C2MUS2	60 kDa chaperonin OS=Thelohanellus kitauei	12.4	3
A0A0C2N442	Ras-related protein Rab-11A OS=Thelohanellus kitauei	5.3	1
A0A0C2N4C0	Cyclin-dependent kinase 9 OS=Thelohanellus kitauei	4.2	1
A0A0C2N4T5	ATP synthase subunit alpha OS=Thelohanellus kitauei	6.1	3
A0A0C2NEB1	Uncharacterized protein OS=Thelohanellus kitauei	6.4	1
A0A4Y6KM02	Cytochrome c oxidase subunit 2 (Fragment) OS=Montipora flabellata	8.9	1
A0A169Q0T5	Glyceraldehyde-3-phosphate dehydrogenase OS=Aurelia sp. SETO	15.2	4
A0A1L2A726	Superoxide dismutase [Cu-Zn] OS=Cyanea capillata	8.4	1
A0A1U9XQR0	Fructose-bisphosphate aldolase OS=Aurelia sp. 1 GW-2014	13.6	5
A0A1U9XQR2	Prolyl 4-hydroxylase subunit alpha-1 OS=Aurelia sp. 1 GW-2014	3.3	1
A0A219XS31	Serine protease 2 (Fragment) OS=Cyanea capillata	8	2
A0A2B4R2A5	RNA polymerase sigma factor RpoD (Fragment) OS=Stylophora pistillata	0.9	1
A0A2B4R2I0	Fumarylacetoacetase (Fragment) OS=Stylophora pistillata	5.1	1
A0A2B4R364	GTP-binding protein TypA/BipA-like OS=Stylophora pistillata	4.5	1
A0A2B4R6Q9	Fumarate hydratase class II OS=Stylophora pistillata	2.4	1
A0A2B4R9G5	Histone H2B OS=Stylophora pistillata	7.3	2
A0A2B4R9Q9	Histone H4 OS=Stylophora pistillata	35.8	11
A0A2B4R9T9	Chaperone protein DnaK OS=Stylophora pistillata	2.3	1
A7RQD8	Predicted protein OS=Nematostella vectensis	22.9	2
Q5FB18	Heat shock protein 70 OS=Pocillopora damicornis	2.4	2
A0A3M6TR29	Hcy-binding domain-containing protein OS=Pocillopora damicornis	5	1
A0A3M6UT08	PCM1_C domain-containing protein (Fragment) OS=Pocillopora damicornis	1.2	2
A0A2B4RC99	Macrophage receptor MARCO OS=Stylophora pistillata	8.4	2
T2M2P0	Coatomer subunit gamma (Fragment) OS=Hydra vulgaris	1.4	1

A7SRN1	Predicted protein OS=Nematostella vectensis	2.4	1
A0A2B4RI23	GTP-binding protein SAR1 OS=Stylophora pistillata	6.8	1
A0A2B4RIF3	Retrovirus-related Pol polyprotein OS=Stylophora pistillata	3.2	1
A0A2B4RJH1	Tubulin beta chain OS=Stylophora pistillata	39.4	13
A0A3M6TIL0	Uncharacterized protein OS=Pocillopora damicornis	6.5	1
Q7YZL5	Tubulin alpha chain (Fragment) OS=Aurelia aurita	32	9
A0A3M6U0I8	Uncharacterized protein OS=Pocillopora damicornis	3.6	1
A0A2B4RPA9	Clathrin heavy chain OS=Stylophora pistillata	8.3	10
A7RT97	Predicted protein OS=Nematostella vectensis	1.7	1
A0A3M6TQ41	Catalase OS=Pocillopora damicornis	5.5	2
Q93116	Ub52 OS=Acropora millepora	41.1	5
A0A2B4RTB1	Tubulin alpha-1C chain OS=Stylophora pistillata	34.5	7
Q2F6G0	Prohibitin (Fragment) OS=Anthopleura elegantissima	10	1
T2M3D0	Nucleolar protein 58 OS=Hydra vulgaris	2.6	1
A0A2B4RVA0	Tubulin alpha chain OS=Stylophora pistillata	16.2	5
A0A3M6UI41	Uncharacterized protein OS=Pocillopora damicornis	13.5	1
A0A3M6U1C8	NAC-A/B domain-containing protein OS=Pocillopora damicornis	6.2	1
A0A3M6U3P0	Uncharacterized protein OS=Pocillopora damicornis	1.5	1
A7SA87	Predicted protein OS=Nematostella vectensis	1.7	1
A0A3M6U791	Phosphoinositide phospholipase C OS=Pocillopora damicornis	4.5	1
A7S494	40S ribosomal protein S27 OS=Nematostella vectensis	15.5	1
T2M4N6	Guanine nucleotide-binding protein subunit beta-4 (Fragment) OS=Hydra vulgaris	3.3	1
A0A2B4RZV5	Uncharacterized protein OS=Stylophora pistillata	4.5	1
A0A3M6THY8	Uncharacterized protein OS=Pocillopora damicornis	1.7	1
A0A2B4S029	Aminopeptidase OS=Stylophora pistillata	2.7	1
A0A2B4S092	Multifunctional fusion protein OS=Stylophora pistillata	0.7	2
A0A3M6TYB3	Uncharacterized protein OS=Pocillopora damicornis	10.8	1
Q9Y207	G protein alpha subunit 3 (Fragment) OS=Hydra vulgaris	5.2	1
A0A2B4S129	Peroxiredoxin-1 OS=Stylophora pistillata	11.6	3
A0A2B4S1U8	Gamma-glutamyltranspeptidase 1 OS=Stylophora pistillata	3.4	1
Q6YCH0	Ribosomal protein S3 (Fragment) OS=Hydra vulgaris	9.7	2
A7SWV8	Predicted protein OS=Nematostella vectensis	3.9	1
A0A2B4S5A3	S-adenosylmethionine synthase OS=Stylophora pistillata	1.1	1
A0A3M6UGG9	Uncharacterized protein OS=Pocillopora damicornis	3.5	2
A0A2B4S643	Doublesex-and mab-3-related transcription factor A2 OS=Stylophora pistillata	3.3	2
A0A2B4S6B0	Tetratricopeptide repeat protein 28 OS=Stylophora pistillata	2.5	1
A0A2B4S7B2	Metabotropic glutamate receptor 3 OS=Stylophora pistillata	0.7	1
A0A2B4S7Q8	RING finger protein nhl-1 OS=Stylophora pistillata	4.9	1
T2M644	Microtubule-associated proteins 1A/1B light chain 3C OS=Hydra vulgaris	13.6	1
T2MEK8	Ras-related protein Rab-1A OS=Hydra vulgaris	8.4	1
A0A2B4SBE9	Alpha-mannosidase OS=Stylophora pistillata	2.7	2
T2M856	Dynein light chain OS=Hydra vulgaris	12.4	1
T2MF62	Small nuclear ribonucleoprotein Sm D2 OS=Hydra vulgaris	8.5	1

A0A2B4SEE8	Putative RNA-directed DNA polymerase from transposon BS OS=Stylophora pistillata	2.3	1
A0A2B4SF23	Uncharacterized protein K02A2.6 OS=Stylophora pistillata	0.7	1
A7T182	Predicted protein OS=Nematostella vectensis	5.3	1
A0A3M6U0P7	Uncharacterized protein OS=Pocillopora damicornis	9.8	2
T2MF68	Small nuclear ribonucleoprotein E OS=Hydra vulgaris	12.6	1
A0A2B4SHV7	E3 ubiquitin-protein ligase DZIP3 OS=Stylophora pistillata	0.4	1
A0A3M6TKN8	Transaldolase OS=Pocillopora damicornis	2.8	1
A7SPP0	ATP synthase subunit beta OS=Nematostella vectensis	20.4	6
A0A3M6V078	Rab GDP dissociation inhibitor OS=Pocillopora damicornis	4.5	1
A0A3M6TT70	V-type proton ATPase proteolipid subunit OS=Pocillopora damicornis	11.7	1
T2MF57	Coatomer subunit alpha OS=Hydra vulgaris	1	1
T2MEI1	AP-2 complex subunit beta (Fragment) OS=Hydra vulgaris	1.5	1
A7SY04	Predicted protein OS=Nematostella vectensis	1.3	1
A0A2B4SRV3	EF-hand domain-containing protein OS=Stylophora pistillata	2.1	1
A7T2Q5	Serine/threonine-protein phosphatase OS=Nematostella vectensis	9.4	2
Q8IAC3	Actin OS=Galaxea fascicularis	28.7	7
A0A2B4ST14	NACHT, LRR and PYD domains-containing protein 12 OS=Stylophora pistillata	0.3	1
A0A2B4STP4	Tubulin beta chain OS=Stylophora pistillata	15.4	12
A0A2B4STW2	Tetrapeptide repeat protein 28 OS=Stylophora pistillata	0.9	1
Q4JG19	Proteasome subunit beta OS=Swiftia exserta	4.9	1
A0A2B4SV29	YqaJ domain-containing protein OS=Stylophora pistillata	3.3	1
A0A2B4SVJ6	Aspartyl aminopeptidase OS=Stylophora pistillata	2.7	1
A0A3M6U4Q7	Uncharacterized protein OS=Pocillopora damicornis	6.6	1
A0A2B4SXX6	Solute carrier organic anion transporter family member 4A1 OS=Stylophora pistillata	3.8	1
A7SXE6	Predicted protein (Fragment) OS=Nematostella vectensis	3.5	1
A7SBR9	Predicted protein OS=Nematostella vectensis	3	1
A7T1M0	RNA-binding protein 8A (Fragment) OS=Nematostella vectensis	12.5	1
A0A2Z5WH73	Myosin heavy chain OS=Aurelia sp. 2017-HT	3.9	6
A0A2Z5WH78	Ser-Thr kinase OS=Aurelia sp. 2017-HT	2.3	1
A0A2Z5WH81	Myosin essential light chain OS=Aurelia sp. 2017-HT	7.3	1
A0A3M6T968	Uncharacterized protein OS=Pocillopora damicornis	12.4	1
T2MD57	Calcium-transporting ATPase OS=Hydra vulgaris	1.7	1
A0A3M6TAC9	BBS1 domain-containing protein OS=Pocillopora damicornis	1.7	1
A0A3M6TIE8	Non-specific serine/threonine protein kinase OS=Pocillopora damicornis	0.8	1
A0A3M6TIP3	Protein kinase domain-containing protein (Fragment) OS=Pocillopora damicornis	1.4	1
A0A3M6TL80	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	1.9	1
A0A3M6TLH9	Uncharacterized protein OS=Pocillopora damicornis	6.7	2
A0A3M6TRE9	Uncharacterized protein OS=Pocillopora damicornis	11.1	1
A0A3M6TST2	Uncharacterized protein OS=Pocillopora damicornis	5.4	1
A0A3M6TVV7	Hcy-binding domain-containing protein OS=Pocillopora damicornis	4.4	1
A0A3M6TYE7	Uncharacterized protein OS=Pocillopora damicornis	6.2	1
A0A3M6U3L0	C2H2-type domain-containing protein (Fragment) OS=Pocillopora damicornis	2	1
A0A3M6U5H6	ANF_receptor domain-containing protein (Fragment) OS=Pocillopora	10.4	1

	damicornis		
A0A3M6U8Y8	Proteasome subunit alpha type OS=Pocillopora damicornis	6.3	1
A0A3M6UGM1	V-type proton ATPase subunit a OS=Pocillopora damicornis	4.4	1
A0A3M6UHG1	Uncharacterized protein OS=Pocillopora damicornis	1.9	1
A0A3M6UPH5	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	3.2	1
A0A3M6UPZ4	Uncharacterized protein OS=Pocillopora damicornis	4.3	2
Q6EIK7	Rab7 OS=Aiptasia pulchella	16.1	3
A0A3M6UZ63	Annexin OS=Pocillopora damicornis	11	6
A0A3M6V263	Isochorismatase domain-containing protein OS=Pocillopora damicornis	5.6	1
A0A3M6V2N5	Adenosylhomocysteinase OS=Pocillopora damicornis	8.3	3
A0A3M6V5E0	Aminopeptidase OS=Pocillopora damicornis	1.2	1
G9IT81	Cytochrome c oxidase subunit 2 OS=Rhizostoma pulmo	13.3	2
A3F9E8	Histone H2B (Fragment) OS=Anacropora matthai	17.9	2
A7RHF7	Eukaryotic translation initiation factor 6 OS=Nematostella vectensis	10.2	1
Q5U9S0	Ubiquitin/ribosomal L40 fusion protein OS=Scleronephthya gracillimum	41.4	5
A7RL59	Predicted protein OS=Nematostella vectensis	5.2	1
A7RL77	Coatomer subunit beta OS=Nematostella vectensis	2.3	2
A7RM97	Predicted protein OS=Nematostella vectensis	13.6	2
A7RNA5	Electron transfer flavoprotein-ubiquinone oxidoreductase OS=Nematostella vectensis	2	1
A7RPG9	Predicted protein OS=Nematostella vectensis	4.4	1
A7SM36	Predicted protein OS=Nematostella vectensis	3.8	1
A7RUX0	Tubulin alpha chain OS=Nematostella vectensis	14.2	5
A7RVC0	Clathrin heavy chain OS=Nematostella vectensis	6.2	8
A7RVD9	Tubulin alpha chain OS=Nematostella vectensis	28	8
A7RXV6	Predicted protein (Fragment) OS=Nematostella vectensis	13	1
A7S1I1	Predicted protein OS=Nematostella vectensis	1.6	1
A7S1I9	Predicted protein OS=Nematostella vectensis	11.8	2
A7S289	Predicted protein OS=Nematostella vectensis	17.9	1
A7S335	Predicted protein OS=Nematostella vectensis	1.6	3
A7S469	Predicted protein OS=Nematostella vectensis	6.9	1
A7S4D2	Triosephosphate isomerase OS=Nematostella vectensis	9.7	2
I2G9C5	Alpha-actinin (Fragment) OS=Nematostella vectensis	3.4	1
A7S4Z2	Predicted protein (Fragment) OS=Nematostella vectensis	5.1	1
A7S690	Predicted protein (Fragment) OS=Nematostella vectensis	20.4	2
A7S7K4	Predicted protein OS=Nematostella vectensis	4.4	1
A7S7R7	Predicted protein OS=Nematostella vectensis	13.3	1
Q7YZK5	Tubulin beta chain (Fragment) OS=Nematostella vectensis	41.6	13
A7S8R3	Beta-galactosidase OS=Nematostella vectensis	1.5	1
A7SC77	Predicted protein OS=Nematostella vectensis	21.5	6
A7SDJ0	Predicted protein (Fragment) OS=Nematostella vectensis	1.5	1
A7SFM4	Predicted protein (Fragment) OS=Nematostella vectensis	2.4	1
A7SHC0	Predicted protein (Fragment) OS=Nematostella vectensis	1.3	1
A7SJZ4	Small nuclear ribonucleoprotein Sm D1 OS=Nematostella vectensis	26.7	2

A7SKY7	Angiotensin-converting enzyme OS=Nematostella vectensis	1	1
A7SPM9	Predicted protein (Fragment) OS=Nematostella vectensis	2.3	1
A7SPQ4	Predicted protein OS=Nematostella vectensis	15.8	3
A7SPV0	Predicted protein (Fragment) OS=Nematostella vectensis	0.6	1
A7SSL5	Predicted protein OS=Nematostella vectensis	6.3	4
A7SX44	Predicted protein (Fragment) OS=Nematostella vectensis	4.3	1
A7SX99	Predicted protein OS=Nematostella vectensis	13.6	1
A7T2X0	Predicted protein (Fragment) OS=Nematostella vectensis	2.3	1
A7T070	Predicted protein OS=Nematostella vectensis	1.3	1
A7TOR0	Predicted protein (Fragment) OS=Nematostella vectensis	4.7	1
A7T288	T-complex protein 1 subunit delta OS=Nematostella vectensis	2.1	1
A7T3D9	Predicted protein OS=Nematostella vectensis	2.9	1
A7TCL7	Histone H2A OS=Nematostella vectensis	41.1	11
A8DX89	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Urticina eques	3.7	1
C1IS27	Clathrin heavy chain (Fragment) OS=Carukia barnesi	16.4	2
I2G9E1	Serine/threonine-protein phosphatase (Fragment) OS=Clytia hemisphaerica	8.1	2
I2G9E9	Myosin II heavy chain, smooth/non-muscle-type (Fragment) OS=Clytia hemisphaerica	3.4	1
K0A063	Beta-actin (Fragment) OS=Chrysaora quinquecirrha	33.7	8
M1E2A8	Calmodulin (Fragment) OS=Rhizostoma octopus	45.6	3
M1T236	Putative flagellar-associated protein (Fragment) OS=Stylophora pistillata	1.5	1
Q56GW1	60S ribosomal protein L12 (Fragment) OS=Hydractinia echinata	16.5	1
Q56GW5	40S ribosomal protein S4 (Fragment) OS=Hydractinia echinata	14.3	1
Q5EN87	Putative tyrosine-rich heat shock protein (Fragment) OS=Aurelia aurita	5.8	1
Q5WR13	Non-muscle actin (Fragment) OS=Hydra viridissima	34.9	4
Q6PTK3	Triosephosphate isomerase (Fragment) OS=Obelia sp. KJP-2004	17.5	3
Q7YZI4	90-kDa heat-shock protein (Fragment) OS=Aurelia aurita	8.9	3
Q7YZK4	Tubulin beta chain (Fragment) OS=Aurelia aurita	41.9	13
Q8I9P3	Serine protease 2 (Fragment) OS=Aurelia aurita	5.1	1
Q9GUZ7	PL10-related protein CnPL10 (Fragment) OS=Hydractinia echinata	10.1	2
Q9NFW1	60S ribosomal protein L12 OS=Hydra vulgaris	9.7	1
R9S2M2	Elongation factor 1-alpha OS=Aurelia aurita	6.9	3
S5ZJ06	Heme-binding protein 1-like protein OS=Aurelia aurita	3.6	1
T2M3F8	Aspartyl aminopeptidase OS=Hydra vulgaris	2.6	1
T2M3I7	RuvB-like helicase OS=Hydra vulgaris	3.5	1
T2M4E1	Beta-ureidopropionase (Fragment) OS=Hydra vulgaris	2.6	1
T2M4S3	BTB/POZ domain-containing protein KCTD5 (Fragment) OS=Hydra vulgaris	4.4	1
T2M5D3	Protein transport protein Sec61 subunit alpha isoform 2 OS=Hydra vulgaris	4.2	1
T2M5K6	Transmembrane 9 superfamily member OS=Hydra vulgaris	1.7	1
T2M6Q7	Transmembrane emp24 domain-containing protein 9 OS=Hydra vulgaris	9.3	3
T2M7H4	Transcription factor BTF3 OS=Hydra vulgaris	8.9	1
T2M7J1	Vacuolar protein sorting-associated protein 35 (Fragment) OS=Hydra vulgaris	6.7	4
T2M7R0	Ubiquitin carboxyl-terminal hydrolase (Fragment) OS=Hydra vulgaris	1.8	1
T2M8L0	Phospholipase B-like OS=Hydra vulgaris	2.9	1

T2M9A6	SH3 domain-containing RING finger protein 3 OS=Hydra vulgaris	1.7	1
T2MCF0	Activating signal cointegrator 1 OS=Hydra vulgaris	2	1
T2MDG4	Flotillin-2 OS=Hydra vulgaris	3.5	1
T2MDJ0	Dihydropyrimidinase (Fragment) OS=Hydra vulgaris	3.1	1
T2MEJ9	Eukaryotic translation initiation factor 6 (Fragment) OS=Hydra vulgaris	7.2	1
T2MEL5	40S ribosomal protein S28 OS=Hydra vulgaris	17.9	1
T2MEP2	40S ribosomal protein S18 OS=Hydra vulgaris	7.1	1
T2MEP4	Small nuclear ribonucleoprotein Sm D1 (Fragment) OS=Hydra vulgaris	7.7	1
T2MET8	WD repeat-containing protein 5 OS=Hydra vulgaris	9.1	2
T2MEY1	60S ribosomal protein L11 (Fragment) OS=Hydra vulgaris	7.2	1
T2MF54	60S ribosomal protein L7a (Fragment) OS=Hydra vulgaris	4.4	1
T2MF63	Serine/threonine-protein phosphatase OS=Hydra vulgaris	29.7	7
T2MFU6	26S proteasome non-ATPase regulatory subunit 7 OS=Hydra vulgaris	3.7	1
T2MFV4	Isoleucyl-tRNA synthetase,cytoplasmic (Fragment) OS=Hydra vulgaris	1.7	2
T2MFY6	Hippocalcin-like protein 1 OS=Hydra vulgaris	21.5	3
T2MG06	Transaldolase OS=Hydra vulgaris	2.7	1
T2MG07	Proteasome subunit alpha type OS=Hydra vulgaris	14.5	2
T2MG36	Myosin-10 OS=Hydra vulgaris	0.7	1
T2MG47	Radixin OS=Hydra vulgaris	2.7	1
T2MGF7	Malate dehydrogenase,mitochondrial OS=Hydra vulgaris	3.5	1
T2MGH4	Proteasome subunit alpha type OS=Hydra vulgaris	3.6	1
T2MGL9	40S ribosomal protein S17-like OS=Hydra vulgaris	7.5	1
T2MGS3	cAMP-dependent protein kinase catalytic subunit alpha OS=Hydra vulgaris	3.4	1
T2MGT7	Glutathione peroxidase (Fragment) OS=Hydra vulgaris	5.6	1
T2MGX7	60S ribosomal protein L13 (Fragment) OS=Hydra vulgaris	7.2	2
T2MGY7	40S ribosomal protein S12 OS=Hydra vulgaris	10.2	1
T2MH46	Filamin-A OS=Hydra vulgaris	0.6	1
T2MHA3	Histone H1.0 OS=Hydra vulgaris	5.2	1
T2MHN7	Citrate synthase OS=Hydra vulgaris	3.4	1
T2MHT5	Heat shock protein HSP 90-alpha OS=Hydra vulgaris	5.5	4
T2MHY4	Argininosuccinate synthase (Fragment) OS=Hydra vulgaris	2.9	1
T2MHZ3	Ornithine aminotransferase,mitochondrial OS=Hydra vulgaris	4.4	1
T2MI35	Splicing factor 3B subunit 1 (Fragment) OS=Hydra vulgaris	1.2	1
T2MIQ9	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial (Fragment) OS=Hydra vulgaris	1.8	1
T2MIT4	Calpain-5 (Fragment) OS=Hydra vulgaris	1.6	1
W8PTQ2	Peroxiredoxin 4 OS=Cyanea capillata	34.4	7
W8Q1J8	Glyceraldehyde-3-phosphate dehydrogenase OS=Cyanea capillata	5.4	2

Table D-3. List of proteins identified (425 proteins) from nematocyst of edible jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were derived from in-gel digestion experiment. Database of taxonomy Cnidaria (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
A7SGU1	Glucose-6-phosphate isomerase OS=Nematostella vectensis	2.7	1
A7RKS5	40S ribosomal protein SA OS=Nematostella vectensis	3.5	1
T2MCI6	Transmembrane emp24 domain-containing protein 2 OS=Hydra vulgaris	4.6	1
E5F7D0	Non-muscle actin II OS=Hydractinia echinata	60.1	19
T2MGY6	Sodium/potassium-transporting ATPase subunit alpha OS=Hydra vulgaris	5.2	3
T2MGR0	60S ribosomal protein L17 OS=Hydra vulgaris	8.7	1
M1G2E5	Ras2 (Fragment) OS=Hydractinia echinata	16.1	2
P38984	ribosomal protein SA OS=Hydra viridissima	4.1	1
P41113	Actin-3 OS=Podocoryna carnea	56.9	18
M1G4Y4	Ras1 (Fragment) OS=Hydractinia echinata	19.6	2
P62184	Calmodulin OS=Renilla reniformis	58.4	4
B1PM92	Calmodulin OS=Acropora muricata	58.4	4
A0A0C2I691	Translation initiation factor IF-2 OS=Thelohanellus kitauei	6.3	1
A0A0C2I839	Cytosol aminopeptidase OS=Thelohanellus kitauei	2.4	1
A0A0C2IKC3	Coiled-coil domain-containing protein 94 OS=Thelohanellus kitauei	12.6	1
A7SRV8	40S ribosomal protein S4 OS=Nematostella vectensis	4.6	1
A0A1V0IGH5	Histone H2B OS=Hydra vulgaris	11.2	1
A0A0C2IV52	Translation initiation factor IF-2 OS=Thelohanellus kitauei	18	3
A0A0C2IZS4	Outer membrane protein TolC OS=Thelohanellus kitauei	3.8	1
A0A0C2J3J1	60 kDa heat shock protein, mitochondrial OS=Thelohanellus kitauei	2.1	1
A0A0C2J513	Ldh_1_N domain-containing protein OS=Thelohanellus kitauei	17.1	1
T2MF79	Transforming protein RhoA OS=Hydra vulgaris	16.7	3
A0A0C2JEY5	6-phosphogluconate dehydrogenase, decarboxylating OS=Thelohanellus kitauei	7	3
A0A0C2JHL7	Uncharacterized protein OS=Thelohanellus kitauei	11.4	1
A0A0C2JSW9	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 OS=Thelohanellus kitauei	1.9	1
A0A0C2M5P0	Outer membrane protein A OS=Thelohanellus kitauei	5.6	2
A0A0C2M5R5	26S protease regulatory subunit 8 OS=Thelohanellus kitauei	12	2
A0A0C2M8T0	Translation initiation factor IF-2 OS=Thelohanellus kitauei	4.1	1
A0A0C2MG55	Uncharacterized protein OS=Thelohanellus kitauei	7	1
A0A0C2MKJ3	Uncharacterized protein OS=Thelohanellus kitauei	2.8	1
A0A0C2MNQ3	Myosin-10 OS=Thelohanellus kitauei	3.2	2
A7RVW7	Predicted protein (Fragment) OS=Nematostella vectensis	6.2	1
A0A0C2MUS2	60 kDa chaperonin OS=Thelohanellus kitauei	16.1	6
A0A0C2N200	Ras-related protein RABA2a OS=Thelohanellus kitauei	5.3	1
A0A0C2N354	ATP synthase subunit beta OS=Thelohanellus kitauei	22.3	6
A0A0C2N442	Ras-related protein Rab-11A OS=Thelohanellus kitauei	5.3	1
A0A0C2N916	Casein kinase I isoform gamma-1 OS=Thelohanellus kitauei	3.9	1
A0A0C4VZ14	78 kDa glycose-regulated protein (Fragment) OS=Capnella imbricata	7.1	2
A0A181ZLN7	Heat shock protein 70 (Fragment) OS=Sinularia cf. cruciata GS-2016	11.5	3
A0A4Y6KM02	Cytochrome c oxidase subunit 2 (Fragment) OS=Montipora flabellata	8.9	1
A0A0N7F1C5	MAC/Perforin domain containing protein OS=Rhopilema esculentum	3	1
A0A0U2E1U9	Cytochrome c oxidase subunit 2 OS=Sagartia ornata	8.1	1

A0A169Q0T5	Glyceraldehyde-3-phosphate dehydrogenase OS=Aurelia sp. SETO	12.8	3
A0A2Z5WH77	Actin-1 OS=Aurelia sp. 2017-HT	67.3	22
A0A1B3IQV5	Histone macroH2A OS=Hydractinia echinata	2.4	1
A0A1B3IQX8	Histone H2A OS=Hydractinia echinata	29	2
A0A1L2A726	Superoxide dismutase [Cu-Zn] OS=Cyanea capillata	8.4	1
A7RFA3	Predicted protein (Fragment) OS=Nematostella vectensis	2.9	1
A0A1U9XQR0	Fructose-bisphosphate aldolase OS=Aurelia sp. 1 GW-2014	17.5	7
A0A288W1V0	Mitogen-activated protein kinase OS=Aurelia aurita	17.3	4
A0A3M6TX36	Protein kinase domain-containing protein OS=Pocillopora damicornis	5.2	1
A0A2B4S3Y5	Uncharacterized protein OS=Stylophora pistillata	1	1
A0A2B4R2A5	RNA polymerase sigma factor RpoD (Fragment) OS=Stylophora pistillata	1.4	1
A0A2B4R2I0	Fumarylacetoacetase (Fragment) OS=Stylophora pistillata	5.1	1
A0A2B4R364	GTP-binding protein TypA/BipA-like OS=Stylophora pistillata	7.5	2
A0A2B4R3E0	NAD-specific glutamate dehydrogenase (Fragment) OS=Stylophora pistillata	1	1
A0A2B4R3V3	Flagellar hook protein FlgE (Fragment) OS=Stylophora pistillata	3.1	1
A0A2B4R6Q9	Fumarate hydratase class II OS=Stylophora pistillata	4	2
A0A2B4R7X3	Endonuclease III-like protein 1 OS=Stylophora pistillata	5.8	1
A0A2B4R9G5	Histone H2B OS=Stylophora pistillata	7.3	2
A0A2B4R9Q9	Histone H4 OS=Stylophora pistillata	36.8	12
A0A2B4R9T9	Chaperone protein DnaK OS=Stylophora pistillata	2.3	1
A7RQD8	Predicted protein OS=Nematostella vectensis	39.8	4
A0A2B4RB68	Transmembrane 9 superfamily member (Fragment) OS=Stylophora pistillata	22.3	2
A0A2B4RCT7	4-hydroxyphenylpyruvate dioxygenase OS=Stylophora pistillata	4	1
A0A2B4RF65	Isocitrate dehydrogenase [NADP] 2 OS=Stylophora pistillata	0.9	1
A7SRN1	Predicted protein OS=Nematostella vectensis	11.1	5
A0A2B4RHH4	Heat shock protein 70 B2 OS=Stylophora pistillata	10.8	3
A0A2B4RHH5	Enoyl-CoA hydratase, mitochondrial OS=Stylophora pistillata	6	1
A0A2B4RI23	GTP-binding protein SAR1 OS=Stylophora pistillata	6.8	1
A0A2B4RIA2	Polyadenylate-binding protein 4 OS=Stylophora pistillata	2.4	1
A0A3M6U0C3	GLTP domain-containing protein OS=Pocillopora damicornis	5.9	2
A0A3M6ULI0	J domain-containing protein OS=Pocillopora damicornis	6.5	1
A0A2B4RJH1	Tubulin beta chain OS=Stylophora pistillata	59.7	24
A0A3M6TIL0	Uncharacterized protein OS=Pocillopora damicornis	6.5	1
A0A2B4RKT3	26S proteasome non-ATPase regulatory subunit 2 OS=Stylophora pistillata	1.7	1
A7RRD6	Predicted protein OS=Nematostella vectensis	1.7	1
A7SH82	Predicted protein OS=Nematostella vectensis	5.9	1
A0A2B4RNK8	Uncharacterized protein OS=Stylophora pistillata	8.7	1
A0A3M6UAJ0	Autophagy-related protein 3 (Fragment) OS=Pocillopora damicornis	6.7	1
A0A3M6TUJ6	Protein kinase domain-containing protein OS=Pocillopora damicornis	1.8	1
A7STE6	Predicted protein OS=Nematostella vectensis	6.5	1
A0A2B4RPA9	Clathrin heavy chain OS=Stylophora pistillata	9.6	13
A0A2B4RQ22	Tyrosine-protein kinase OS=Stylophora pistillata	3.7	2
A7SQS1	Malate dehydrogenase OS=Nematostella vectensis	4.7	1
A0A2B4RQI4	Proteasome subunit beta OS=Stylophora pistillata	8.6	2

A0A3M6V4M9	Uncharacterized protein OS=Pocillopora damicornis	11.9	3
A0A2B4RQY2	Ubiquitin-conjugating enzyme E2 L3 OS=Stylophora pistillata	21.4	2
A0A2B4RQZ5	Glutathione reductase, mitochondrial OS=Stylophora pistillata	2.3	1
A0A2B4RRR8	Dynein beta chain, ciliary OS=Stylophora pistillata	0.5	1
Q93116	Ub52 OS=Acropora millepora	36.4	4
A0A2B4RTB1	Tubulin alpha-1C chain OS=Stylophora pistillata	53.4	10
A0A2B4SVG2	EGF-like domain-containing protein OS=Stylophora pistillata	5.8	1
A7RXR8	Predicted protein OS=Nematostella vectensis	12.2	1
Q2F6G0	Prohibitin (Fragment) OS=Anthopleura elegantissima	10	1
T2M3D0	Nucleolar protein 58 OS=Hydra vulgaris	2.6	1
A0A2B4RVA0	Tubulin alpha chain OS=Stylophora pistillata	18.2	6
A0A2B4RW25	Pre-mRNA-processing-splicing factor 8 OS=Stylophora pistillata	1.6	3
A0A3M6U1C8	NAC-A/B domain-containing protein OS=Pocillopora damicornis	6.2	1
A0A3M6U3P0	Uncharacterized protein OS=Pocillopora damicornis	1.5	1
A0A3M6UGY3	UBIQUITIN_CONJUGAT_2 domain-containing protein OS=Pocillopora damicornis	9.9	1
A0A2B4RX45	Coiled-coil domain-containing protein 138 OS=Stylophora pistillata	1.9	1
A0A2B4RXI4	Ras-related protein Rab-5B OS=Stylophora pistillata	5.6	1
A0A3M6TNT3	Coatomer subunit delta OS=Pocillopora damicornis	2.4	1
A0A2B4S092	Multifunctional fusion protein OS=Stylophora pistillata	1.7	5
A0A3M6TYB3	Uncharacterized protein OS=Pocillopora damicornis	10.8	1
L0AUB3	Alpha q G protein OS=Acropora palmata	10.2	3
A0A2B4S129	Peroxiredoxin-1 OS=Stylophora pistillata	8.4	2
A0A2B4S132	Uncharacterized protein OS=Stylophora pistillata	1.1	1
T2MJH6	rRNA/tRNA 2-O-methyltransferase fibrillar-like protein 1 OS=Hydra vulgaris	7.3	1
A0A2B4S1U8	Gamma-glutamyltranspeptidase 1 OS=Stylophora pistillata	3.4	1
A7RSQ0	Predicted protein (Fragment) OS=Nematostella vectensis	1.5	1
A0A3M6UUK9	Lipoyl-binding domain-containing protein OS=Pocillopora damicornis	2.8	1
A0A2B4S2W7	Major vault protein OS=Stylophora pistillata	6	4
A7SWV8	Predicted protein OS=Nematostella vectensis	3.9	1
A0A2B4S3I9	Non-specific serine/threonine protein kinase OS=Stylophora pistillata	4.9	3
A0A3M6TR43	AA_TRNA_LIGASE_II domain-containing protein OS=Pocillopora damicornis	3.1	2
T2MEG1	Cell division control protein 42 homolog OS=Hydra vulgaris	17.8	3
A0A2B4S5A3	S-adenosylmethionine synthase OS=Stylophora pistillata	1.2	2
A0A3M6UGG9	Uncharacterized protein OS=Pocillopora damicornis	13.5	9
A7SLT6	6-phosphogluconate dehydrogenase, decarboxylating OS=Nematostella vectensis	4.5	2
A0A2B4S643	Doublesex-and mab-3-related transcription factor A2 OS=Stylophora pistillata	3.3	1
A0A3M6UQS3	UBA_e1_C domain-containing protein OS=Pocillopora damicornis	1.4	1
A0A2B4SC49	Actin-related protein 3 OS=Stylophora pistillata	23.2	5
T2M856	Dynein light chain OS=Hydra vulgaris	24.7	2
A0A3M6T7R7	Small nuclear ribonucleoprotein Sm D2 OS=Pocillopora damicornis	16.1	2
A7RFJ1	Predicted protein OS=Nematostella vectensis	7.7	1
A7SS49	Predicted protein OS=Nematostella vectensis	10.5	3
A0A2B4SE68	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Stylophora pistillata	3	1

A0A2B4SFU3	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Stylophora pistillata	12.1	2
A0A2B4SGD6	Centrosome and spindle pole-associated protein 1 OS=Stylophora pistillata	1.1	1
T2MF68	Small nuclear ribonucleoprotein E OS=Hydra vulgaris	12.6	1
A7RVJ0	Serine/threonine-protein phosphatase OS=Nematostella vectensis	13.1	4
A0A3M6U8V1	E3 ubiquitin-protein ligase OS=Pocillopora damicornis	1.5	1
A0A3M6TKN8	Transaldolase OS=Pocillopora damicornis	7.2	3
A7SAS1	Predicted protein OS=Nematostella vectensis	23.1	2
A0A3M6TVL9	Uncharacterized protein OS=Pocillopora damicornis	2.1	2
A7SPP0	ATP synthase subunit beta OS=Nematostella vectensis	40.1	10
A0A2B4SJQ6	Rab GDP dissociation inhibitor OS=Stylophora pistillata	7.2	2
A0A3M6UYR9	Sm domain-containing protein OS=Pocillopora damicornis	15.5	1
A0A3M6V0P1	RPN2_C domain-containing protein (Fragment) OS=Pocillopora damicornis	2.2	1
A0A2B4SLN3	Gamma-aminobutyric acid type B receptor subunit 2 OS=Stylophora pistillata	0.4	1
A0A3M6TT70	V-type proton ATPase proteolipid subunit OS=Pocillopora damicornis	11.7	1
A7RV73	Vacuolar protein sorting-associated protein 29 OS=Nematostella vectensis	7.1	1
A7SHU3	Predicted protein OS=Nematostella vectensis	32.1	6
A0A2B4SQT0	Unconventional myosin-Ie OS=Stylophora pistillata	1	1
T2MF57	Coatomer subunit alpha OS=Hydra vulgaris	1.9	2
A0A3M6UDV1	WD_REPEATS_REGION domain-containing protein OS=Pocillopora damicornis	3.8	1
A0A3M6V090	Serine/threonine-protein phosphatase OS=Pocillopora damicornis	13.7	2
A0A2B4STP6	Kinesin-like protein KIF28P OS=Stylophora pistillata	1.4	1
A0A2B4SU54	Collagen alpha-1(XIV) chain OS=Stylophora pistillata	0.6	1
A0A2B4SUW9	Isocitrate dehydrogenase [NADP] OS=Stylophora pistillata	5.3	2
A0A3M6U1Z1	Uncharacterized protein OS=Pocillopora damicornis	0.9	1
A0A2B4SV07	Tubulin beta chain OS=Stylophora pistillata	57.6	24
A0A3M6TU98	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	9.9	1
A7T8C0	Predicted protein (Fragment) OS=Nematostella vectensis	3.3	1
A0A2B4SWD0	Proteasome subunit alpha type OS=Stylophora pistillata	14.1	3
A0A3M6UEM1	Uncharacterized protein OS=Pocillopora damicornis	13.7	1
A0A3M6UTM8	Uncharacterized protein OS=Pocillopora damicornis	2.6	2
A0A2B4SXX6	Solute carrier organic anion transporter family member 4A1 OS=Stylophora pistillata	3.8	1
A0A2B4SYF4	GTP-binding protein YPT1 OS=Stylophora pistillata	5	1
A0A2B4SYS5	Sodium/potassium-transporting ATPase subunit alpha OS=Stylophora pistillata	5.8	3
A0A2B4SZL5	Radixin OS=Stylophora pistillata	8.5	3
A0A2B4SZV5	Ras GTPase-activating-like protein IQGAP1 OS=Stylophora pistillata	1.6	2
A0A2B4T1C4	ATP synthase subunit alpha OS=Stylophora pistillata	27.9	11
A7SBR9	Predicted protein OS=Nematostella vectensis	4.7	2
A7T1M0	RNA-binding protein 8A (Fragment) OS=Nematostella vectensis	12.5	1
A7SB93	Predicted protein OS=Nematostella vectensis	12	2
A0A2Z5WH73	Myosin heavy chain OS=Aurelia sp. 2017-HT	6.1	8
A0A2Z5WH78	Ser-Thr kinase OS=Aurelia sp. 2017-HT	2.3	1
A0A2Z5WH79	Tropomyosin-2 OS=Aurelia sp. 2017-HT	5.7	1
A0A2Z5WH80	Myosin regulatory light chain OS=Aurelia sp. 2017-HT	22.2	3

A0A2Z5WH81	Myosin essential light chain OS=Aurelia sp. 2017-HT	7.3	1
A0A343FMY2	Cytochrome c oxidase subunit 2 OS=Nemopilema nomurai	5.7	1
A0A3M6T475	Actin-related protein 2/3 complex subunit 4 OS=Pocillopora damicornis	17.3	3
A0A3M6T8X3	Calcium-transporting ATPase OS=Pocillopora damicornis	1.5	1
A0A3M6T968	Uncharacterized protein OS=Pocillopora damicornis	12.4	1
A7S1T2	Predicted protein OS=Nematostella vectensis	5.5	2
T2MD57	Calcium-transporting ATPase OS=Hydra vulgaris	3.3	3
A0A3M6TBF7	Uncharacterized protein OS=Pocillopora damicornis	6.9	1
A7SXV0	Predicted protein OS=Nematostella vectensis	3	1
A0A3M6THH7	Actin-related protein 2 OS=Pocillopora damicornis	14.1	4
A0A3M6TLH9	Uncharacterized protein OS=Pocillopora damicornis	7.7	4
A0A3M6TMJ8	A2M_recep domain-containing protein OS=Pocillopora damicornis	1.5	1
A0A3M6TQM6	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	6	1
A0A3M6TST2	Uncharacterized protein OS=Pocillopora damicornis	5.4	1
A0A3M6TVV7	Hcy-binding domain-containing protein OS=Pocillopora damicornis	4.4	1
A0A3M6TW19	Sodium/potassium-transporting ATPase subunit alpha (Fragment) OS=Pocillopora damicornis	4.5	3
A0A3M6TWG3	PHB domain-containing protein (Fragment) OS=Pocillopora damicornis	4.6	2
A0A3M6TYE7	Uncharacterized protein OS=Pocillopora damicornis	6.2	1
A0A3M6U2Z6	Uncharacterized protein OS=Pocillopora damicornis	7.4	1
A0A3M6U3X8	Uncharacterized protein OS=Pocillopora damicornis	3.2	1
A0A3M6U454	Histone H2A OS=Pocillopora damicornis	17.4	2
A0A3M6U7U8	Uncharacterized protein OS=Pocillopora damicornis	5.3	3
A0A3M6U8Y8	Proteasome subunit alpha type OS=Pocillopora damicornis	12.2	3
A0A3M6UB81	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	1.2	1
A7RMA8	Predicted protein OS=Nematostella vectensis	4.5	1
A0A3M6UGM1	V-type proton ATPase subunit a OS=Pocillopora damicornis	4.4	1
A0A3M6UHG1	Uncharacterized protein OS=Pocillopora damicornis	1.9	1
A0A3M6UIW6	ABC transporter domain-containing protein OS=Pocillopora damicornis	1.2	1
A0A3M6UJY5	Transket_pyr domain-containing protein OS=Pocillopora damicornis	1.3	1
A0A3M6UN42	DUF4709 domain-containing protein OS=Pocillopora damicornis	2.1	1
A0A3M6UP81	Uncharacterized protein OS=Pocillopora damicornis	48.9	15
A0A3M6UQA3	Calponin-homology (CH) domain-containing protein OS=Pocillopora damicornis	5.8	1
A0A3M6US90	Uncharacterized protein OS=Pocillopora damicornis	4.8	1
A0A3M6UUF7	Uncharacterized protein OS=Pocillopora damicornis	4.1	1
A0A3M6UYC1	cGMP-dependent protein kinase OS=Pocillopora damicornis	1.7	1
A0A3M6UZ63	Annexin OS=Pocillopora damicornis	10.6	9
A0A3M6V263	Isochorismatase domain-containing protein OS=Pocillopora damicornis	5.6	1
A0A3M6V2N5	Adenosylhomocysteinase OS=Pocillopora damicornis	8.3	3
A0A4V1H7U6	Cytochrome c oxidase subunit 2 OS=Stomolophus sp. CG-2019	23.4	3
T2MEW7	Ras-related protein Rab-10 OS=Hydra vulgaris	22.7	4
A0S5V7	Mitochondrial succinate dehydrogenase flavoprotein subunit (Fragment) OS=Hydra vulgaris	6.7	2
A3F9E8	Histone H2B (Fragment) OS=Anacropora matthai	9.4	1
IIYAQ8	Beta-catenin OS=Clytia hemisphaerica	3	2

A7REV0	Anoctamin (Fragment) OS=Nematostella vectensis	1.6	1
A7RGP8	Predicted protein OS=Nematostella vectensis	5.5	4
A7RGV0	Predicted protein OS=Nematostella vectensis	3.5	1
A7RHF7	Eukaryotic translation initiation factor 6 OS=Nematostella vectensis	10.2	1
A7RIF0	T-complex protein 1 subunit eta OS=Nematostella vectensis	4	2
Q5U9S0	Ubiquitin/ribosomal L40 fusion protein OS=Scleronephthya gracillimum	36.7	4
A7RJD9	Predicted protein OS=Nematostella vectensis	19	3
A7RL59	Predicted protein OS=Nematostella vectensis	5.2	1
A7RL77	Coatomer subunit beta OS=Nematostella vectensis	2.3	2
A7RLY5	Predicted protein OS=Nematostella vectensis	2.2	1
A7RMZ4	Predicted protein OS=Nematostella vectensis	5.4	1
A7RPG9	Predicted protein OS=Nematostella vectensis	4.4	1
A7RQR3	10-formyltetrahydrofolate dehydrogenase OS=Nematostella vectensis	4.9	3
A7RRK0	Predicted protein (Fragment) OS=Nematostella vectensis	8.9	1
A7T836	Predicted protein (Fragment) OS=Nematostella vectensis	2.7	1
A7RT97	Predicted protein OS=Nematostella vectensis	2.8	2
A7RUT1	Tubulin alpha chain OS=Nematostella vectensis	51.1	18
A7RVC0	Clathrin heavy chain OS=Nematostella vectensis	7.4	10
A7RXX2	Thymidine phosphorylase OS=Nematostella vectensis	2.4	1
E7BTP8	Rab14 OS=Aiptasia pulchella	26.3	5
B5KVJ1	Small GTP-binding protein Rab4 OS=Aiptasia pulchella	7.4	1
A7S0B5	Predicted protein (Fragment) OS=Nematostella vectensis	1.7	1
A7S1I1	Predicted protein OS=Nematostella vectensis	1.6	1
A7S1I9	Predicted protein OS=Nematostella vectensis	11.8	2
A7S214	Predicted protein OS=Nematostella vectensis	49.7	8
A7S260	Predicted protein OS=Nematostella vectensis	3.1	1
A7S378	Isocitrate dehydrogenase [NADP] OS=Nematostella vectensis	3.4	1
A7S392	Predicted protein OS=Nematostella vectensis	1.5	1
A7S405	60S ribosomal protein L13 OS=Nematostella vectensis	4.7	1
A7S469	Predicted protein OS=Nematostella vectensis	6.9	1
A7S4X0	Predicted protein OS=Nematostella vectensis	4.6	4
A7S4Z2	Predicted protein (Fragment) OS=Nematostella vectensis	5.1	1
A7S5Z0	Predicted protein OS=Nematostella vectensis	6.9	2
A7S616	Predicted protein OS=Nematostella vectensis	39.4	5
A7S690	Predicted protein (Fragment) OS=Nematostella vectensis	20.4	2
A7S6N2	Predicted protein (Fragment) OS=Nematostella vectensis	2.8	1
A7S7K4	Predicted protein OS=Nematostella vectensis	7.9	2
A7SAK1	Predicted protein OS=Nematostella vectensis	3.2	1
A7SC77	Predicted protein OS=Nematostella vectensis	18.7	4
A7SCJ3	Succinate dehydrogenase (quinone) (Fragment) OS=Nematostella vectensis	6.7	2
A7SDY3	Tubulin alpha chain OS=Nematostella vectensis	44.3	16
A7SEB1	Predicted protein OS=Nematostella vectensis	60.5	18
A7SFJ3	Predicted protein OS=Nematostella vectensis	9	3
A7SG05	GTP-binding nuclear protein OS=Nematostella vectensis	20.7	4

A7TCF2	Peptidyl-prolyl cis-trans isomerase (Fragment) OS=Nematostella vectensis	26.4	1
A7SG62	Predicted protein OS=Nematostella vectensis	7.3	1
A7SHC0	Predicted protein (Fragment) OS=Nematostella vectensis	2.2	3
A7SJL4	Predicted protein OS=Nematostella vectensis	3.4	2
Q8WRT4	Beta-catenin (Fragment) OS=Nematostella vectensis	6.1	2
A7SMS0	Coatomer subunit beta OS=Nematostella vectensis	4.4	3
A7T514	Predicted protein OS=Nematostella vectensis	2.6	1
A7SPM9	Predicted protein (Fragment) OS=Nematostella vectensis	2.3	1
A7SPQ4	Predicted protein OS=Nematostella vectensis	15.8	2
A7SPW3	Predicted protein (Fragment) OS=Nematostella vectensis	7.4	1
A7SQ60	Predicted protein OS=Nematostella vectensis	6.6	2
A7SQV3	Proteasome subunit beta OS=Nematostella vectensis	9.7	2
A7SSL5	Predicted protein OS=Nematostella vectensis	4.6	3
A7T5Y2	Predicted protein OS=Nematostella vectensis	5.5	1
A7SX44	Predicted protein (Fragment) OS=Nematostella vectensis	4.3	1
A7SX99	Predicted protein OS=Nematostella vectensis	13.6	1
A7SZN8	Predicted protein OS=Nematostella vectensis	3.1	1
A7T0Q5	Predicted protein OS=Nematostella vectensis	4.1	1
A7T3D9	Predicted protein OS=Nematostella vectensis	2.9	1
A7T409	Predicted protein OS=Nematostella vectensis	5.8	1
A7T4C2	Predicted protein (Fragment) OS=Nematostella vectensis	76.7	7
A7TBN5	Predicted protein (Fragment) OS=Nematostella vectensis	8.5	1
A7TCL7	Histone H2A OS=Nematostella vectensis	37.2	11
A8DRV3	Vacuolar ATP synthase subunit B (Fragment) OS=Urticina eques	20.7	2
A8DVF1	Predicted protein (Fragment) OS=Nematostella vectensis	4.6	1
B2KTD5	Dickkopf protein 3 OS=Clytia hemisphaerica	7.9	1
C0JP85	Ribosomal protein S2 (Fragment) OS=Carybdea marsupialis	14.7	1
C1IS27	Clathrin heavy chain (Fragment) OS=Carukia barnesi	23.5	3
C1IS28	Clathrin heavy chain (Fragment) OS=Carukia barnesi	43.5	8
D1FX76	Thypedin (Fragment) OS=Chironex fleckeri	5.1	2
I2G9E9	Myosin II heavy chain, smooth/non-muscle-type (Fragment) OS=Clytia hemisphaerica	10.6	3
I6ZY10	Elongation factor 2 (Fragment) OS=Myxidium coryphaenoideum	9.7	2
K0A063	Beta-actin (Fragment) OS=Chrysaora quinquecirrha	69	19
M1E2A8	Calmodulin (Fragment) OS=Rhizostoma octopus	45.6	4
O76969	Ribosomal protein L9 (Fragment) OS=Podocoryna carnea	6	1
Q0H8V3	Heat shock protein 70 (Fragment) OS=Cnidaria environmental sample	12.2	2
Q56GW1	60S ribosomal protein L12 (Fragment) OS=Hydractinia echinata	16.5	1
Q56GW5	40S ribosomal protein S4 (Fragment) OS=Hydractinia echinata	14.3	1
Q5EN86	S-adenosylhomocysteine hydrolase (Fragment) OS=Aurelia aurita	19.3	2
Q5EN87	Putative tyrosine-rich heat shock protein (Fragment) OS=Aurelia aurita	5.8	1
Q5EN91	Putative 3-hydroxyacyl-Coenzyme A dehydrogenase (Fragment) OS=Aurelia aurita	19.4	3
Q5EN93	Heat shock protein Hsp70 (Fragment) OS=Aurelia aurita	6.5	2
Q5WR13	Non-muscle actin (Fragment) OS=Hydra viridissima	62.2	9

Q6PTK3	Triosephosphate isomerase (Fragment) OS=Obelia sp. KJP-2004	13.3	2
Q6YCH0	Ribosomal protein S3 (Fragment) OS=Hydra vulgaris	24.4	5
Q7YZI4	90-kDa heat-shock protein (Fragment) OS=Aurelia aurita	12.6	4
Q7YZJ5	Elongation factor 2 (Fragment) OS=Aurelia aurita	10.3	1
Q7YZK4	Tubulin beta chain (Fragment) OS=Aurelia aurita	64.3	23
Q8MUA5	Protein kinase B OS=Hydra vulgaris	2.8	1
Q9NFW1	60S ribosomal protein L12 OS=Hydra vulgaris	9.7	1
R9S2H2	Uncharacterized protein (Fragment) OS=Aurelia aurita	0.5	1
R9S2M2	Elongation factor 1-alpha OS=Aurelia aurita	8.8	4
T2M3F8	Aspartyl aminopeptidase OS=Hydra vulgaris	2.6	1
T2M3I7	RuvB-like helicase OS=Hydra vulgaris	6.6	2
T2M486	Vacuolar protein sorting-associated protein 29 OS=Hydra vulgaris	12.6	1
T2M492	Dynein heavy chain 9, axonemal (Fragment) OS=Hydra vulgaris	0.3	1
T2M4E1	Beta-ureidopropionase (Fragment) OS=Hydra vulgaris	2.6	1
T2M4N6	Guanine nucleotide-binding protein subunit beta-4 (Fragment) OS=Hydra vulgaris	17.3	5
T2M559	Probable cysteinyl-tRNA synthetase, mitochondrial (Fragment) OS=Hydra vulgaris	2	1
T2M5B3	Phospholipid-transporting ATPase (Fragment) OS=Hydra vulgaris	5.8	3
T2M5D3	Protein transport protein Sec61 subunit alpha isoform 2 OS=Hydra vulgaris	8.4	3
T2M5K6	Transmembrane 9 superfamily member OS=Hydra vulgaris	1.7	1
T2M5M6	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (Fragment) OS=Hydra vulgaris	1.9	1
T2M644	Microtubule-associated proteins 1A/1B light chain 3C OS=Hydra vulgaris	26.4	2
T2M6Q7	Transmembrane emp24 domain-containing protein 9 OS=Hydra vulgaris	9.3	2
T2M6Z7	26S proteasome non-ATPase regulatory subunit 1 (Fragment) OS=Hydra vulgaris	1.5	1
T2M7H4	Transcription factor BTF3 OS=Hydra vulgaris	8.9	1
T2M7J1	Vacuolar protein sorting-associated protein 35 (Fragment) OS=Hydra vulgaris	8.4	5
T2M7M5	Ubiquitin thioesterase OS=Hydra vulgaris	5.3	1
T2M7N8	Ras-related protein Rab-8B OS=Hydra vulgaris	17.4	3
T2M7R2	Protein TFG OS=Hydra vulgaris	4.9	1
T2M870	AP-2 complex subunit mu (Fragment) OS=Hydra vulgaris	3.2	1
T2M8F7	Actin-related protein 2/3 complex subunit 1A (Fragment) OS=Hydra vulgaris	3.8	1
T2M8N4	Glutaryl-CoA dehydrogenase, mitochondrial OS=Hydra vulgaris	3.7	1
T2M9A6	SH3 domain-containing RING finger protein 3 OS=Hydra vulgaris	1.7	1
T2M9D4	Prostaglandin reductase 2 (Fragment) OS=Hydra vulgaris	6.8	1
T2M9Q3	Sorting nexin OS=Hydra vulgaris	3.5	1
T2MCX5	Vacuolar protein sorting-associated protein 26B (Fragment) OS=Hydra vulgaris	7.4	2
T2MD34	Serine/threonine protein phosphatase 2A regulatory subunit OS=Hydra vulgaris	2.8	1
T2MD44	Major vault protein OS=Hydra vulgaris	5.6	7
T2MDB0	Eukaryotic initiation factor 4A-II OS=Hydra vulgaris	5.4	2
T2MDG4	Flotillin-2 OS=Hydra vulgaris	6	3
T2MDI5	Septin-6 (Fragment) OS=Hydra vulgaris	5.8	2
T2MDK8	Spliceosome RNA helicase DDX39B OS=Hydra vulgaris	7.6	3
T2MDT0	Cytoplasmic dynein 1 heavy chain 1 OS=Hydra vulgaris	1	3
T2ME03	Quinone oxidoreductase OS=Hydra vulgaris	3.7	1

T2ME25	Guanine nucleotide-binding protein G(I) subunit alpha-1 OS=Hydra vulgaris	9	3
T2ME63	2-oxoglutarate dehydrogenase,mitochondrial OS=Hydra vulgaris	1.4	1
T2ME64	Disks large homolog 1 OS=Hydra vulgaris	1.5	1
T2ME66	Ras-related protein Rab-11A OS=Hydra vulgaris	20.2	4
T2MEA3	Myosin-1e (Fragment) OS=Hydra vulgaris	1.6	1
T2MEB5	ADP-ribosylation factor 1 OS=Hydra vulgaris	49.7	7
T2MEH3	Casein kinase II subunit alpha OS=Hydra vulgaris	10.6	3
T2MEH6	Dynein light chain Tctex-type 1 OS=Hydra vulgaris	30.1	2
T2MEI1	AP-2 complex subunit beta (Fragment) OS=Hydra vulgaris	7.2	5
T2MEJ9	Eukaryotic translation initiation factor 6 (Fragment) OS=Hydra vulgaris	7.2	1
T2MEK4	60S ribosomal protein L8 OS=Hydra vulgaris	5.4	2
T2MEK8	Ras-related protein Rab-1A OS=Hydra vulgaris	39.6	5
T2MEL5	40S ribosomal protein S28 OS=Hydra vulgaris	17.9	1
T2MEN5	Clathrin heavy chain OS=Hydra vulgaris	8.6	10
T2MEP2	40S ribosomal protein S18 OS=Hydra vulgaris	7.1	1
T2MEP4	Small nuclear ribonucleoprotein Sm D1 (Fragment) OS=Hydra vulgaris	7.7	1
T2MEQ7	26S protease regulatory subunit 4 OS=Hydra vulgaris	6.1	2
T2MEV1	Tubulin beta chain (Fragment) OS=Hydra vulgaris	31.8	15
T2MEW2	Actin-related protein 3 OS=Hydra vulgaris	15.1	3
T2MEY1	60S ribosomal protein L11 (Fragment) OS=Hydra vulgaris	7.2	1
T2MEY5	Actin-related protein 2/3 complex subunit 4 OS=Hydra vulgaris	11.9	3
T2MF30	40S ribosomal protein S13 (Fragment) OS=Hydra vulgaris	19.5	4
T2MF54	60S ribosomal protein L7a (Fragment) OS=Hydra vulgaris	4.4	1
T2MF93	Ras-related protein Rab-14 (Fragment) OS=Hydra vulgaris	28.4	4
T2MFE1	Actin-related protein 2 OS=Hydra vulgaris	4.8	2
T2MFG0	Transmembrane emp24 domain-containing protein 10 (Fragment) OS=Hydra vulgaris	11.5	4
T2MFH7	Poly(RC)-binding protein 3 (Fragment) OS=Hydra vulgaris	4.1	1
T2MFJ8	Protein transport protein Sec24C OS=Hydra vulgaris	1.3	1
T2MFM1	Transitional endoplasmic reticulum ATPase (Fragment) OS=Hydra vulgaris	10.4	5
T2MFM6	Ribonuclease UK114 OS=Hydra vulgaris	7.4	1
T2MFQ3	Coatamer subunit beta (Fragment) OS=Hydra vulgaris	3.1	3
T2MFR8	Ras-related protein Rab-7a OS=Hydra vulgaris	34	8
T2MFU6	26S proteasome non-ATPase regulatory subunit 7 OS=Hydra vulgaris	5.2	1
T2MFY6	Hippocalcin-like protein 1 OS=Hydra vulgaris	27.2	4
T2MFZ7	Erythrocyte band 7 integral membrane protein OS=Hydra vulgaris	8.6	2
T2MFZ8	V-type proton ATPase catalytic subunit A OS=Hydra vulgaris	7.1	2
T2MG07	Proteasome subunit alpha type OS=Hydra vulgaris	14.5	2
T2MG36	Myosin-10 OS=Hydra vulgaris	3.3	6
T2MG37	Glycine cleavage system P protein OS=Hydra vulgaris	1.7	1
T2MG47	Radixin OS=Hydra vulgaris	6.3	3
T2MG58	Multidrug resistance-associated protein 1 (Fragment) OS=Hydra vulgaris	1.2	1
T2MG74	Serine hydroxymethyltransferase,mitochondrial OS=Hydra vulgaris	2.2	1
T2MG86	Vesicle-fusing ATPase OS=Hydra vulgaris	1.6	1

T2MGF1	Pyruvate kinase OS=Hydra vulgaris	1.9	1
T2MGF7	Malate dehydrogenase,mitochondrial OS=Hydra vulgaris	3.5	1
T2MGG5	Proteasome subunit alpha type OS=Hydra vulgaris	6.1	1
T2MGG7	ADP-ribosylation factor-like protein 3 OS=Hydra vulgaris	6.1	1
T2MGH4	Proteasome subunit alpha type OS=Hydra vulgaris	3.6	1
T2MGI7	ADP/ATP translocase 3 (Fragment) OS=Hydra vulgaris	7	3
T2MGJ0	Polyadenylate-binding protein OS=Hydra vulgaris	2.7	1
T2MGL9	40S ribosomal protein S17-like OS=Hydra vulgaris	7.5	1
T2MGQ4	ER lumen protein retaining receptor 2 OS=Hydra vulgaris	12.6	2
T2MGR5	60S ribosomal protein L7 (Fragment) OS=Hydra vulgaris	3.4	1
T2MGS3	cAMP-dependent protein kinase catalytic subunit alpha OS=Hydra vulgaris	8.3	2
T2MGX7	60S ribosomal protein L13 (Fragment) OS=Hydra vulgaris	4.7	1
T2MGY7	40S ribosomal protein S12 OS=Hydra vulgaris	10.2	1
T2MGZ6	ATP synthase subunit alpha OS=Hydra vulgaris	13	6
T2MH20	Glutamate dehydrogenase OS=Hydra vulgaris	5.7	3
T2MH23	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial (Fragment) OS=Hydra vulgaris	2.5	1
T2MH41	78 kDa glucose-regulated protein OS=Hydra vulgaris	11.4	6
T2MH44	Vacuolar proton pump subunit B (Fragment) OS=Hydra vulgaris	10.2	3
T2MH46	Filamin-A OS=Hydra vulgaris	0.9	2
T2MHA3	Histone H1.0 OS=Hydra vulgaris	5.2	1
T2MHF1	Elongation factor 2 OS=Hydra vulgaris	3.4	2
T2MHI3	Flotillin-1 (Fragment) OS=Hydra vulgaris	6.3	2
T2MHI5	Alpha-actinin-1 OS=Hydra vulgaris	4.8	4
T2MHJ0	Non-specific serine/threonine protein kinase OS=Hydra vulgaris	5.8	2
T2MHN7	Citrate synthase OS=Hydra vulgaris	2.6	1
T2MHT5	Heat shock protein HSP 90-alpha OS=Hydra vulgaris	8.2	6
T2MHU7	Protein disulfide-isomerase OS=Hydra vulgaris	2.4	1
T2MHX4	Myosin-Id OS=Hydra vulgaris	1.2	1
T2MHY4	Argininosuccinate synthase (Fragment) OS=Hydra vulgaris	2.9	1
T2MI35	Splicing factor 3B subunit 1 (Fragment) OS=Hydra vulgaris	2.4	2
T2MI99	ATP-binding cassette sub-family B member 7, mitochondrial OS=Hydra vulgaris	1.7	1
T2MIB9	AP-2 complex subunit alpha OS=Hydra vulgaris	3.1	2
T2MIT4	Calpain-5 (Fragment) OS=Hydra vulgaris	1.6	1
T2MIU1	Nucleolar protein 56 (Fragment) OS=Hydra vulgaris	7.3	3
T2MIZ1	Arp2/3 complex 34 kDa subunit OS=Hydra vulgaris	3.7	1
T2MJJ5	Myosin regulatory light chain 12B OS=Hydra vulgaris	33.5	4
W8Q1J8	Glyceraldehyde-3-phosphate dehydrogenase OS=Cyanea capillata	10.1	2

2. In-solution digestion

2.1 Nematocyst extracted by 2% SDS couple with sonication and digested with trypsin enzyme

Table D-4. List of proteins identified (253 proteins) from nematocyst of edible jellyfish by using extraction of SDS coupled with sonication. The proteins were derived from in-solution digestion experiment. Database of taxonomy Cnidaria (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
E5F7D0	Non-muscle actin II OS=Hydractinia echinata	38.6	11
T2MGY6	Sodium/potassium-transporting ATPase subunit alpha OS=Hydra vulgaris	5.2	3
T2MGR0	60S ribosomal protein L17 OS=Hydra vulgaris	8.7	1
P38984	40S ribosomal protein SA OS=Hydra viridissima	4.1	1
P62184	Calmodulin OS=Renilla reniformis	65.8	6
B3EZK6	Ribosomal protein S5 (Fragment) OS=Cyanea capillata	5.3	1
B1PM92	Calmodulin OS=Acropora muricata	65.8	6
A0A069DMD7	Putative cnidarian restricted protein (Fragment) OS=Clytia hemisphaerica	6.8	1
B7T139	SUEL-type lectin domain-containing protein OS=Acropora millepora	3.4	1
A7TC67	Predicted protein (Fragment) OS=Nematostella vectensis	53.8	3
A0A1V0IGH5	Histone H2B OS=Hydra vulgaris	11.2	1
A0A0C2J3J1	60 kDa heat shock protein, mitochondrial OS=Thelohanellus kitauei	2.1	1
A0A0C2JBA7	40S ribosomal protein S23 OS=Thelohanellus kitauei	8.4	1
A0A0C2M3V7	V-type proton ATPase subunit B OS=Thelohanellus kitauei	10.2	2
C1IJE5	Smooth muscle myosin heavy chain 11 isoform-like protein (Fragment) OS=Myxobolus cerebralis	5.5	1
A0A0C2MQB3	Pol polyprotein OS=Thelohanellus kitauei	7.7	1
A0A0C2MSI4	NFATC2-interacting protein OS=Thelohanellus kitauei	8	1
A7RVW7	Predicted protein (Fragment) OS=Nematostella vectensis	6.2	1
A0A0C2N200	Ras-related protein RABA2a OS=Thelohanellus kitauei	5.3	1
A0A0C2N354	ATP synthase subunit beta OS=Thelohanellus kitauei	15.4	5
A0A0C2N9G6	Uncharacterized protein OS=Thelohanellus kitauei	1	1
A0A169Q0T5	Glyceraldehyde-3-phosphate dehydrogenase OS=Aurelia sp. SETO	6.8	2
T2MHP0	Histone H2A OS=Hydra vulgaris	30.2	2
A0A1B3IQX8	Histone H2A OS=Hydractinia echinata	32.1	3
A7RIE6	Predicted protein (Fragment) OS=Nematostella vectensis	14.7	1
A0A1L2A726	Superoxide dismutase [Cu-Zn] OS=Cyanea capillata	8.4	1
A0A1U9XQR0	Fructose-bisphosphate aldolase OS=Aurelia sp. 1 GW-2014	7.8	3
A0A224ASV7	Heat shock protein 90 OS=Acropora tenuis	4.5	3
A0A2B4R2I0	Fumarylacetoacetase (Fragment) OS=Stylophora pistillata	5.1	1
A0A2B4R8X2	Spliceosome RNA helicase Ddx39b OS=Stylophora pistillata	3	1
A0A2B4R9G5	Histone H2B OS=Stylophora pistillata	6.6	1
A0A2B4R9Q9	Histone H4 OS=Stylophora pistillata	39.6	13
A0A2B4R9T9	Chaperone protein DnaK OS=Stylophora pistillata	2.3	1
A7RQD8	Predicted protein OS=Nematostella vectensis	39.8	3
A0A2B4RB68	Transmembrane 9 superfamily member (Fragment) OS=Stylophora pistillata	7.6	1
A0A2B4RCT7	4-hydroxyphenylpyruvate dioxygenase OS=Stylophora pistillata	4.9	1
A0A2B4RD95	Collagen-like protein 4 OS=Stylophora pistillata	10.1	1

A0A2B4RE11	Putative cation efflux system protein SiIA OS=Stylophora pistillata	0.5	1
A7RU39	Predicted protein OS=Nematostella vectensis	7.1	1
A0A2B4REM0	Uncharacterized protein OS=Stylophora pistillata	2	1
A0A3M6UBM5	Uncharacterized protein OS=Pocillopora damicornis	0.8	1
A0A2B4RH47	Centlein OS=Stylophora pistillata	1.7	1
A0A2B4RHG2	V-type proton ATPase catalytic subunit A OS=Stylophora pistillata	8.1	3
A0A2B4RHH4	Heat shock protein 70 B2 OS=Stylophora pistillata	6	1
A0A2B4RIN1	Neurogenic locus notch-like protein 2 OS=Stylophora pistillata	3.4	1
A0A2B4RJ03	Actin-related protein 2/3 complex subunit 4 OS=Stylophora pistillata	5	1
A0A2B4RJH1	Tubulin beta chain OS=Stylophora pistillata	53.4	20
A0A2B4RKT3	26S proteasome non-ATPase regulatory subunit 2 OS=Stylophora pistillata	1.7	1
A7SH82	Predicted protein OS=Nematostella vectensis	5.9	1
A0A2B4RPA9	Clathrin heavy chain OS=Stylophora pistillata	6.2	7
I2G9E3	F-actin-capping protein subunit beta (Fragment) OS=Clytia hemisphaerica	5	1
A7RT97	Predicted protein OS=Nematostella vectensis	2.7	2
A0A2B4RQQ6	Eukaryotic initiation factor 4A-III OS=Stylophora pistillata	6.2	3
Q93116	Ub52 OS=Acropora millepora	36.4	4
A0A2B4RSY7	ADP-ribosylation factor 1 OS=Stylophora pistillata	8.3	1
A0A2B4RTB1	Tubulin alpha-1C chain OS=Stylophora pistillata	49.4	12
A0A2B4RTH4	Phosphoenolpyruvate carboxykinase, cytosolic [GTP] OS=Stylophora pistillata	2.2	1
A0A3M6U7L4	Thioredoxin domain-containing protein OS=Pocillopora damicornis	5.6	1
A0A3M6USJ4	GOLD domain-containing protein OS=Pocillopora damicornis	13.7	2
Q2F6G0	Prohibitin (Fragment) OS=Anthopleura elegantissima	10	1
A0A3M6UI41	Uncharacterized protein OS=Pocillopora damicornis	29.3	3
A0A2B4RW25	Pre-mRNA-processing-splicing factor 8 OS=Stylophora pistillata	0.9	1
A0A2B4RX45	Coiled-coil domain-containing protein 138 OS=Stylophora pistillata	1.9	1
T2M4N6	Guanine nucleotide-binding protein subunit beta-4 (Fragment) OS=Hydra vulgaris	3.3	1
A0A2B4S029	Aminopeptidase OS=Stylophora pistillata	2.7	1
L0AUB3	Alpha q G protein OS=Acropora palmata	3.1	1
A0A2B4S1U8	Gamma-glutamyltranspeptidase 1 OS=Stylophora pistillata	3.4	1
T2MER0	40S ribosomal protein S14 OS=Hydra vulgaris	9.3	2
A0A2B4S250	Acyl-CoA synthetase family member 2, mitochondrial OS=Stylophora pistillata	2.4	1
Q6YCH0	Ribosomal protein S3 (Fragment) OS=Hydra vulgaris	18.5	4
A7RUL8	Predicted protein (Fragment) OS=Nematostella vectensis	3.1	1
A0A2B4S317	Phosphate carrier protein, mitochondrial OS=Stylophora pistillata	9.3	2
A0A3M6UYZ8	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	4.7	1
A0A2B4S3W2	Uncharacterized protein OS=Stylophora pistillata	1.4	1
A7SFJ3	Predicted protein OS=Nematostella vectensis	4.4	1
A0A3M6UK04	Uncharacterized protein OS=Pocillopora damicornis	1.2	3
A0A2B4S4R7	Proto-oncogene tyrosine-protein kinase receptor Ret OS=Stylophora pistillata	1.4	1
A0A3M6UGG9	Uncharacterized protein OS=Pocillopora damicornis	5.3	3
A0A2B4S643	Doublesex-and mab-3-related transcription factor A2 OS=Stylophora pistillata	3.3	1
A0A2B4S6Z1	AT-rich interactive domain-containing protein 4B OS=Stylophora pistillata	3	1

A7TBT4	Predicted protein (Fragment) OS=Nematostella vectensis	6.7	1
T2M644	Microtubule-associated proteins 1A/1B light chain 3C OS=Hydra vulgaris	13.6	1
A0A3M6TD98	Uncharacterized protein OS=Pocillopora damicornis	13.8	2
A0A2B4S9N3	CHY-type domain-containing protein OS=Stylophora pistillata	1.1	1
T2MEK8	Ras-related protein Rab-1A OS=Hydra vulgaris	16.8	3
A0A2B4SE68	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Stylophora pistillata	3	1
A0A2B4SGD6	Centrosome and spindle pole-associated protein 1 OS=Stylophora pistillata	1.1	1
A0A2B4SH58	Furin-1 OS=Stylophora pistillata	0.4	1
A7SJH7	Predicted protein OS=Nematostella vectensis	3.3	1
A7RVJ0	Serine/threonine-protein phosphatase OS=Nematostella vectensis	5.2	1
A0A3M6TKN8	Transaldolase OS=Pocillopora damicornis	3.7	1
A0A3M6TVL9	Uncharacterized protein OS=Pocillopora damicornis	1.9	1
A7SPP0	synthase subunit beta OS=Nematostella vectensis	30.3	9
A0A3M6TT70	V-type proton ATPase proteolipid subunit OS=Pocillopora damicornis	11.7	1
A7RV73	Vacuolar protein sorting-associated protein 29 OS=Nematostella vectensis	7.1	1
A7SHU3	Predicted protein OS=Nematostella vectensis	14.2	2
A0A3M6TRH7	Uncharacterized protein OS=Pocillopora damicornis	1.1	3
A0A3M6UD35	Coatomer subunit alpha OS=Pocillopora damicornis	1.6	2
A0A2B4SR94	NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Stylophora pistillata	2.9	1
A7SJK8	AP complex subunit beta OS=Nematostella vectensis	2	2
A0A3M6UDV1	WD_REPEATS_REGION domain-containing protein OS=Pocillopora damicornis	3.8	1
A0A2B4SS23	Protein transport protein Sec61 subunit alpha isoform 2 OS=Stylophora pistillata	9.6	4
A0A3M6V2N5	Adenosylhomocysteinase OS=Pocillopora damicornis	6.2	2
A0A2B4SUV2	Stress-70 protein, mitochondrial OS=Stylophora pistillata	2.4	1
A0A2B4SYS5	Sodium/potassium-transporting ATPase subunit alpha OS=Stylophora pistillata	4.3	2
A0A2B4SYV9	Small nuclear ribonucleoprotein Sm D1 OS=Stylophora pistillata	9.2	1
A0A3M6TZ50	Uncharacterized protein OS=Pocillopora damicornis	3.6	1
A0A2B4T1C4	ATP synthase subunit alpha OS=Stylophora pistillata	16.7	7
A7SBR9	Predicted protein OS=Nematostella vectensis	6.4	2
Q7YZL5	Tubulin alpha chain (Fragment) OS=Aurelia aurita	47.7	12
A0A2Z5WH73	Myosin heavy chain OS=Aurelia sp. 2017-HT	10.8	19
A0A2Z5WH78	Ser-Thr kinase OS=Aurelia sp. 2017-HT	2.3	1
A0A2Z5WH82	Tropomyosin-1 OS=Aurelia sp. 2017-HT	13.2	2
A0A3M6T8X3	Calcium-transporting ATPase OS=Pocillopora damicornis	3.7	2
A0A3M6T968	Uncharacterized protein OS=Pocillopora damicornis	12.4	1
A0A3M6TAP5	DWNN domain-containing protein OS=Pocillopora damicornis	1.4	1
A0A3M6TEN5	Uncharacterized protein OS=Pocillopora damicornis	2.3	1
A7SXV0	Predicted protein OS=Nematostella vectensis	3	1
A0A3M6TG79	Histone H4 (Fragment) OS=Pocillopora damicornis	55.4	7
A0A3M6TK27	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	1.6	1
A7SQ60	Predicted protein OS=Nematostella vectensis	6.4	2
A0A3M6TLH9	Uncharacterized protein OS=Pocillopora damicornis	7.7	2
A0A3M6TMX1	Receptor expression-enhancing protein OS=Pocillopora damicornis	7.9	1

T2MJT0	26S proteasome non-ATPase regulatory subunit 14 OS=Hydra vulgaris	12.6	2
A0A3M6TYE7	Uncharacterized protein OS=Pocillopora damicornis	6.2	1
A0A3M6U454	Histone H2A OS=Pocillopora damicornis	17.4	2
A0A3M6U653	Uncharacterized protein OS=Pocillopora damicornis	0.7	1
A0A3M6U8F9	PHB domain-containing protein OS=Pocillopora damicornis	2.9	1
A0A3M6UGM1	V-type proton ATPase subunit a OS=Pocillopora damicornis	4.4	1
A0A3M6UH20	Uncharacterized protein OS=Pocillopora damicornis	0.9	1
A0A3M6UHG1	Uncharacterized protein OS=Pocillopora damicornis	1.9	1
A0A3M6UP81	Uncharacterized protein OS=Pocillopora damicornis	34.6	8
A7RL80	Predicted protein OS=Nematostella vectensis	6.9	1
A7T6G0	Annexin OS=Nematostella vectensis	5.5	2
A0A3M6UZ82	PCI domain-containing protein OS=Pocillopora damicornis	3	1
A0A3M6V6C8	Uncharacterized protein OS=Pocillopora damicornis	5.3	1
G9IT81	Cytochrome c oxidase subunit 2 OS=Rhizostoma pulmo	13.3	2
A0S5U2	Heat shock protein 70 OS=Hydra vulgaris	4	2
A0S5V5	EF-hand domain-containing protein OS=Hydra vulgaris	7.5	1
A7REV0	Anoctamin (Fragment) OS=Nematostella vectensis	1.6	1
T2M6S6	Coiled-coil domain-containing protein 94 OS=Hydra vulgaris	2.9	1
A7RGP5	Signal recognition particle 54 kDa protein OS=Nematostella vectensis	2.2	1
A7RH22	Predicted protein OS=Nematostella vectensis	1.7	1
A7RHF7	Eukaryotic translation initiation factor 6 OS=Nematostella vectensis	10.2	1
A7RJL4	Histone H2A OS=Nematostella vectensis	48.4	3
A7RL77	Coatomer subunit beta OS=Nematostella vectensis	1	1
A7RPX5	Histone H2A (Fragment) OS=Nematostella vectensis	25	2
A7RRG9	Predicted protein OS=Nematostella vectensis	14.9	1
A7T836	Predicted protein (Fragment) OS=Nematostella vectensis	3.3	2
A7RU78	Predicted protein OS=Nematostella vectensis	8.9	1
A7RUX0	Tubulin alpha chain OS=Nematostella vectensis	24.5	7
A7RVD9	Tubulin alpha chain OS=Nematostella vectensis	33.3	10
A7S3I0	Predicted protein (Fragment) OS=Nematostella vectensis	4.4	3
A7S3K4	Predicted protein OS=Nematostella vectensis	3.5	1
A7S428	Predicted protein OS=Nematostella vectensis	2.7	1
Q6PTK3	Triosephosphate isomerase (Fragment) OS=Obelia sp. KJP-2004	7.1	1
A7S4X0	Predicted protein OS=Nematostella vectensis	2.5	2
A7S5Z0	Predicted protein OS=Nematostella vectensis	9.9	3
A7S690	Predicted protein (Fragment) OS=Nematostella vectensis	20.4	2
Q7YZL6	Tubulin alpha chain (Fragment) OS=Nematostella vectensis	27.1	8
T2M3I7	RuvB-like helicase OS=Hydra vulgaris	3.1	1
A7S7H8	Predicted protein OS=Nematostella vectensis	1	1
A7S7K4	Predicted protein OS=Nematostella vectensis	7.9	2
A7SFM4	Predicted protein (Fragment) OS=Nematostella vectensis	2.4	1
A7SG05	GTP-binding nuclear protein OS=Nematostella vectensis	10.1	2
A7SG62	Predicted protein OS=Nematostella vectensis	7.3	1
A7SJL4	Predicted protein OS=Nematostella vectensis	3.4	2

A7SMN3	Predicted protein OS=Nematostella vectensis	3.9	1
A7SMZ7	Dynein light chain roadblock OS=Nematostella vectensis	12.5	1
A7SN59	Predicted protein OS=Nematostella vectensis	1.1	1
A7SPN7	Glycerol-3-phosphate dehydrogenase OS=Nematostella vectensis	1.9	1
A7SPQ4	Predicted protein OS=Nematostella vectensis	16.5	3
A7SQP1	Predicted protein OS=Nematostella vectensis	12.6	2
A7SRK8	Adenosylhomocysteinase OS=Nematostella vectensis	5.8	2
A7SRV8	40S ribosomal protein S4 OS=Nematostella vectensis	3.8	1
A7SWR9	Predicted protein OS=Nematostella vectensis	8.6	2
A7SX99	Predicted protein OS=Nematostella vectensis	13.6	1
A7T1L2	Histone H2B OS=Nematostella vectensis	15.6	1
A7TCL7	Histone H2A OS=Nematostella vectensis	41.7	12
A8DV31	Histone H4 (Fragment) OS=Nematostella vectensis	68.7	7
B2KTD5	Dickkopf protein 3 OS=Clytia hemisphaerica	7.9	1
C0JP85	Ribosomal protein S2 (Fragment) OS=Carybdea marsupialis	24.1	2
C1IS27	Clathrin heavy chain (Fragment) OS=Carukia barnesi	16.4	2
C1IS28	Clathrin heavy chain (Fragment) OS=Carukia barnesi	30.9	7
E9A111	Ribosomal protein S6 kinase OS=Hydra vulgaris	1.3	1
I2G9E9	Myosin II heavy chain, smooth/non-muscle-type (Fragment) OS=Clytia hemisphaerica	6.5	3
I6ZY10	Elongation factor 2 (Fragment) OS=Myxidium coryphaenoideum	6	1
M1E2A8	Calmodulin (Fragment) OS=Rhizostoma octopus	45.6	4
M1H3W2	Putative late embryogenesis protein (Fragment) OS=Stylophora pistillata	3.7	1
M1T236	Putative flagellar-associated protein (Fragment) OS=Stylophora pistillata	1.5	1
Q56GW1	60S ribosomal protein L12 (Fragment) OS=Hydractinia echinata	16.5	1
Q56GW5	40S ribosomal protein S4 (Fragment) OS=Hydractinia echinata	14.3	1
Q5EN86	S-adenosylhomocysteine hydrolase (Fragment) OS=Aurelia aurita	14.9	1
Q5EN87	Putative tyrosine-rich heat shock protein (Fragment) OS=Aurelia aurita	5.8	1
Q5FB16	Ubiquitin-ribosomal protein CEP52 fusion protein (Fragment) OS=Pocillopora damicornis	46	4
Q5XPR4	NaK-ATPase alpha subunit (Fragment) OS=Hydractinia echinata	6.6	1
Q6B4R5	Elongation factor 1-alpha OS=Scleronephthya gracillimum	4.8	2
Q6RFF9	Mitochondrial 60 kDa heat shock protein OS=Anemonia viridis	1.9	1
Q7YZ14	90-kDa heat-shock protein (Fragment) OS=Aurelia aurita	8.9	2
Q7YZJ5	Elongation factor 2 (Fragment) OS=Aurelia aurita	15.5	3
Q9NFW1	60S ribosomal protein L12 OS=Hydra vulgaris	9.7	1
R9S2H2	Uncharacterized protein (Fragment) OS=Aurelia aurita	0.5	1
R9S2M2	Elongation factor 1-alpha OS=Aurelia aurita	4.8	2
T2M2P5	RuvB-like helicase OS=Hydra vulgaris	6.1	2
T2M338	Stomatin-like protein 2 OS=Hydra vulgaris	3	1
T2M3N8	Septin-9 OS=Hydra vulgaris	2.2	1
T2M4N0	Ras-related GTP-binding protein C OS=Hydra vulgaris	3.7	1
T2M5D3	Protein transport protein Sec61 subunit alpha isoform 2 OS=Hydra vulgaris	7.6	2
T2M6L6	T-complex protein 1 subunit eta OS=Hydra vulgaris	4.9	2
T2M6Q7	Transmembrane emp24 domain-containing protein 9 OS=Hydra vulgaris	9.3	2

T2M8N1	Transportin-1 OS=Hydra vulgaris	1.4	1
T2M9Q3	Sorting nexin OS=Hydra vulgaris	3.5	1
T2MAR5	E3 ubiquitin-protein ligase RBBP6 OS=Hydra vulgaris	1.3	1
T2MD09	Splicing factor 3B subunit 3 OS=Hydra vulgaris	1.1	1
T2MD44	Major vault protein OS=Hydra vulgaris	2.7	3
T2MDB0	Eukaryotic initiation factor 4A-II OS=Hydra vulgaris	5.9	2
T2MEB5	ADP-ribosylation factor 1 OS=Hydra vulgaris	8.3	1
T2MEJ9	Eukaryotic translation initiation factor 6 (Fragment) OS=Hydra vulgaris	7.2	1
T2MEL5	40S ribosomal protein S28 OS=Hydra vulgaris	17.9	1
T2MEP2	40S ribosomal protein S18 OS=Hydra vulgaris	12.9	2
T2MEW9	Calcineurin subunit B type 1 OS=Hydra vulgaris	6.5	1
T2MEY1	60S ribosomal protein L11 (Fragment) OS=Hydra vulgaris	7.2	1
T2MEY3	T-complex protein 1 subunit beta (Fragment) OS=Hydra vulgaris	3.8	2
T2MF54	60S ribosomal protein L7a (Fragment) OS=Hydra vulgaris	8.2	2
T2MF60	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Hydra vulgaris	4.8	1
T2MFG0	Transmembrane emp24 domain-containing protein 10 (Fragment) OS=Hydra vulgaris	6.2	2
T2MFK0	Isocitrate dehydrogenase [NADP],mitochondrial (Fragment) OS=Hydra vulgaris	3.6	1
T2MFM1	Transitional endoplasmic reticulum ATPase (Fragment) OS=Hydra vulgaris	3.6	2
T2MFP2	40S ribosomal protein S9 OS=Hydra vulgaris	8.4	2
T2MFQ3	Coatomer subunit beta (Fragment) OS=Hydra vulgaris	1	1
T2MFY6	Hippocalcin-like protein 1 OS=Hydra vulgaris	7.3	1
T2MFZ7	Erythrocyte band 7 integral membrane protein OS=Hydra vulgaris	4.3	1
T2MG36	Myosin-10 OS=Hydra vulgaris	1.1	3
T2MG86	Vesicle-fusing ATPase OS=Hydra vulgaris	1.6	1
T2MGG7	ADP-ribosylation factor-like protein 3 OS=Hydra vulgaris	6.1	1
T2MGR5	60S ribosomal protein L7 (Fragment) OS=Hydra vulgaris	3.4	1
T2MGW5	Endoplasmic reticulum chaperone protein OS=Hydra vulgaris	2.7	3
T2MGX7	60S ribosomal protein L13 (Fragment) OS=Hydra vulgaris	8.1	2
T2MGZ6	ATP synthase subunit alpha OS=Hydra vulgaris	7.3	4
T2MH23	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial (Fragment) OS=Hydra vulgaris	2.5	1
T2MH41	78 kDa glucose-regulated protein OS=Hydra vulgaris	6	3
T2MH46	Filamin-A OS=Hydra vulgaris	0.6	1
T2MHH5	Myosin-6 OS=Hydra vulgaris	1.7	4
T2MHI3	Flotillin-1 (Fragment) OS=Hydra vulgaris	6.3	2
T2MHJ7	60 kDa heat shock protein,mitochondrial (Fragment) OS=Hydra vulgaris	2	1
T2MHT5	Heat shock protein HSP 90-alpha OS=Hydra vulgaris	3.3	3
T2MHT8	60S acidic ribosomal protein P0 OS=Hydra vulgaris	4.1	1
T2MHY4	Argininosuccinate synthase (Fragment) OS=Hydra vulgaris	2.9	1
T2MIB9	AP-2 complex subunit alpha OS=Hydra vulgaris	1.2	1
T2MIV7	Endothelial differentiation-related factor 1 OS=Hydra vulgaris	10.1	1
T2MJ45	Calpain-9 (Fragment) OS=Hydra vulgaris	2	1
T2MJJ5	Myosin regulatory light chain 12B OS=Hydra vulgaris	22.9	3
W8Q1J8	Glyceraldehyde-3-phosphate dehydrogenase OS=Cyanea capillata	9.6	2

2.2 Nematocyst extracted by PBS buffer couple with ultrasonication and digested with trypsin enzyme

Table D-5. List of proteins identified (158 proteins) from nematocyst of edible jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were derived from in-solution digestion experiment. Database of taxonomy Cnidaria (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
E5F7D0	Non-muscle actin II OS=Hydractinia echinata	44.7	14
A8DV16	Predicted protein (Fragment) OS=Nematostella vectensis	20.3	1
T2MGR0	60S ribosomal protein L17 OS=Hydra vulgaris	8.7	1
B1PM92	Calmodulin OS=Acropora muricata	30.2	3
A0A069DLY1	VEGF related ligand OS=Clytia hemisphaerica	3.4	1
A0A0C2I691	Translation initiation factor IF-2 OS=Thelohanellus kitauei	6.3	1
A0A0C2IQJ8	Uncharacterized protein OS=Thelohanellus kitauei	14.2	1
A0A1V0IGH5	Histone H2B OS=Hydra vulgaris	11.2	1
A0A0C2IV52	Translation initiation factor IF-2 OS=Thelohanellus kitauei	15	1
A0A0C2J3J1	60 kDa heat shock protein, mitochondrial OS=Thelohanellus kitauei	2.1	1
A0A0C2JL79	60S acidic ribosomal protein P0 OS=Thelohanellus kitauei	4.9	1
A0A0C2MG61	Uncharacterized protein OS=Thelohanellus kitauei	9.4	1
A0A0C2MJF1	Peroxiredoxin-1 OS=Thelohanellus kitauei	5	1
A0A0C2MJV4	Putative isomerase YbhH OS=Thelohanellus kitauei	4.1	1
A0A0C2MUS2	60 kDa chaperonin OS=Thelohanellus kitauei	5.7	1
A0A0C2N354	ATP synthase subunit beta OS=Thelohanellus kitauei	9.9	4
A0A0C2N4C2	Glucose-6-phosphate 1-dehydrogenase OS=Thelohanellus kitauei	16.6	1
A0A0C2N4T5	ATP synthase subunit alpha OS=Thelohanellus kitauei	6.1	3
A0A0C2N9G6	Uncharacterized protein OS=Thelohanellus kitauei	1.5	2
A0A0C2NH50	Uncharacterized protein OS=Thelohanellus kitauei	9	1
A0A169Q0T5	Glyceraldehyde-3-phosphate dehydrogenase OS=Aurelia sp. SETO	4.5	1
A0A181ZLG6	Tubulin alpha chain (Fragment) OS=Sinularia cf. cruciata GS-2016	11.6	3
A0A1U9XQR0	Fructose-bisphosphate aldolase OS=Aurelia sp. 1 GW-2014	3.9	1
A2T3F8	Cytochrome c oxidase subunit 2 OS=Savalia savaglia	4.4	1
Q7YZI5	90-kDa heat-shock protein (Fragment) OS=Nematostella vectensis	4.2	2
A0A2B4R364	GTP-binding protein TypA/BipA-like OS=Stylophora pistillata	3	1
A0A3M6TUD1	NACHT domain-containing protein (Fragment) OS=Pocillopora damicornis	2.1	1
A0A2B4R4N1	Chaperone protein ClpB (Fragment) OS=Stylophora pistillata	1.6	1
A0A2B4R884	Uncharacterized protein YqaJ OS=Stylophora pistillata	3.9	1
A7RQD8	Predicted protein OS=Nematostella vectensis	16.1	1
A0A2B4RBC2	NFX1-type zinc finger-containing protein 1 OS=Stylophora pistillata	0.8	2
A0A2B4RBT6	Putative serine/threonine-protein kinase roco5 OS=Stylophora pistillata	0.7	1
A0A2B4RF06	Myosin-9 OS=Stylophora pistillata	0.4	1

A0A2B4RF66	Peroxiredoxin OS=Stylophora pistillata	12.1	1
A0A3M6UBM5	Uncharacterized protein OS=Pocillopora damicornis	0.8	1
A0A2B4RHH5	Enoyl-CoA hydratase, mitochondrial OS=Stylophora pistillata	6	1
A0A3M6TI71	Glutamate dehydrogenase OS=Pocillopora damicornis	2.3	1
M1SUP7	Tubulin beta chain (Fragment) OS=Stylophora pistillata	27.5	7
A0A3M6TIL0	Uncharacterized protein OS=Pocillopora damicornis	6.5	1
A0A2B4RNS7	Uncharacterized protein OS=Stylophora pistillata	5.1	1
A0A2B4RNY4	Neurabin-1 OS=Stylophora pistillata	1.3	1
C1IS27	Clathrin heavy chain (Fragment) OS=Carukia barnesi	7.5	1
A7RT97	Predicted protein OS=Nematostella vectensis	1.7	1
A0A2B4RQY2	Ubiquitin-conjugating enzyme E2 L3 OS=Stylophora pistillata	9.7	1
A0A2B4RS60	Guanidinobutyrase OS=Stylophora pistillata	7.6	1
A0A2B4RSY7	ADP-ribosylation factor 1 OS=Stylophora pistillata	8.3	1
A0A3M6TB89	Uncharacterized protein OS=Pocillopora damicornis	0.2	1
A0A2B4RTB1	Tubulin alpha-1C chain OS=Stylophora pistillata	12.4	4
A0A2B4SVG2	EGF-like domain-containing protein OS=Stylophora pistillata	5.8	1
A0A2B4RWB7	Uncharacterized protein OS=Stylophora pistillata	2.6	1
A0A2B4RX27	Acylamino-acid-releasing enzyme OS=Stylophora pistillata	1.5	1
A0A2B4RXA8	TNF receptor-associated factor 2 OS=Stylophora pistillata	2.4	1
A0A2B4RZG3	Putative G-protein coupled receptor 112 OS=Stylophora pistillata	1.9	1
A0A2B4S092	Multifunctional fusion protein OS=Stylophora pistillata	0.7	1
A0A2B4S0H6	Uncharacterized protein K02A2.6 OS=Stylophora pistillata	2.6	1
A0A2B4S1S9	Putative AAA domain-containing protein ycf46 OS=Stylophora pistillata	3.3	1
T2MERO	40S ribosomal protein S14 OS=Hydra vulgaris	8.6	1
A0A2B4S3H8	Leucine-rich repeat and calponin-likey domain-containing protein 1 OS=Stylophora pistillata	0.6	1
A0A3M6UK04	Uncharacterized protein OS=Pocillopora damicornis	0.4	1
A0A2B4S5E4	ADP-ribosylation factor 6 OS=Stylophora pistillata	8.6	1
A7SJ61	Predicted protein OS=Nematostella vectensis	1.5	1
A0A3M6TI13	10-formyltetrahydrofolate dehydrogenase OS=Pocillopora damicornis	1.2	1
A0A2B4S771	Fibropellin-1 OS=Stylophora pistillata	0.5	1
A0A2B4S9R9	Uncharacterized protein OS=Stylophora pistillata	1.4	1
A0A2B4SBD4	Orexin receptor type 2 OS=Stylophora pistillata	7.2	1
A0A2B4SCT3	EH domain-binding protein 1 OS=Stylophora pistillata	1.1	1
A0A2B4SE68	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Stylophora pistillata	3	1
A0A2B4SEX1	Uncharacterized protein OS=Stylophora pistillata	0.8	1
A0A2B4SGD6	Centrosome and spindle pole-associated protein 1 OS=Stylophora pistillata	1.1	1
A0A3M6TVL9	Uncharacterized protein OS=Pocillopora damicornis	2.1	1
A7SPP0	ATP synthase subunit beta OS=Nematostella vectensis	19	6
A0A2B4SMN6	G-protein coupled receptor GRL101 OS=Stylophora pistillata	6.3	1
A7SHU3	Predicted protein OS=Nematostella vectensis	6.6	1
A0A2B4SR94	NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Stylophora pistillata	2.9	1
A7RME1	Adenosylhomocysteinase OS=Nematostella vectensis	3.5	1
A0A2B4SUVO	60S ribosomal protein L13 OS=Stylophora pistillata	4.4	1

A7S2L5	Predicted protein OS=Nematostella vectensis	0.2	1
A0A2B4SYS5	Sodium/potassium-transporting ATPase subunit alpha OS=Stylophora pistillata	2.5	1
A0A2B4T333	Rotatin OS=Stylophora pistillata	1.4	1
A0A2Z5WH73	Myosin heavy chain OS=Aurelia sp. 2017-HT	1.3	2
A0A3M6T6Y2	OTU domain-containing protein OS=Pocillopora damicornis	3.3	1
A0A3M6TF63	Uncharacterized protein OS=Pocillopora damicornis	0.5	1
A0A3M6TIP1	Uncharacterized protein OS=Pocillopora damicornis	3.1	1
A0A3M6TJ99	Uncharacterized protein OS=Pocillopora damicornis	5.8	1
A0A3M6TJK2	Uncharacterized protein OS=Pocillopora damicornis	1.7	1
A0A3M6TK27	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	1.6	2
A0A3M6TSA1	Uncharacterized protein OS=Pocillopora damicornis	0.4	1
A0A3M6TYE7	Uncharacterized protein OS=Pocillopora damicornis	6.2	1
Q7YZJ5	Elongation factor 2 (Fragment) OS=Aurelia aurita	5.2	1
A0A3M6U1H0	Uncharacterized protein OS=Pocillopora damicornis	1.2	1
A0A3M6U1V1	Uncharacterized protein OS=Pocillopora damicornis	1.5	1
A7S690	Predicted protein (Fragment) OS=Nematostella vectensis	10.5	1
A0A3M6UGM1	V-type proton ATPase subunit a OS=Pocillopora damicornis	4.4	1
A0A3M6UHC4	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	0.6	1
A0A3M6UHG1	Uncharacterized protein OS=Pocillopora damicornis	1.9	1
A0A3M6UP81	Uncharacterized protein OS=Pocillopora damicornis	40.4	11
A7RT62	Predicted protein OS=Nematostella vectensis	5.4	1
A0A3M6UUD8	Uncharacterized protein OS=Pocillopora damicornis	0.4	1
A0A3M6UYC1	cGMP-dependent protein kinase OS=Pocillopora damicornis	1.7	1
A7T6G0	Annexin OS=Nematostella vectensis	5.5	2
A0A3M6UZ98	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	4.4	1
A0A3M6V4D5	Uncharacterized protein OS=Pocillopora damicornis	3.1	1
A0A410N5R8	Calmodulin (Fragment) OS=Macrorhynchia hornelli	23.4	2
A0A5P8FSD8	Guanylate cyclase OS=Acropora digitifera	1.4	1
A3F9E8	Histone H2B (Fragment) OS=Anacropora matthai	12	1
A7RNE1	Predicted protein OS=Nematostella vectensis	3	1
A7RQR3	10-formyltetrahydrofolate dehydrogenase OS=Nematostella vectensis	1.4	1
A8DVY3	Predicted protein OS=Nematostella vectensis	8.3	1
C1IS28	Clathrin heavy chain (Fragment) OS=Carukia barnesi	2.9	1
A7RYJ3	Metalloendopeptidase (Fragment) OS=Nematostella vectensis	1	1
E7BTP8	Rab14 OS=Aiptasia pulchella	6.9	2
A7S3I0	Predicted protein (Fragment) OS=Nematostella vectensis	2.8	2
A7S5Z0	Predicted protein OS=Nematostella vectensis	2.8	1
A7S7K4	Predicted protein OS=Nematostella vectensis	4.4	1
A7SAK1	Predicted protein OS=Nematostella vectensis	3.2	1
A7SC40	Predicted protein OS=Nematostella vectensis	2.5	1
A7SG05	GTP-binding nuclear protein OS=Nematostella vectensis	11.1	2
A7SG62	Predicted protein OS=Nematostella vectensis	7.3	1
A7SHC0	Predicted protein (Fragment) OS=Nematostella vectensis	2.1	2
A7SJL4	Predicted protein OS=Nematostella vectensis	1.2	1

A7SMZ7	Dynein light chain roadblock OS=Nematostella vectensis	12.5	1
A7SNP7	Predicted protein OS=Nematostella vectensis	3.1	1
A7SPQ4	Predicted protein OS=Nematostella vectensis	9	2
A7SQE6	Predicted protein OS=Nematostella vectensis	0.7	1
A7SVE5	Predicted protein OS=Nematostella vectensis	5	1
A7SX99	Predicted protein OS=Nematostella vectensis	13.6	1
A7T270	Predicted protein OS=Nematostella vectensis	9.1	1
I2G9E9	Myosin II heavy chain, smooth/non-muscle-type (Fragment) OS=Clytia hemisphaerica	4.4	1
K0A063	Beta-actin (Fragment) OS=Chrysaora quinquecirrha	51.5	14
M1E2P9	Calmodulin (Fragment) OS=Rhizostoma octopus	22.8	1
Q56GW1	60S ribosomal protein L12 (Fragment) OS=Hydractinia echinata	16.5	1
Q5EN87	Putative tyrosine-rich heat shock protein (Fragment) OS=Aurelia aurita	5.8	1
Q5EN93	Heat shock protein Hsp70 (Fragment) OS=Aurelia aurita	3.5	1
Q5FB16	Ubiquitin-ribosomal protein CEP52 fusion protein (Fragment) OS=Pocillopora damicornis	15	1
Q6RFF9	Mitochondrial 60 kDa heat shock protein OS=Anemonia viridis	1.7	1
Q7YZI4	90-kDa heat-shock protein (Fragment) OS=Aurelia aurita	8.2	2
Q9NFW1	60S ribosomal protein L12 OS=Hydra vulgaris	9.7	1
R9S2H2	Uncharacterized protein (Fragment) OS=Aurelia aurita	0.5	1
R9S2M2	Elongation factor 1-alpha OS=Aurelia aurita	4.8	2
T2MEY7	60S ribosomal protein L30 (Fragment) OS=Hydra vulgaris	4.9	1
T2M5A4	GrpE protein homolog (Fragment) OS=Hydra vulgaris	4.8	1
T2M5M6	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (Fragment) OS=Hydra vulgaris	1.9	1
T2M866	Phosphomannomutase (Fragment) OS=Hydra vulgaris	4.2	1
T2M9L6	Carbohydrate sulfotransferase OS=Hydra vulgaris	1.7	1
T2MD44	Major vault protein OS=Hydra vulgaris	1.2	2
T2ME66	Ras-related protein Rab-11A OS=Hydra vulgaris	6	1
T2MEF1	Amidophosphoribosyltransferase OS=Hydra vulgaris	6.1	1
T2MEY1	60S ribosomal protein L11 (Fragment) OS=Hydra vulgaris	7.2	1
T2MF20	RNA polymerase II elongation factor ELL OS=Hydra vulgaris	2	1
T2MF60	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Hydra vulgaris	4.8	1
T2MFG0	Transmembrane emp24 domain-containing protein 10 (Fragment) OS=Hydra vulgaris	4	1
T2MFY6	Hippocalcin-like protein 1 OS=Hydra vulgaris	7.3	1
T2MGZ6	ATP synthase subunit alpha OS=Hydra vulgaris	6.1	3
T2MH46	Filamin-A OS=Hydra vulgaris	0.6	1
T2MHJ7	60 kDa heat shock protein,mitochondrial (Fragment) OS=Hydra vulgaris	2	1
T2MHT5	Heat shock protein HSP 90-alpha OS=Hydra vulgaris	3.6	3
T2MHY4	Argininosuccinate synthase (Fragment) OS=Hydra vulgaris	2.9	1
T2MIK6	Mediator of RNA polymerase II transcription subunit 6 (Fragment) OS=Hydra vulgaris	4.2	1

2.3 Nematocyst extracted by PBS buffer couple with ultrasonication and digested with PNGase and trypsin enzyme

Table D-6. List of proteins identified (91 proteins) from nematocyst of edible jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were derived from in-solution digestion experiment. Database of taxonomy Cnidaria (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
A0A069DLP7	Putative cnidarian restricted protein OS=Clytia hemisphaerica	1.4	1
A8DV16	Predicted protein (Fragment) OS=Nematostella vectensis	20.3	1
B1PM92	Calmodulin OS=Acropora muricata	22.8	2
A0A0C2I691	Translation initiation factor IF-2 OS=Thelohanellus kitauei	6.3	1
A0A0C2IV52	Translation initiation factor IF-2 OS=Thelohanellus kitauei	15	2
A0A0C2JTE8	Uncharacterized protein OS=Thelohanellus kitauei	4.6	1
A0A0C2M6X7	Vigilin OS=Thelohanellus kitauei	1.3	1
C1IJE5	Smooth muscle myosin heavy chain 11 isoform-like protein (Fragment) OS=Myxobolus cerebralis	5.5	1
A0A0C2MTF3	U5 small nuclear ribonucleoprotein helicase OS=Thelohanellus kitauei	2.1	1
A0A0C2N354	ATP synthase subunit beta OS=Thelohanellus kitauei	6.4	2
A0A0C2N4T5	ATP synthase subunit alpha OS=Thelohanellus kitauei	3.3	2
A0A0C2N6G3	Uncharacterized protein OS=Thelohanellus kitauei	7.1	1
L0I703	Calmodulin (Fragment) OS=Schuchertinia conchicola	18.6	1
A0A2Z5WH77	Actin-1 OS=Aurelia sp. 2017-HT	41.5	12
A7SDX9	Tubulin alpha chain OS=Nematostella vectensis	12.9	3
A0A1U9XQR0	Fructose-bisphosphate aldolase OS=Aurelia sp. 1 GW-2014	3.9	1
Q7YZI5	90-kDa heat-shock protein (Fragment) OS=Nematostella vectensis	4.2	2
A0A2B4R884	Uncharacterized protein YqaJ OS=Stylophora pistillata	3.9	1
M1SUP7	Tubulin beta chain (Fragment) OS=Stylophora pistillata	11.2	3
A0A2B4RJK3	Neurogenic locus notch-like protein 2 OS=Stylophora pistillata	0.3	1
A0A3M6TIL0	Uncharacterized protein OS=Pocillopora damicornis	6.5	1
A0A3M6UMI9	Poly [ADP-ribose] polymerase OS=Pocillopora damicornis	1.6	1
A0A2B4RM42	THAP-type domain-containing protein OS=Stylophora pistillata	1.9	1
A0A2B4RNY4	Neurabin-1 OS=Stylophora pistillata	1.3	1
A0A2B4RPA9	Clathrin heavy chain OS=Stylophora pistillata	0.9	1
A7RT97	Predicted protein OS=Nematostella vectensis	1.7	1
A0A2B4RRF8	Serine/threonine-protein kinase DCLK1 OS=Stylophora pistillata	1.1	1
A0A2B4RSY7	ADP-ribosylation factor 1 OS=Stylophora pistillata	8.3	1
A0A2B4RTB1	Tubulin alpha-1C chain OS=Stylophora pistillata	17.7	3
A0A2B4RWB7	Uncharacterized protein OS=Stylophora pistillata	2.6	1
A0A2B4S1E6	RNA-directed DNA polymerase from mobile element jockey OS=Stylophora pistillata	1.8	1
A0A2B4S7E1	Uncharacterized protein OS=Stylophora pistillata	0.8	1
A0A2B4SCK6	Retrovirus-related Pol polyprotein from transposon 17.6 OS=Stylophora pistillata	1.4	1
A7SPP0	ATP synthase subunit beta OS=Nematostella vectensis	10.3	2
A0A2B4S JL5	Uncharacterized protein OS=Stylophora pistillata	8.2	1
A0A2B4SNJ2	Schlafen family member 13 OS=Stylophora pistillata	2.7	1

A0A2B4SQD7	Acyl-coenzyme A oxidase OS=Stylophora pistillata	1.9	1
A0A2B4SR92	Collagen alpha-2(I) chain OS=Stylophora pistillata	0.7	1
A0A3M6TPE2	Uncharacterized protein OS=Pocillopora damicornis	4.1	1
A0A2B4SYK6	Uncharacterized protein OS=Stylophora pistillata	0.5	1
A0A2B4SYS5	Sodium/potassium-transporting ATPase subunit alpha OS=Stylophora pistillata	2.5	1
A0A2Z5WH73	Myosin heavy chain OS=Aurelia sp. 2017-HT	1.4	2
A0A3M6T7E4	ANK_REP_REGION domain-containing protein OS=Pocillopora damicornis	5.9	1
A0A3M6T8X3	Calcium-transporting ATPase OS=Pocillopora damicornis	1.5	1
A0A3M6TEN3	BTB domain-containing protein OS=Pocillopora damicornis	2.6	1
A0A3M6TK27	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	1.6	1
A0A3M6TLH9	Uncharacterized protein OS=Pocillopora damicornis	3.7	1
A0A3M6TSG0	Uncharacterized protein OS=Pocillopora damicornis	1.3	1
Q7YZJ5	Elongation factor 2 (Fragment) OS=Aurelia aurita	5.2	1
A0A3M6UDZ0	TIR domain-containing protein OS=Pocillopora damicornis	3.9	1
A0A3M6UMM4	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	11.7	1
A0A3M6UP68	Uncharacterized protein OS=Pocillopora damicornis	0.6	1
A0A3M6UP81	Uncharacterized protein OS=Pocillopora damicornis	38.3	10
A0A3M6UYC1	cGMP-dependent protein kinase OS=Pocillopora damicornis	1.7	1
A7T6G0	Annexin OS=Nematostella vectensis	5.1	1
A0A3M6V0Z0	Uncharacterized protein OS=Pocillopora damicornis	2	1
A0A3M6V268	ANK_REP_REGION domain-containing protein OS=Pocillopora damicornis	0.7	1
A0A410N5R8	Calmodulin (Fragment) OS=Macrorhynchia hornelli	13.5	1
A7RFT6	Dihydrolipoyl dehydrogenase OS=Nematostella vectensis	3.5	1
A7RH24	Predicted protein (Fragment) OS=Nematostella vectensis	0.8	1
A7RLG8	Predicted protein OS=Nematostella vectensis	1	1
A7RNA0	Predicted protein OS=Nematostella vectensis	2	1
A7RQR3	10-formyltetrahydrofolate dehydrogenase OS=Nematostella vectensis	1.4	1
A7RT78	Predicted protein OS=Nematostella vectensis	0.8	1
A7S7K4	Predicted protein OS=Nematostella vectensis	4.4	1
A7SG62	Predicted protein OS=Nematostella vectensis	7.3	1
A7SP73	Predicted protein OS=Nematostella vectensis	2.5	1
A7SPQ4	Predicted protein OS=Nematostella vectensis	9	1
A7T1L2	Histone H2B OS=Nematostella vectensis	15.6	1
C1IS28	Clathrin heavy chain (Fragment) OS=Carukia barnesi	9	1
G8H6N5	Xeroderma pigmentosum group D OS=Hydra vulgaris	3.6	1
I2G9E9	Myosin II heavy chain, smooth/non-muscle-type (Fragment) OS=Clytia hemisphaerica	7.8	2
M1RYL5	Ubiquitin-like protein OS=Stylophora pistillata	22.5	2
Q56GW1	60S ribosomal protein L12 (Fragment) OS=Hydractinia echinata	16.5	1
Q5EN87	Putative tyrosine-rich heat shock protein (Fragment) OS=Aurelia aurita	5.8	1
Q5FB16	Ubiquitin-ribosomal protein CEP52 fusion protein (Fragment) OS=Pocillopora damicornis	15	1
Q5XPR4	NaK-ATPase alpha subunit (Fragment) OS=Hydractinia echinata	6.6	1
Q7YZI4	90-kDa heat-shock protein (Fragment) OS=Aurelia aurita	11.3	3
Q9NFW1	60S ribosomal protein L12 OS=Hydra vulgaris	9.7	1

R9S2H2	Uncharacterized protein (Fragment) OS=Aurelia aurita	0.5	1
R9S2M2	Elongation factor 1-alpha OS=Aurelia aurita	4.8	2
T2MEY1	60S ribosomal protein L11 (Fragment) OS=Hydra vulgaris	7.2	1
T2MG36	Myosin-10 OS=Hydra vulgaris	1.4	2
T2MGD2	Cytosol aminopeptidase OS=Hydra vulgaris	3.1	1
T2MGF9	Serine/threonine-protein kinase receptor OS=Hydra vulgaris	5.4	1
T2MGG2	Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment) OS=Hydra vulgaris	4	1
T2MGZ6	ATP synthase subunit alpha OS=Hydra vulgaris	3.3	2
T2MH46	Filamin-A OS=Hydra vulgaris	0.6	1
T2MHJ7	60 kDa heat shock protein,mitochondrial (Fragment) OS=Hydra vulgaris	2	1
T2MIE3	Importin-13 (Fragment) OS=Hydra vulgaris	0.6	1
T2MJJ5	Myosin regulatory light chain 12B OS=Hydra vulgaris	10.6	1

3. Top-down proteomics

Table D-7. List of protein identified from nematocyst of edible jellyfish by using extraction of SDS coupled with sonication. Proteins without digestion were analyzed by top-down proteomics experiment. Taxonomy Cnidaria database (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
U5KIJ7	Cytochrome c oxidase subunit III (Fragment) OS=Leiopathes sp. JSL4870-1	100	1

Table D-8. List of proteins identified (2 proteins) from nematocyst of edible jellyfish by using extraction of PBS buffer coupled with ultrasonication. Proteins without digestion were analyzed by top-down proteomics experiment. Taxonomy Cnidaria database (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
A0A3M6U9V1	Uncharacterized protein OS=Pocillopora damicornis	100	1
A0A5J6Y2U5	Cytochrome oxidase subunit 3 (Fragment) OS=Rhodactis indosinensis	100	1



APPENDIX E

Protein identified from edible jellyfish toxin using database of taxonomy Cnidaria and
keyword toxin

1. In-gel digestion

1.1 Identification of protein from crude of tentacle

Table E-1. List of proteins identified (9 proteins) from crude tentacles of edible jellyfish. These proteins identified were derived from in-gel digestion experiment. Database of taxonomy Cnidaria and keyword toxin (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
Q9GNN8	Toxin CaTX-A OS=Carybdea alata	Cytolysis, Hemolysis	13.4	2
A0A2B4SA86	Thrombospondin-1 OS=Stylophora pistillata	Toxin	2.9	2
A0A2B4SQL7	Metalloendopeptidase OS=Stylophora pistillata	Hydrolase, Metalloprotease, Protease, Toxin	1.3	1
A0A2B4SWG8	Retinol dehydrogenase 12 OS=Stylophora pistillata	Toxin	2.9	1
A0A3M6TK48	Uncharacterized protein OS=Pocillopora damicornis	Hydrolase, Protease, Serine protease, Toxin	4.7	3
A0A3M6TTZ7	Metalloendopeptidase (Fragment) OS=Pocillopora damicornis	Hydrolase, Metalloprotease, Protease, Toxin	6.8	2
A0A3M6UY54	Uncharacterized protein OS=Pocillopora damicornis	Toxin	1.4	6
A0A3M6V0Y5	Metalloendopeptidase OS=Pocillopora damicornis	Hydrolase, Metalloprotease, Protease, Toxin	3.1	2
A0A3M6V2T1	ShKT domain-containing protein OS=Pocillopora damicornis	Toxin	5.5	2

1.2 Identification of protein from nematocyst

Table E-2. List of proteins identified (9 proteins) from nematocyst of edible jellyfish by using extraction of SDS coupled with sonication. The proteins were derived from in-gel digestion experiment. Database of taxonomy Cnidaria and keyword toxin (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
Q8WS88	Phospholipase A2 A2-hormotoxin-Apt1a OS=Adamsia palliata	Hydrolase, Toxin	5.1	1
A0A2B4SA86	Thrombospondin-1 OS=Stylophora pistillata	Toxin	0.9	1
A0A2B4SIN1	Pathogenesis-related leaf protein 4 OS=Stylophora pistillata	Toxin	1.7	2
A0A2B4SWG8	Retinol dehydrogenase 12 OS=Stylophora pistillata	Toxin	2.9	1
A0A3M6TKE4	Uncharacterized protein OS=Pocillopora damicornis	Toxin	3.2	1
A0A3M6TPP5	Uncharacterized protein OS=Pocillopora damicornis	Hydrolase, Metalloprotease, Protease, Toxin	4.1	2
A0A3M6TQD4	Uncharacterized protein OS=Pocillopora damicornis	Toxin	2	2
A0A3M6UY54	Uncharacterized protein OS=Pocillopora damicornis	Toxin	0.4	2
A0A3M6UZV0	Metalloendopeptidase OS=Pocillopora damicornis	Hydrolase, Metalloprotease, Protease, Toxin	3.3	2

Table E-3. List of proteins identified (8 proteins) from nematocyst of edible jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were derived from in-gel digestion experiment. Database of taxonomy Cnidaria and keyword toxin (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P0DN04	U-actitoxin-Avd10a OS= <i>Anemonia viridis</i>	Ion channel impairing toxin, Neurotoxin, Potassium channel impairing toxin, Toxin, Voltage-gated potassium channel impairing toxin	9.3	1
A0A2B4T1C5	Hemicentin-1 OS= <i>Stylophora pistillata</i>	Toxin	0.4	1
A0A3M6TK48	Uncharacterized protein OS= <i>Pocillopora damicornis</i>	Hydrolase, Protease, Serine protease, Toxin	1	1
A0A3M6TTZ7	Metalloendopeptidase (Fragment) OS= <i>Pocillopora damicornis</i>	Hydrolase, Metalloprotease, Protease, Toxin	2	1
A0A3M6UXV7	Uncharacterized protein (Fragment) OS= <i>Pocillopora damicornis</i>	Toxin	1.7	2
A0A3M6UY54	Uncharacterized protein OS= <i>Pocillopora damicornis</i>	Toxin	2.9	9
A0A4U8YUA8	Metalloendopeptidase OS= <i>Oulactis</i> sp.	Hydrolase, Metalloprotease, Protease, Toxin	0.8	1
A7SA78	Metalloendopeptidase (Fragment) OS= <i>Nematostella vectensis</i>	Hydrolase, Metalloprotease, Protease, Toxin	7.7	1

2. In-solution digestion

2.1 Nematocyst extracted by 2% SDS couple with sonication and digested with trypsin enzyme

Table E-4. List of proteins identified (8 proteins) from nematocyst of edible jellyfish by using extraction of SDS coupled with sonication. The proteins were derived from in-solution digestion experiment. Database of taxonomy Cnidaria and keyword toxin (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
B1B5I8	KappaPI-stichotoxin-Shd2a OS= <i>Stichodactyla haddoni</i>	Ion channel impairing toxin, Potassium channel impairing toxin, Protease inhibitor, Serine protease inhibitor, Toxin, Voltage-gated potassium channel impairing toxin	42	1

A0A2B4RNQ4	ShKT domain-containing protein OS=Stylophora pistillata	Toxin	3.6	1
A0A2B4SA86	Thrombospondin-1 OS=Stylophora pistillata	Toxin	0.9	1
A0A2B4SSB6	Metalloendopeptidase OS=Stylophora pistillata	Hydrolase, Metalloprotease, Protease, Toxin	5.7	3
A0A2B4SWG8	Retinol dehydrogenase 12 OS=Stylophora pistillata	Toxin	2.9	1
A0A3M6UY54	Uncharacterized protein OS=Pocillopora damicornis	Toxin	1	3
A0A3M6UYN9	ShKT domain-containing protein OS=Pocillopora damicornis	Toxin	5.2	1
A7SCA9	Predicted protein OS=Nematostella vectensis	Toxin	12.8	1

2.2 Nematocyst extracted by PBS buffer couple with ultrasonication and digested with trypsin enzyme

Table E-5. List of proteins identified (11 proteins) from nematocyst of edible jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were derived from in-solution digestion experiment. Database of taxonomy Cnidaria and keyword toxin (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P69930	Delta-actitoxin-Amc2a OS=Antheopsis maculata	Neurotoxin, Toxin	20	1
P86462	Toxin Bcg III 28.78 (Fragment) OS=Bunodosoma cangicum	Ion channel impairing toxin, Toxin	73	1
A0A3M6TQD4	Uncharacterized protein OS=Pocillopora damicornis	Toxin	0.9	2
A0A2B4SA86	Thrombospondin-1 OS=Stylophora pistillata	Toxin	7.4	5
A0A2B4SHB7	Hemicentin-1 OS=Stylophora pistillata	Toxin	6.5	3
A0A3M6T4M3	Uncharacterized protein OS=Pocillopora damicornis	Toxin	1.8	1
A0A3M6UVW0	Metalloendopeptidase OS=Pocillopora damicornis	Hydrolase, Metalloprotease, Protease, Toxin	6.8	3
A0A3M6UY54	Uncharacterized protein OS=Pocillopora damicornis	Toxin	0.8	3
A0A3M6UZV0	Metalloendopeptidase OS=Pocillopora damicornis	Hydrolase, Metalloprotease, Protease, Toxin	1.6	1
A7S9H4	Predicted protein OS=Nematostella vectensis	Toxin	0.8	1
A7SQR7	Metalloendopeptidase (Fragment) OS=Nematostella vectensis	Hydrolase, Metalloprotease, Protease, Toxin	12.2	1

2.3 Nematocyst extracted by PBS buffer couple with ultrasonication and digested with PNGase and trypsin enzyme

Table E-6. List of proteins identified (24 proteins) from nematocyst of edible jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were derived from in-solution digestion experiment. Database of taxonomy Cnidaria and keyword toxin (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
E2S062	Kappa-stichotoxin-Shd5a OS=Stichodactyla haddoni	Ion channel impairing toxin, Neurotoxin, Potassium channel impairing toxin, Toxin, Voltage-gated potassium channel impairing toxin	29.7	1
A0A0S1M157	Sodium channel toxin protein (Fragment) OS=Anemonia sulcata	Ion channel, Neurotoxin, Toxin	31.3	1
A0A2B4RCC1	Uncharacterized protein OS=Stylophora pistillata	Toxin	11.2	1
A0A2B4RII3	Metalloendopeptidase OS=Stylophora pistillata	Hydrolase, Metalloprotease, Protease, Toxin	3.4	2
A0A3M6V6A0	Uncharacterized protein OS=Pocillopora damicornis	Hydrolase, Protease, Serine protease, Toxin	7.2	1
A0A2B4SE56	Cell wall protein PRY3 OS=Stylophora pistillata	Toxin	5.1	1
A0A2B4SWG8	Retinol dehydrogenase 12 OS=Stylophora pistillata	Toxin	2.9	1
A0A3M6T9J1	Uncharacterized protein OS=Pocillopora damicornis	Toxin	4.6	1
A0A3M6TK48	Uncharacterized protein OS=Pocillopora damicornis	Hydrolase, Protease, Serine protease, Toxin	3.1	2
A0A3M6TQ50	Uncharacterized protein OS=Pocillopora damicornis	Hydrolase, Protease, Serine protease, Toxin	2.7	1
A0A3M6TX77	Uncharacterized protein OS=Pocillopora damicornis	Toxin	1.9	1
A0A3M6TYG6	Uncharacterized protein OS=Pocillopora damicornis	Toxin	6.3	1
A0A3M6UD47	Metalloendopeptidase (Fragment) OS=Pocillopora damicornis	Hydrolase, Metalloprotease, Protease, Toxin	7.2	2
A0A3M6UDC3	ShKT domain-containing protein (Fragment) OS=Pocillopora damicornis	Toxin	3.9	2
A0A3M6UWW3	Metalloendopeptidase (Fragment) OS=Pocillopora damicornis	Hydrolase, Metalloprotease, Protease, Toxin	6	1
A0A3M6UX25	Metalloendopeptidase OS=Pocillopora damicornis	Hydrolase, Metalloprotease, Protease, Toxin	3.4	1
A0A3M6UXW8	ShKT domain-containing protein (Fragment) OS=Pocillopora damicornis	Toxin	5.1	1
A0A3M6UY54	Uncharacterized protein OS=Pocillopora damicornis	Toxin	0.3	1
A0A3M6UZV0	Metalloendopeptidase OS=Pocillopora damicornis	Hydrolase, Metalloprotease, Protease, Toxin	5.9	2
A0A3M6V0Y3	Metalloendopeptidase OS=Pocillopora damicornis	Hydrolase, Metalloprotease, Protease, Toxin	2.6	1
A0A3M6V2T1	ShKT domain-containing protein OS=Pocillopora damicornis	Toxin	2.2	1
A0A4D8XPG1	mRNA OS=Oulactis sp.	Toxin	30.9	1
A0A4U8YU89	mRNA (Fragment) OS=Oulactis sp.	Toxin	5.7	1
A7SQR8	Metalloendopeptidase (Fragment) OS=Nematostella vectensis	Hydrolase, Metalloprotease, Protease, Toxin	8.3	1



APPENDIX F

Protein identified from edible jellyfish toxin using database of keyword toxin

1. In-gel digestion

1.1 Identification of protein from crude of tentacle

Table F-1. List of proteins identified (23 proteins) from crude tentacles of edible jellyfish. These proteins identified were derived from in-gel digestion experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P00610	Basic phospholipase A2 OS=Hydrophis schistosus	Blood coagulation cascade inhibiting toxin, Hemostasis impairing toxin, Hydrolase, Myotoxin, Neurotoxin, Presynaptic neurotoxin, Toxin	13.4	1
Q48258	Vacuolating cytotoxin autotransporter OS=Helicobacter pylori	Toxin	1.4	1
Q593B6	Coagulation factor V OS=Pseudonaja textilis	Prothrombin activator, Toxin	0.7	1
A0A087CVT3	Ribonuclease VapC OS=Bifidobacterium ruminantium	Hydrolase, Nuclease, Toxin	9.6	1
A0A0K2SES2	Conotoxin Superfamily T OS=Conus episcopatus	N/A	33.3	1
A0A0K9RKN2	rRNA N-glycosidase OS=Spinacia oleracea	Hydrolase, Protein synthesis inhibitor, Toxin	10.6	1
A0A0Q3VY71	Uncharacterized protein OS=Bacillus sp. FJAT-25509	Hydrolase, Toxin	2.6	1
A0A1G9W2D8	Ribonuclease VapC OS=Allokutzneria albata	Hydrolase, Nuclease, Toxin	19.3	1
A0A1I2DKJ5	Ribonuclease VapC OS=Blastococcus sp. DSM 46838	Hydrolase, Nuclease, Toxin	9.6	1
A0A437NML3	Ribonuclease VapC OS=Rhizobium sp. RMa-01	Hydrolase, Nuclease, Toxin	6.6	1
A0A1T1ZLG4	Cytolethal distending toxin subunit A OS=Campylobacter coli	Cytotoxins, Toxin	8.1	1
A0A1W5IH15	Cry1Db-like protein OS=Bacillus thuringiensis	Toxin	2	1
A0A2B3LBN2	Ricin B-type lectin domain-containing protein OS=Bacillus thuringiensis	Toxin	1.7	1
A0A2P9AP98	Ribonuclease VapC OS=Mesorhizobium delmotii	Hydrolase, Nuclease, Toxin	12	1
A0A350MUL1	Ribonuclease VapC OS=Actinobacteria bacterium	Hydrolase, Nuclease, Toxin	17.1	1
A0A3C1G0X6	Ribonuclease VapC OS=Nitrospiraceae bacterium	Hydrolase, Nuclease, Toxin	21.8	1
A0A3L6PD81	rRNA N-glycosidase OS=Panicum miliaceum	Hydrolase, Lyase, Protein synthesis inhibitor, Toxin	1.3	1
A0A402DR21	Ribonuclease VapC OS=Cellulomonas biazotea	Hydrolase, Nuclease, Toxin	14.3	1
A0A5R9P826	Ribonuclease VapC OS=Rhizobium sp. JKLM12A2	N/A	13.4	1
A0A4U2NI39	Thiol-activated cytolysin OS=Bacillus cereus	Cytolysis	2.5	1
A0A534U3Q3	Ribonuclease VapC OS=Deltaproteobacteria bacterium	Hydrolase, Nuclease, Toxin	13.1	1
A9ZP30	Non-structural glycoprotein 4 OS=Human rotavirus A	Enterotoxin, Ion channel, Toxin, Viral ion channel	5.7	1
B4SBA4	Ribonuclease VapC OS=Pelodictyon phaeoclathratiforme (strain DSM 5477 / BU-1)	Hydrolase, Nuclease, Toxin	20.8	1

1.2 Identification of protein from nematocyst

Table F-2. List of proteins identified (21 proteins) from nematocyst of edible jellyfish by using extraction of SDS coupled with sonication. The proteins were derived from in-gel digestion experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P00610	Basic phospholipase A2 OS=Hydrophis schistosus	Blood coagulation cascade inhibiting toxin, Hemostasis impairing toxin, Hydrolase, Myotoxin, Neurotoxin, Presynaptic neurotoxin, Toxin	13.4	1
P0CY67	Conotoxin Bu9 (Fragment) OS=Conus bullatus	Ion channel impairing toxin, Neurotoxin, Toxin	33.3	1
P55126	Iron-regulated protein FrpA OS=Neisseria meningitidis serogroup C	Toxin	1.3	1
Q593B6	Coagulation factor V OS=Pseudonaja textilis	Prothrombin activator, Toxin	0.7	1
A0Q0M2	Thiol-activated cytolysin OS=Clostridium novyi (strain NT)	Cytolysis	1.9	1
A0A4U2ZS53	Thiol-activated cytolysin (Fragment) OS=Bacillus mycoides	Cytolysis	13.2	1
A0A087CVT3	Ribonuclease VapC OS=Bifidobacterium ruminantium	Hydrolase, Nuclease, Toxin	9.6	1
A0A0K9RKN2	rRNA N-glycosidase OS=Spinacia oleracea	Hydrolase, Protein synthesis inhibitor, Toxin	10.6	1
A0A1F6LI84	Ribonuclease VapC OS=Candidatus Lindowbacteria bacterium RIFCSPLOWO2_12_FULL_62_27	Hydrolase, Nuclease, Toxin	6.7	1
A0A549T543	Ribonuclease VapC OS=Rhizobium straminoryzae	Hydrolase, Nuclease, Toxin	6.9	1
A0A437NML3	Ribonuclease VapC OS=Rhizobium sp. RMa-01	Hydrolase, Nuclease, Toxin	6.6	1
A0A1W5IH15	Cry1Db-like protein OS=Bacillus thuringiensis	Toxin	2	1
A0A2N4Y7R1	Ribonuclease VapC OS=Rhizobium sp. TH135	Hydrolase, Nuclease, Toxin	19.3	1
A0A2W7APJ0	Ribonuclease VapC OS=Leptolyngbya sp.	Hydrolase, Nuclease, Toxin	19.4	1
A0A350MUL1	Ribonuclease VapC OS=Actinobacteria bacterium	Hydrolase, Nuclease, Toxin	17.1	1
A0A3B6PJD9	rRNA N-glycosidase OS=Triticum aestivum	Hydrolase, Protein synthesis inhibitor, Toxin	4.1	1
A0A3L6PD81	rRNA N-glycosidase OS=Panicum miliaceum	Hydrolase, Lyase, Protein synthesis inhibitor, Toxin	1.3	1
A0A3L6Q3F6	rRNA N-glycosidase OS=Panicum miliaceum	Hydrolase, Protein synthesis inhibitor, Toxin	2.9	2
A0A534P8F5	Ribonuclease VapC OS=Deltaproteobacteria bacterium	Hydrolase, Nuclease, Toxin	25	1
H0SVJ0	Ribonuclease VapC OS=Bradyrhizobium sp. STM 3809	Hydrolase, Nuclease, Toxin	6.3	1
Q5P893	Ribonuclease VapC OS=Aromatoleum aromaticum (strain EbN1)	Hydrolase, Nuclease, Toxin	6.8	1

Table F-3. List of proteins identified (12 proteins) from nematocyst of edible jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were derived from in-gel digestion experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P00610	Basic phospholipase A2 OS=Hydrophis schistosus	Blood coagulation cascade inhibiting toxin, Hemostasis impairing toxin, Hydrolase, Myotoxin, Neurotoxin, Presynaptic neurotoxin, Toxin	47.1	4
Q7SZN0	Venom prothrombin activator pseutarin-C non-catalytic subunit OS=Pseudonaja textilis	Blood coagulation cascade activating toxin, Hemostasis impairing toxin, Prothrombin activator, Toxin	2.2	2
A0A014PKY9	Clostridium neurotoxin-like protein OS=Metarhizium robertsii	Neurotoxin, Toxin	1	1
A0A0K9RKN2	rRNA N-glycosidase OS=Spinacia oleracea	Hydrolase, Protein synthesis inhibitor, Toxin	10.6	1
A0A179BSN6	Ribonuclease VapC OS=Rhizobium leguminosarum	Hydrolase, Nuclease, Toxin	7.4	1
A0A1J5AHB9	Ribonuclease VapC OS=Anaerolineae bacterium CG2_30_64_16	Hydrolase, Nuclease, Toxin	8.7	1
A0A549T543	Ribonuclease VapC OS=Rhizobium straminoryzae	Hydrolase, Nuclease, Toxin	6.9	1
A0A238DNE9	Ribonuclease VapC OS=Thiomonas sp. X19	Hydrolase, Nuclease, Toxin	10.3	1
A0A2M7GQU3	Ribonuclease VapC OS=Rhodospirillales bacterium CG15_BIG_FIL_POST_REV_8_21_14_020_66_15	Hydrolase, Nuclease, Toxin	10.4	1
A0A2W0BS89	Ribonuclease VapC OS=Acidobacteria bacterium	Hydrolase, Nuclease, Toxin	13	1
A0A350MUL1	Ribonuclease VapC OS=Actinobacteria bacterium	Hydrolase, Nuclease, Toxin	17.1	1
A0A3D1BN09	Ribonuclease VapC OS=Nitrospiraceae bacterium	Hydrolase, Nuclease, Toxin	9.6	1

2. In-solution digestion

2.1 Nematocyst extracted by 2% SDS couple with sonication and digested with trypsin enzyme

Table F-4. List of proteins identified (31 proteins) from nematocyst of edible jellyfish by using extraction of SDS coupled with sonication. The proteins were derived from in-solution digestion experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P30894	Venom nerve growth factor OS=Daboia russelii	Growth factor, Metalloenzyme inhibitor, Metalloprotease inhibitor, Protease inhibitor, Toxin	16.2	1
A0A069IQI1	Ribonuclease VapC OS=Brevundimonas sp. EAKA	Hydrolase, Nuclease, Toxin	9.3	1
A0A0K2S9V1	Conotoxin Superfamily T OS=Conus episcopatus	N/A	26	1
A0A0K9RKN2	rRNA N-glycosidase OS=Spinacia oleracea	Hydrolase, Protein synthesis inhibitor, Toxin	10.6	1

A0A0S6W3Y2	Ribonuclease VapC OS=Candidatus Moduliflexus flocculans	Hydrolase, Nuclease, Toxin	15.2	1
A0A0U1TZ19	Knot1 domain-containing protein OS=Isometrus maculatus	N/A	14.8	1
A0A1E7IUN9	Ribonuclease VapC OS=Desulfobacteriales bacterium S5133MH4	Hydrolase, Nuclease, Toxin	6	1
A0A1F6LI84	Ribonuclease VapC OS=Candidatus Lindowbacteria bacterium RIFCSPLOWO2_12_FULL_62_27	Hydrolase, Nuclease, Toxin	6.7	1
A0A1I2DKJ5	Ribonuclease VapC OS=Blastococcus sp. DSM 46838	Hydrolase, Nuclease, Toxin	9.6	1
A0A2N3RS75	Ribonuclease VapC OS=Fibrobacter sp. UWT1	Endonuclease, Hydrolase, Nuclease, Toxin	8.4	1
A0A1Q3NFJ3	Ribonuclease VapC OS=Solirubrobacteriales bacterium 67-14	Hydrolase, Nuclease, Toxin	7.9	1
A0A1Q8QGL7	Ribonuclease VapC OS=Desulfovibrio sp. DV	Hydrolase, Nuclease, Toxin	9	1
A0A1S1SRK3	Ribonuclease VapC OS=Rhizobium sp. LCM 4573	Hydrolase, Nuclease, Toxin	11.8	1
A0A1V4EQ29	Ribonuclease VapC OS=Microbispora sp. GKU 823	Hydrolase, Nuclease, Toxin	14.7	1
A0A1W9KWW0	Ribonuclease VapC OS=Rhodoferrax ferrireducens	Hydrolase, Nuclease, Toxin	14.5	1
A0A2B3PYJ5	Uncharacterized protein OS=Bacillus thuringiensis	Toxin	3	1
A0A2B9TT38	Uncharacterized protein (Fragment) OS=Bacillus cereus	Toxin	3.2	1
A0A2K2DAV7	Uncharacterized protein (Fragment) OS=Brachypodium distachyon	N/A	13.3	1
A0A3A4MWW3	Thiol-activated cytolysin OS=Streptococcus pseudopneumoniae	N/A	1.5	1
A0A3A5KFP5	Ribonuclease VapC OS=Mesorhizobium waimense	Hydrolase, Nuclease, Toxin	7.2	1
A0A3C0HI99	Ribonuclease VapC OS=Xanthomonadaceae bacterium	Hydrolase, Nuclease, Toxin	13.8	1
A0A3E2TR35	Ribonuclease VapC OS=Coprococcus catus	Hydrolase, Nuclease, Toxin	15.4	1
A0A3S0EIC5	Ribonuclease VapC OS=Rhizobiales bacterium	Hydrolase, Nuclease, Toxin	6.3	1
A0A443PL30	rRNA N-glycosidase OS=Cinnamomum micranthum f. kanehirae	Hydrolase, Protein synthesis inhibitor, Toxin	38.5	1
A0A453SS91	rRNA N-glycosidase OS=Aegilops tauschii subsp. strangulata	Hydrolase, Protein synthesis inhibitor, Toxin	5.6	1
A0A4D8XKT5	mRNA OS=Oulactis sp.	Toxin	48.7	1
A0A532DU08	Ribonuclease VapC OS=Nitrospira sp.	Hydrolase, Nuclease, Toxin	14.4	1
A0A533HZM6	Ribonuclease VapC OS=Paracoccus denitrificans	Hydrolase, Nuclease, Toxin	7.5	1
A0A5M8SDQ8	Ribonuclease VapC OS=Acidobacteria bacterium AB60	Hydrolase, Nuclease, Toxin	13.5	1
A9ZP30	Non-structural glycoprotein 4 OS=Human rotavirus A	Enterotoxin, Ion channel, Toxin, Viral ion channel	5.7	1
NILSG2	Cry OS=Bacillus sp. GeD10	Toxin	3.3	1

2.2 Nematocyst extracted by PBS buffer couple with ultrasonication and digested with trypsin enzyme

Table F-5. List of proteins identified (2 proteins) from nematocyst of edible jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were

derived from in-solution digestion experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P0C8U7	Alpha-conotoxin-like PuSG1.2 OS=Conus pulicarius	Acetylcholine receptor inhibiting toxin, Ion channel impairing toxin, Neurotoxin, Postsynaptic neurotoxin, Toxin	66.7	1
A0A0K9RKN2	rRNA N-glycosidase OS=Spinacia oleracea	Hydrolase, Protein synthesis inhibitor, Toxin	10.6	1

2.3 Nematocyst extracted by PBS buffer couple with ultrasonication and digested with PNGase and trypsin enzyme

Table F-6. List of proteins identified (8 proteins) from nematocyst of edible jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were derived from in-solution digestion experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
Q2G1X0	Alpha-hemolysin OS=Staphylococcus aureus (strain NCTC 8325)	Hemolysis, Toxin	7.2	2
Q41358	Ribosome-inactivating protein SNAI OS=Sambucus nigra	Hydrolase, Protein synthesis inhibitor, Toxin	6	1
Q593B6	Coagulation factor V OS=Pseudonaja textilis	Prothrombin activator, Toxin	0.5	1
S0F1N7	Omega-hexatoxin-Hvn1b OS=Hadronyche venenata	Calcium channel impairing toxin, Ion channel impairing toxin, Toxin, Voltage-gated calcium channel impairing toxin	51.2	1
A0A1E8D1W9	Ribonuclease VapC OS=Humibacillus sp. DSM 29435	Hydrolase, Nuclease, Toxin	29.4	1
A0A4D8XKT5	mRNA OS=Oulactis sp.	Toxin	48.7	1
A0A560JB51	Ribonuclease VapC OS=Nitrospirillum amazonense	Hydrolase, Nuclease, Toxin	6	1
A0A5K7ZGL4	Ribonuclease VapC OS=Desulfosarcina ovata	Hydrolase, Nuclease, Toxin	4.4	1

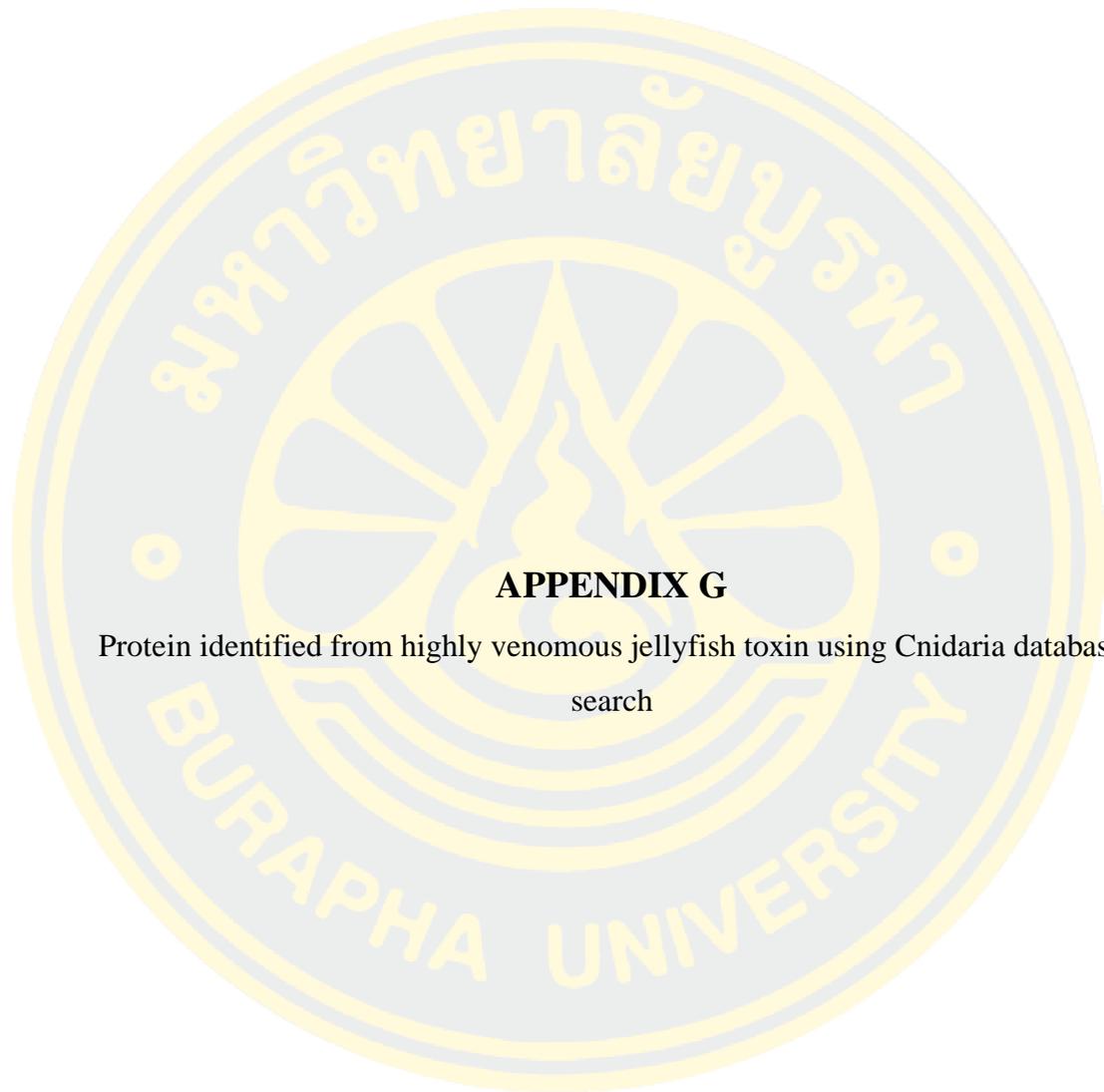
3. Top-down proteomics

Table F-7. List of protein identified (4 proteins) from nematocyst of edible jellyfish by using extraction of SDS coupled with sonication. Proteins without digestion were analyzed by top-down proteomics experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P0C249	Contryphan-In OS=Conus inscriptus	Ion channel impairing toxin, Neurotoxin, Toxin	100	1
P0DKZ4	Bradykinin-potentiating peptide 8a OS=Bothrops cotiara	Hypotensive agent, Metalloenzyme inhibitor, Metalloprotease inhibitor, Protease inhibitor, Toxin	100	1

Q7LZF4	Snake venom serine protease IVa (Fragment) OS=Cerastes cerastes	Hypotensive agent, Metalloenzyme inhibitor, Metalloprotease inhibitor, Protease inhibitor, Toxin	100	1
Q7M3P1	U28-ctenitoxin-Pn1a (Fragment) OS=Phoneutria nigriventer	Toxin	100	1





APPENDIX G

Protein identified from highly venomous jellyfish toxin using Cnidaria database
search

1. In-gel digestion

1.1 Identification of protein from crude of tentacle

Table G-1. List of proteins identified (384 proteins) from crude tentacles of highly venomous jellyfish. These proteins identified were derived from in-gel digestion experiment. Database of taxonomy Cnidaria (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
A0A3M6UR37	Eukaryotic translation initiation factor 3 subunit I OS=Pocillopora damicornis	3.8	1
T2MCI6	Transmembrane emp24 domain-containing protein 2 OS=Hydra vulgaris	4.6	1
T2MGY6	Sodium/potassium-transporting ATPase subunit alpha OS=Hydra vulgaris	4.6	3
P38984	40S ribosomal protein SA OS=Hydra viridissima	4.1	1
M1G4Y4	Ras1 (Fragment) OS=Hydractinia echinata	19.1	2
P62184	Calmodulin OS=Renilla reniformis	58.4	4
B1PM92	Calmodulin OS=Acropora muricata	58.4	4
A0A069DMJ2	Glutamate deshydrogenase (Fragment) OS=Clytia hemisphaerica	4.2	2
A0A0C2I839	Cytosol aminopeptidase OS=Thelohanellus kitauei	2.4	1
A0A1V0IGH5	Histone H2B OS=Hydra vulgaris	11.2	1
A0A0C2JBA7	40S ribosomal protein S23 OS=Thelohanellus kitauei	8.4	1
A0A0C2JEY5	6-phosphogluconate dehydrogenase, decarboxylating OS=Thelohanellus kitauei	10.3	4
A0A0C2JSW9	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 OS=Thelohanellus kitauei	1.9	1
A0A0C2M5P0	Outer membrane protein A OS=Thelohanellus kitauei	5.6	2
A0A0C2MK04	Uncharacterized protein OS=Thelohanellus kitauei	24.6	1
A0A0C2MMZ6	Eukaryotic initiation factor 4A-III OS=Thelohanellus kitauei	5.8	2
C1IJE5	Smooth muscle myosin heavy chain 11 isoform-like protein (Fragment) OS=Myxobolus cerebralis	5.5	1
A0A0C2MT43	Heat shock protein HSP 90-alpha 1 OS=Thelohanellus kitauei	1.7	1
A0A0C2MUS2	60 kDa chaperonin OS=Thelohanellus kitauei	8	3
A0A0C2N1N8	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Thelohanellus kitauei	4.8	1
A0A0C2N200	Ras-related protein RABA2a OS=Thelohanellus kitauei	5.3	1
A0A0C2N354	ATP synthase subunit beta OS=Thelohanellus kitauei	9	3
A0A0C2N442	Ras-related protein Rab-11A OS=Thelohanellus kitauei	5.3	1
A0A0C2NF10	60S ribosomal protein L28 OS=Thelohanellus kitauei	7.2	1
A0A0C4VZ14	78 kDa glucose-regulated protein (Fragment) OS=Capnella imbricata	16.4	5
A0A2B4STX3	Heat shock protein 70 B2 OS=Stylophora pistillata	6.1	3
A0A0K0K658	Cytochrome c oxidase subunit 2 OS=Myriopathes japonica	6.4	1
A0A3M6T9A7	Uncharacterized protein OS=Pocillopora damicornis	4.1	1
A0A142I2D1	Cytochrome c oxidase subunit 3 (Fragment) OS=Phyllorhiza punctata	6.2	1
A0A169Q0T5	Glyceraldehyde-3-phosphate dehydrogenase OS=Aurelia sp. SETO	6.8	2
A0A2Z5WH77	Actin-1 OS=Aurelia sp. 2017-HT	52.4	18
A0A1L2A726	Superoxide dismutase [Cu-Zn] OS=Cyanea capillata	24	4
A0A1U9XQR0	Fructose-bisphosphate aldolase OS=Aurelia sp. 1 GW-2014	6.6	2

A0A2B4QXZ5	ATP-dependent Clp protease ATP-binding subunit ClpX (Fragment) OS=Stylophora pistillata	2.2	1
A0A2B4R364	GTP-binding protein TypA/BipA-like OS=Stylophora pistillata	7.5	2
A0A2B4R6Q9	Fumarate hydratase class II OS=Stylophora pistillata	4	2
A0A2B4R9G5	Histone H2B OS=Stylophora pistillata	7.3	2
A0A2B4R9Q9	Histone H4 OS=Stylophora pistillata	38.2	14
A0A2B4R9T9	Chaperone protein DnaK OS=Stylophora pistillata	2.3	1
A0A2B4RAR4	60S ribosomal protein L4 (Fragment) OS=Stylophora pistillata	7.4	2
A7RQD8	Predicted protein OS=Nematostella vectensis	39.8	4
A0A3M6TR29	Hcy-binding domain-containing protein OS=Pocillopora damicornis	4.7	2
A7RVK9	Predicted protein OS=Nematostella vectensis	3.8	1
T2MHV0	Aldehyde dehydrogenase,mitochondrial OS=Hydra vulgaris	2.3	1
T2MEZ1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial (Fragment) OS=Hydra vulgaris	3.6	1
A0A2B4RFD1	Cytoplasmic dynein 2 heavy chain 1 OS=Stylophora pistillata	0.3	1
A0A2B4RG26	Dual specificity protein kinase shkC OS=Stylophora pistillata	1.4	1
A0A2B4RHG2	V-type proton ATPase catalytic subunit A OS=Stylophora pistillata	9.4	4
A0A2B4RHH5	Enoyl-CoA hydratase, mitochondrial OS=Stylophora pistillata	6	1
A0A2B4RI23	GTP-binding protein SAR1 OS=Stylophora pistillata	6.8	1
A0A2B4RI26	Proteasome subunit alpha type OS=Stylophora pistillata	3.5	1
A0A3M6TI71	Glutamate dehydrogenase OS=Pocillopora damicornis	2.3	1
A7SSV8	Polyadenylate-binding protein OS=Nematostella vectensis	1.9	1
A0A3M6V529	Ribosomal_L23eN domain-containing protein (Fragment) OS=Pocillopora damicornis	7.5	1
A7SRJ0	Non-specific serine/threonine protein kinase OS=Nematostella vectensis	2.2	1
A0A2B4RJH1	Tubulin beta chain OS=Stylophora pistillata	47.7	20
A0A2B4RKG6	U6 snRNA-associated Sm-like protein LSm8 OS=Stylophora pistillata	21.3	1
A0A2B4RKT3	26S proteasome non-ATPase regulatory subunit 2 OS=Stylophora pistillata	1.7	1
A0A2B4RKT5	Actin-related protein 2 OS=Stylophora pistillata	6.5	2
A0A3M6V3V6	Uncharacterized protein OS=Pocillopora damicornis	13.7	3
A0A2B4RPA9	Clathrin heavy chain OS=Stylophora pistillata	3.7	5
A0A2B4RPD3	Endoplasmic reticulum chaperone protein OS=Stylophora pistillata	2.7	2
A0A2B4RQE8	GDP-mannose 4,6 dehydratase OS=Stylophora pistillata	4.1	1
A7SQS1	Malate dehydrogenase OS=Nematostella vectensis	4.7	1
A0A2B4RQQ6	Eukaryotic initiation factor 4A-III OS=Stylophora pistillata	10.2	3
A0A2B4RQZ5	Glutathione reductase, mitochondrial OS=Stylophora pistillata	2.3	1
A0A2B4SU65	Catalase OS=Stylophora pistillata	3	1
Q93116	Ub52 OS=Acropora millepora	36.4	4
A0A2B4RU67	Peroxiredoxin-4 OS=Stylophora pistillata	12.9	3
A0A2B4RU80	Coatomer subunit beta OS=Stylophora pistillata	3.2	2
I2G9E1	Serine/threonine-protein phosphatase (Fragment) OS=Clytia hemisphaerica	4.5	2
Q2F6G0	Prohibitin (Fragment) OS=Anthopleura elegantissima	10	1
A0A3M6UCM8	MPN domain-containing protein OS=Pocillopora damicornis	0.5	1
A0A2B4RWB5	Elongation factor 1-gamma OS=Stylophora pistillata	2.6	1
A0A2B4RXI4	Ras-related protein Rab-5B OS=Stylophora pistillata	11.1	2
A0A3M6UGZ3	NTP_transferase domain-containing protein OS=Pocillopora damicornis	5.8	1

A0A3M6TBX6	40S ribosomal protein S27 OS=Pocillopora damicornis	38.1	3
A0A3M6TNT3	Coatomer subunit delta OS=Pocillopora damicornis	2.4	1
A0A2B4S092	Multifunctional fusion protein OS=Stylophora pistillata	1.4	3
L0AUB3	Alpha q G protein OS=Acropora palmata	3.1	1
T2MIU1	Nucleolar protein 56 (Fragment) OS=Hydra vulgaris	2.5	1
A0A3M6V6P2	FAA_hydrolase domain-containing protein OS=Pocillopora damicornis	3.2	1
A0A2B4S129	Peroxiredoxin-1 OS=Stylophora pistillata	8.4	2
A0A3M6T6R6	Uncharacterized protein OS=Pocillopora damicornis	4.6	2
A7RRA1	Predicted protein OS=Nematostella vectensis	14.5	1
A0A2B4S2W7	Major vault protein OS=Stylophora pistillata	3.9	3
A7SWV8	Predicted protein OS=Nematostella vectensis	3.9	1
E0YPA3	Heat shock protein 70 OS=Seriatopora hystrix	5.4	3
A0A3M6TSC5	Uncharacterized protein OS=Pocillopora damicornis	2.2	1
T2MEG1	Cell division control protein 42 homolog OS=Hydra vulgaris	21.5	3
Q8WRT4	Beta-catenin (Fragment) OS=Nematostella vectensis	6.3	2
A0A3M6UUZ3	Uncharacterized protein OS=Pocillopora damicornis	6.1	1
A0A2B4S5N4	Alanine--tRNA ligase, cytoplasmic OS=Stylophora pistillata	1.4	1
A0A3M6UAY9	AAA domain-containing protein OS=Pocillopora damicornis	8.9	3
A0A3M6UGG9	Uncharacterized protein OS=Pocillopora damicornis	9.9	7
A7SLT6	6-phosphogluconate dehydrogenase, decarboxylating OS=Nematostella vectensis	2.1	1
A0A2B4S6M0	Tubulin alpha-1D chain OS=Stylophora pistillata	40.1	17
A0A2B4S6V6	Filamin-A OS=Stylophora pistillata	0.8	3
A0A2B4S6W5	PWWP domain-containing protein 2A OS=Stylophora pistillata	2.1	1
A0A3M6TI13	10-formyltetrahydrofolate dehydrogenase OS=Pocillopora damicornis	1.8	2
D1FNZ6	Ribosomal protein L16p/L10e (Fragment) OS=Carukia barnesi	12.7	2
A0A2B4S8M8	Aminopeptidase OS=Stylophora pistillata	1.2	1
A7SU78	Predicted protein OS=Nematostella vectensis	8.1	3
T2MEK8	Ras-related protein Rab-1A OS=Hydra vulgaris	31.7	5
A7S3B3	Predicted protein OS=Nematostella vectensis	7.9	2
J3T9N7	PL10 OS=Euphyllia ancora	5.2	3
T2M856	Dynein light chain OS=Hydra vulgaris	12.4	1
A7RFJ1	Predicted protein OS=Nematostella vectensis	7.7	1
A7SJD2	Predicted protein (Fragment) OS=Nematostella vectensis	3.6	1
A0A2B4SH13	Mechanosensory protein 2 OS=Stylophora pistillata	11.6	3
A0A2B4SE68	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Stylophora pistillata	3	1
A7T1P0	Ribosomal protein L19 OS=Nematostella vectensis	4.6	1
A7SLQ2	Predicted protein OS=Nematostella vectensis	10.2	4
A0A3M6U2E3	40S ribosomal protein S8 OS=Pocillopora damicornis	7.7	1
A0A3M6U683	AAA domain-containing protein OS=Pocillopora damicornis	4.5	1
A7RRK9	Predicted protein (Fragment) OS=Nematostella vectensis	3.7	1
A7T7R5	Predicted protein OS=Nematostella vectensis	3.6	1
A7ST94	Predicted protein OS=Nematostella vectensis	13.2	3
A7RK04	Predicted protein OS=Nematostella vectensis	6.7	1

A0A3M6U381	Uncharacterized protein OS=Pocillopora damicornis	7	1
A0A3M6UNP0	Serine/threonine-protein phosphatase OS=Pocillopora damicornis	7.6	3
A7SAS1	Predicted protein OS=Nematostella vectensis	25.6	4
A7SPP0	synthase subunit beta OS=Nematostella vectensis	17.3	5
T2MGG2	Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment) OS=Hydra vulgaris	5.9	1
A0A3M6TT74	Uncharacterized protein OS=Pocillopora damicornis	1	1
A0A2B4SMR1	Proteasome subunit beta OS=Stylophora pistillata	7.2	1
A0A3M6TT70	V-type proton ATPase proteolipid subunit OS=Pocillopora damicornis	11.7	1
Q58I86	Leonardo protein (Fragment) OS=Hydractinia echinata	26.3	2
A7RV73	Vacuolar protein sorting-associated protein 29 OS=Nematostella vectensis	7.1	1
A0A3M6TLJ1	SH3 domain-containing protein OS=Pocillopora damicornis	2.7	1
A0A2B4SPX6	Plastin-3 OS=Stylophora pistillata	0.9	1
A7SKL5	Predicted protein (Fragment) OS=Nematostella vectensis	3	1
A7SHU3	Predicted protein OS=Nematostella vectensis	34.4	6
A0A2B4SR64	Glutamate dehydrogenase OS=Stylophora pistillata	4.7	2
A0A2B4SRE9	AP complex subunit beta OS=Stylophora pistillata	3.7	3
A0A2B4SSG8	Actin, cytoplasmic OS=Stylophora pistillata	23	4
A0A3M6V2N5	Adenosylhomocysteinase OS=Pocillopora damicornis	2.8	1
A7T2Q5	Serine/threonine-protein phosphatase OS=Nematostella vectensis	9.4	2
A0A2B4SSS4	Polyamine-modulated factor 1-binding protein 1 OS=Stylophora pistillata	1.5	2
A0A2B4STS3	Guanylate cyclase OS=Stylophora pistillata	1.2	1
A0A2B4STV7	Dihydropyrimidine dehydrogenase [NADP(+)] OS=Stylophora pistillata	3.2	2
A0A2B4SU54	Collagen alpha-1(XIV) chain OS=Stylophora pistillata	0.6	1
Q4JG19	Proteasome subunit beta OS=Swiftia exserta	4.9	1
A0A2B4SV07	Tubulin beta chain OS=Stylophora pistillata	46	20
A7SQP1	Predicted protein OS=Nematostella vectensis	15.2	3
A0A3M6TU98	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	9.9	1
A0A3M6TL78	Uncharacterized protein OS=Pocillopora damicornis	1.4	1
A7RID7	Predicted protein OS=Nematostella vectensis	5.9	1
A0A3M6TM92	Proteasome subunit alpha type OS=Pocillopora damicornis	16	2
A0A3M6TPE2	Uncharacterized protein OS=Pocillopora damicornis	4.1	1
A0A3M6T9T2	Coatomer subunit beta OS=Pocillopora damicornis	2.2	2
A0A3M6U4Q7	Uncharacterized protein OS=Pocillopora damicornis	6.6	1
A7T2C3	Predicted protein OS=Nematostella vectensis	1.1	1
A0A2B4SZV5	Ras GTPase-activating-like protein IQGAP1 OS=Stylophora pistillata	1.4	2
A0A2B4T1C4	ATP synthase subunit alpha OS=Stylophora pistillata	23.9	10
A7T1M0	RNA-binding protein 8A (Fragment) OS=Nematostella vectensis	12.5	1
A7SB93	Predicted protein OS=Nematostella vectensis	14.1	2
Q7YZL5	Tubulin alpha chain (Fragment) OS=Aurelia aurita	56.2	17
A0A2Z5WH73	Myosin heavy chain OS=Aurelia sp. 2017-HT	13.2	26
A0A2Z5WH78	Ser-Thr kinase OS=Aurelia sp. 2017-HT	6.6	3
A0A2Z5WH80	Myosin regulatory light chain OS=Aurelia sp. 2017-HT	56.7	8
A0A2Z5WH81	Myosin essential light chain OS=Aurelia sp. 2017-HT	16	2

A0A2Z5WH82	Tropomyosin-1 OS=Aurelia sp. 2017-HT	4.1	1
A7RK57	Predicted protein (Fragment) OS=Nematostella vectensis	2.5	1
A0A3M6T656	Uncharacterized protein OS=Pocillopora damicornis	0.2	1
A7S2J5	Predicted protein OS=Nematostella vectensis	32	5
A7S1T2	Predicted protein OS=Nematostella vectensis	5.5	2
A0A3M6T9K8	Thioredoxin domain-containing protein OS=Pocillopora damicornis	5	1
A0A3M6TG47	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	2.8	1
A0A3M6TIE8	Non-specific serine/threonine protein kinase OS=Pocillopora damicornis	0.8	1
A0A3M6TJC0	Uncharacterized protein OS=Pocillopora damicornis	2.4	1
A0A3M6TLD9	Uncharacterized protein OS=Pocillopora damicornis	10.6	2
A0A3M6TPH2	RuvB-like helicase OS=Pocillopora damicornis	6.7	2
A0A3M6TST2	Uncharacterized protein OS=Pocillopora damicornis	5.4	1
A0A3M6TT35	Uncharacterized protein OS=Pocillopora damicornis	5.8	4
A0A3M6TVL9	Uncharacterized protein OS=Pocillopora damicornis	2.1	1
A0A3M6TVV7	Hcy-binding domain-containing protein OS=Pocillopora damicornis	4.4	1
A0A3M6U1Z2	Uncharacterized protein OS=Pocillopora damicornis	5.2	2
A0A3M6U269	Uncharacterized protein OS=Pocillopora damicornis	4.1	2
A0A3M6U454	Histone H2A OS=Pocillopora damicornis	17.4	2
A0A3M6U4P1	Uncharacterized protein OS=Pocillopora damicornis	2.9	1
A0A3M6U507	Calponin-homology (CH) domain-containing protein OS=Pocillopora damicornis	5.4	1
A7SK13	Predicted protein OS=Nematostella vectensis	1	1
A0A3M6UGM1	V-type proton ATPase subunit a OS=Pocillopora damicornis	4.4	1
A0A3M6UGS0	Uncharacterized protein OS=Pocillopora damicornis	4.2	1
A0A3M6UH78	S4 RNA-binding domain-containing protein OS=Pocillopora damicornis	18.8	6
T2M3D0	Nucleolar protein 58 OS=Hydra vulgaris	5.7	2
A0A3M6UKT7	Uncharacterized protein OS=Pocillopora damicornis	4.8	3
A0A3M6UP81	Uncharacterized protein OS=Pocillopora damicornis	46.3	14
A0A3M6UX10	EGF-like domain-containing protein OS=Pocillopora damicornis	0.7	1
A0A3M6UXC6	Uncharacterized protein OS=Pocillopora damicornis	3.3	1
A0A3M6UYC1	cGMP-dependent protein kinase OS=Pocillopora damicornis	1.7	1
A0A3M6UZ63	Annexin OS=Pocillopora damicornis	9.7	4
A0A3M6V116	Uncharacterized protein OS=Pocillopora damicornis	0.7	1
A0A3M6V235	Uncharacterized protein OS=Pocillopora damicornis	1	1
A0A515L5S5	Beta-tubulin (Fragment) OS=Porites lutea	29.7	4
A3F9E8	Histone H2B (Fragment) OS=Anacropora matthai	9.4	1
A4UAH1	Beta-catenin OS=Podocoryna carnea	4.3	2
A7RGP3	Predicted protein (Fragment) OS=Nematostella vectensis	13.4	1
A7RHF7	Eukaryotic translation initiation factor 6 OS=Nematostella vectensis	10.2	1
A7RHP7	Superoxide dismutase OS=Nematostella vectensis	4.1	1
A7RHS7	Predicted protein OS=Nematostella vectensis	4.6	4
A7RIF0	T-complex protein 1 subunit eta OS=Nematostella vectensis	4.8	2
Q5U9S0	Ubiquitin/ribosomal L40 fusion protein OS=Scleronephthya gracillimum	36.7	4
A7RJD9	Predicted protein OS=Nematostella vectensis	19	2

A7RKR4	Predicted protein OS=Nematostella vectensis	1.3	1
A7RLF6	Predicted protein (Fragment) OS=Nematostella vectensis	7.5	1
A7RMQ8	Proteasome subunit alpha type OS=Nematostella vectensis	8.6	1
A7RN37	Predicted protein OS=Nematostella vectensis	6.5	2
A7RNE1	Predicted protein OS=Nematostella vectensis	3	1
A7RNH9	Predicted protein OS=Nematostella vectensis	4.3	2
A7RQD2	Predicted protein OS=Nematostella vectensis	3.1	2
A7RQF7	Predicted protein OS=Nematostella vectensis	8.7	2
A7RQR3	10-formyltetrahydrofolate dehydrogenase OS=Nematostella vectensis	1.4	1
A7RRG4	Actin-related protein 2/3 complex subunit 4 OS=Nematostella vectensis	16.7	2
A7RRK0	Predicted protein (Fragment) OS=Nematostella vectensis	8.9	1
A7RT97	Predicted protein OS=Nematostella vectensis	4.5	4
A7RU93	Predicted protein OS=Nematostella vectensis	12	2
A7RUF9	Predicted protein (Fragment) OS=Nematostella vectensis	8.9	2
A7RUT6	Kinesin-like protein (Fragment) OS=Nematostella vectensis	1.6	1
A7RVC0	Clathrin heavy chain OS=Nematostella vectensis	4.7	6
A7RVD9	Tubulin alpha chain OS=Nematostella vectensis	41.5	14
A7RVT1	Predicted protein OS=Nematostella vectensis	1.2	1
A7S018	Obg-like ATPase 1 OS=Nematostella vectensis	3.8	1
A7S0L1	Vacuolar proton pump subunit B OS=Nematostella vectensis	5.1	2
A7S183	Predicted protein OS=Nematostella vectensis	4.2	1
A7S1I1	Predicted protein OS=Nematostella vectensis	1.6	1
A7S214	Predicted protein OS=Nematostella vectensis	38.7	7
A7S260	Predicted protein OS=Nematostella vectensis	2.8	1
A7S289	Predicted protein OS=Nematostella vectensis	17.9	1
A7S2F7	Isocitrate dehydrogenase [NADP] OS=Nematostella vectensis	5.4	2
A7S2Z9	Dimethylaniline monooxygenase [N-oxide-forming] OS=Nematostella vectensis	1.9	1
A7S394	Aminopeptidase (Fragment) OS=Nematostella vectensis	1.4	1
A7S310	Predicted protein (Fragment) OS=Nematostella vectensis	2.8	2
T2MEK4	60S ribosomal protein L8 OS=Hydra vulgaris	3.9	1
A7S5Z0	Predicted protein OS=Nematostella vectensis	2.8	1
A7S7K4	Predicted protein OS=Nematostella vectensis	7.9	2
A7S8H2	Predicted protein OS=Nematostella vectensis	2.5	1
A7S8Z2	RuvB-like helicase OS=Nematostella vectensis	4.9	2
T2MF79	Transforming protein RhoA OS=Hydra vulgaris	29.2	3
A7SAZ3	Acetyl-coenzyme A synthetase OS=Nematostella vectensis	2	1
A7SCK6	Predicted protein OS=Nematostella vectensis	11.3	2
A7SD28	Predicted protein OS=Nematostella vectensis	7.1	1
A7SDY3	Tubulin alpha chain OS=Nematostella vectensis	44.6	17
A7SF39	Predicted protein OS=Nematostella vectensis	3.3	1
A7SFE5	Predicted protein OS=Nematostella vectensis	2.4	1
A7SFJ6	Predicted protein OS=Nematostella vectensis	1	1
A7SG05	GTP-binding nuclear protein OS=Nematostella vectensis	10.1	2

A7SHH5	Protein disulfide-isomerase (Fragment) OS=Nematostella vectensis	2.5	1
A7SJR5	Predicted protein OS=Nematostella vectensis	1.2	1
A7SMZ7	Dynein light chain roadblock OS=Nematostella vectensis	12.5	1
A7SPM9	Predicted protein (Fragment) OS=Nematostella vectensis	2.3	1
A7SPQ4	Predicted protein OS=Nematostella vectensis	16.5	3
A7SSL5	Predicted protein OS=Nematostella vectensis	8.4	5
A7SU70	Predicted protein OS=Nematostella vectensis	5.6	1
A7SUX1	Predicted protein OS=Nematostella vectensis	1.5	1
A7SVT6	Predicted protein OS=Nematostella vectensis	1	1
A7SW17	Predicted protein (Fragment) OS=Nematostella vectensis	2.8	2
A7SWC2	Predicted protein OS=Nematostella vectensis	2.8	1
A7SWR9	Predicted protein OS=Nematostella vectensis	8.6	2
A7SXN2	Peptidyl-prolyl cis-trans isomerase OS=Nematostella vectensis	25.2	2
A7SZW4	Purple acid phosphatase (Fragment) OS=Nematostella vectensis	1.9	1
A7T284	Predicted protein OS=Nematostella vectensis	11.5	2
A7T3D9	Predicted protein OS=Nematostella vectensis	2.9	1
A7TCL7	Histone H2A OS=Nematostella vectensis	38.9	13
A8DX89	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Urticina eques	8.4	2
B3EZK6	Ribosomal protein S5 (Fragment) OS=Cyanea capillata	22.8	3
B5MG02	Beta tubulin (Fragment) OS=Cirripathes sp. TW24	31.2	5
C1IS27	Clathrin heavy chain (Fragment) OS=Carukia barnesi	8.8	1
C1IS28	Clathrin heavy chain (Fragment) OS=Carukia barnesi	14.4	3
D1FP08	Ribosomal protein L35Ae OS=Malo kingi	13.3	2
E1CKX4	Nematogalectin-related OS=Aurelia aurita	8	2
E9AI11	Ribosomal protein S6 kinase OS=Hydra vulgaris	1.3	1
G3LIV9	Heat shock cognate protein 71 OS=Hydractinia echinata	6.9	5
G8DM04	Cytochrome c oxidase subunit 2 OS=Chrysaora quinquecirrha	6.9	1
G9ISX7	Cytochrome c oxidase subunit 2 OS=Pelagia noctiluca	8.1	1
I2G9E9	Myosin II heavy chain, smooth/non-muscle-type (Fragment) OS=Clytia hemisphaerica	3.4	1
K0A063	Beta-actin (Fragment) OS=Chrysaora quinquecirrha	56.1	16
M1E2A8	Calmodulin (Fragment) OS=Rhizostoma octopus	42.6	3
O01715	Protein kinase C OS=Hydra vulgaris	1.8	1
O44222	Voltage-gated calcium channel beta subunit OS=Cyanea capillata	2.4	1
Q0H8V3	Heat shock protein 70 (Fragment) OS=Cnidaria environmental sample	12.2	2
Q2XWU1	Rab11 protein OS=Aiptasia pulchella	22.5	5
Q56GW1	60S ribosomal protein L12 (Fragment) OS=Hydractinia echinata	16.5	1
Q56GW5	40S ribosomal protein S4 (Fragment) OS=Hydractinia echinata	14.3	1
Q5EN79	Ganglioside M2 activator-like protein OS=Aurelia aurita	12.3	3
Q5EN88	Actin-related protein 2/3 complex subunit 5 OS=Aurelia aurita	7.3	1
Q5EN91	Putative 3-hydroxyacyl-Coenzyme A dehydrogenase (Fragment) OS=Aurelia aurita	32.6	4
Q6PTK3	Triosephosphate isomerase (Fragment) OS=Obelia sp. KJP-2004	11.8	2
Q6YCH0	Ribosomal protein S3 (Fragment) OS=Hydra vulgaris	13	3
Q7YZI4	90-kDa heat-shock protein (Fragment) OS=Aurelia aurita	16	5

Q7YZK4	Tubulin beta chain (Fragment) OS=Aurelia aurita	50.6	18
Q8WP37	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Dendronephthya klunzingeri	4.3	1
Q967E1	Heat shock protein 90 OS=Dendronephthya klunzingeri	6.5	4
Q967H6	Nucleoside diphosphate kinase OS=Hydra vulgaris	6	1
Q9GUZ6	PL10-related protein CnPL10 (Fragment) OS=Sandaria malayensis	32.8	3
R9S2M2	Elongation factor 1-alpha OS=Aurelia aurita	17.1	7
S5LXY9	ELAV OS=Hydractinia echinata	2.6	1
T2M2P5	RuvB-like helicase OS=Hydra vulgaris	8.4	3
T2M2X1	Adenylate kinase isoenzyme 5 OS=Hydra vulgaris	3.3	2
T2M3D1	Eukaryotic translation initiation factor 3 subunit L OS=Hydra vulgaris	2.5	1
T2M3I7	RuvB-like helicase OS=Hydra vulgaris	6.6	2
T2M4D5	Leucyl-tRNA synthetase,cytoplasmic (Fragment) OS=Hydra vulgaris	1.6	1
T2M4N6	Guanine nucleotide-binding protein subunit beta-4 (Fragment) OS=Hydra vulgaris	6.7	2
T2M5D3	Protein transport protein Sec61 subunit alpha isoform 2 OS=Hydra vulgaris	4.2	2
T2M5K6	Transmembrane 9 superfamily member OS=Hydra vulgaris	1.7	1
T2M644	Microtubule-associated proteins 1A/1B light chain 3C OS=Hydra vulgaris	32.8	3
T2M694	Prohibitin OS=Hydra vulgaris	3.8	1
T2M6B6	Ethanolamine-phosphate cytidyltransferase OS=Hydra vulgaris	3.5	2
T2M6G7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Hydra vulgaris	1.4	1
T2M9L4	Cleavage and polyadenylation specificity factor subunit 7 OS=Hydra vulgaris	2.6	1
T2MAB0	Staphylococcal nuclease domain-containing protein OS=Hydra vulgaris	2.6	2
T2MBN1	Kynurenine--oxoglutarate transaminase 3 OS=Hydra vulgaris	2.9	1
T2MCN2	26S proteasome non-ATPase regulatory subunit 6 (Fragment) OS=Hydra vulgaris	3.3	1
T2MCX1	10-formyltetrahydrofolate dehydrogenase OS=Hydra vulgaris	1.3	1
T2MCX5	Vacuolar protein sorting-associated protein 26B (Fragment) OS=Hydra vulgaris	4	1
T2MD22	RalA-binding protein 1 (Fragment) OS=Hydra vulgaris	1.8	1
T2MD34	Serine/threonine protein phosphatase 2A regulatory subunit OS=Hydra vulgaris	2.8	1
T2MD44	Major vault protein OS=Hydra vulgaris	2.7	3
T2MDB0	Eukaryotic initiation factor 4A-II OS=Hydra vulgaris	5.9	2
T2MDF0	Histone-binding protein RBBP4 OS=Hydra vulgaris	3	1
T2MDG4	Flotillin-2 OS=Hydra vulgaris	9.1	3
T2MDK8	Spliceosome RNA helicase DDX39B OS=Hydra vulgaris	7.6	3
T2MDS7	Src substrate cortactin OS=Hydra vulgaris	3.7	1
T2MDU7	ADP-ribosylation factor 5 OS=Hydra vulgaris	19.6	2
T2MEB5	ADP-ribosylation factor 1 OS=Hydra vulgaris	38.7	6
T2MEB6	26S protease regulatory subunit 8 OS=Hydra vulgaris	10.5	3
T2MEH3	Casein kinase II subunit alpha OS=Hydra vulgaris	5.1	1
T2MEI1	AP-2 complex subunit beta (Fragment) OS=Hydra vulgaris	5	4
T2MEI3	40S ribosomal protein S21 (Fragment) OS=Hydra vulgaris	17.3	1
T2MEN2	40S ribosomal protein S6 OS=Hydra vulgaris	4.8	1
T2MEN5	Clathrin heavy chain OS=Hydra vulgaris	6.1	7
T2MEP2	40S ribosomal protein S18 OS=Hydra vulgaris	17.4	3
T2MEQ7	26S protease regulatory subunit 4 OS=Hydra vulgaris	5.7	2

T2MES1	40S ribosomal protein S15a OS=Hydra vulgaris	10.8	1
T2MET3	Ras-related protein R-Ras2 OS=Hydra vulgaris	18.7	3
T2MET7	Signal transducer and activator of transcription OS=Hydra vulgaris	1.3	1
T2MEV1	Tubulin beta chain (Fragment) OS=Hydra vulgaris	31.6	14
T2MEW9	Calcineurin subunit B type 1 OS=Hydra vulgaris	5.9	1
T2MEY1	60S ribosomal protein L11 (Fragment) OS=Hydra vulgaris	7.2	1
T2MF07	60S ribosomal protein L23a (Fragment) OS=Hydra vulgaris	9.6	1
T2MF38	Adenylate kinase OS=Hydra vulgaris	4.1	2
T2MF93	Ras-related protein Rab-14 (Fragment) OS=Hydra vulgaris	29.9	6
T2MFD2	60S ribosomal protein L26 OS=Hydra vulgaris	6.2	2
T2MFH7	Poly(RC)-binding protein 3 (Fragment) OS=Hydra vulgaris	4.1	1
T2MFJ1	Stress-70 protein, mitochondrial (Fragment) OS=Hydra vulgaris	8.2	3
T2MFM1	Transitional endoplasmic reticulum ATPase (Fragment) OS=Hydra vulgaris	13.1	7
T2MFR0	26S protease regulatory subunit 6B OS=Hydra vulgaris	4.7	2
T2MFR8	Ras-related protein Rab-7a OS=Hydra vulgaris	37.4	8
T2MFU8	Rab GDP dissociation inhibitor (Fragment) OS=Hydra vulgaris	6.3	2
T2MFY6	Hippocalcin-like protein 1 OS=Hydra vulgaris	17.8	3
T2MG06	Transaldolase OS=Hydra vulgaris	6.2	2
T2MG27	26S protease regulatory subunit 7 OS=Hydra vulgaris	5.7	2
T2MG36	Myosin-10 OS=Hydra vulgaris	1.7	5
T2MG47	Radixin OS=Hydra vulgaris	4.3	2
T2MG56	Coatomer subunit delta OS=Hydra vulgaris	3.9	2
T2MG68	Proteasome subunit beta OS=Hydra vulgaris	6.2	1
T2MGA3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Hydra vulgaris	3.7	2
T2MGD8	Eukaryotic initiation factor 4A-III (Fragment) OS=Hydra vulgaris	5	2
T2MGF7	Malate dehydrogenase, mitochondrial OS=Hydra vulgaris	13.7	3
T2MGR0	60S ribosomal protein L17 OS=Hydra vulgaris	14.2	2
T2MGS3	cAMP-dependent protein kinase catalytic subunit alpha OS=Hydra vulgaris	3.4	1
T2MGT2	Transketolase OS=Hydra vulgaris	3.5	2
T2MGX7	60S ribosomal protein L13 (Fragment) OS=Hydra vulgaris	4.7	1
T2MGZ6	ATP synthase subunit alpha OS=Hydra vulgaris	17.2	7
T2MH18	Adenosylhomocysteinase OS=Hydra vulgaris	4.6	2
T2MH23	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial (Fragment) OS=Hydra vulgaris	2.5	1
T2MH41	78 kDa glucose-regulated protein OS=Hydra vulgaris	8.4	6
T2MH44	Vacuolar proton pump subunit B (Fragment) OS=Hydra vulgaris	6	2
T2MH46	Filamin-A OS=Hydra vulgaris	0.9	3
T2MH95	Vinculin OS=Hydra vulgaris	1	1
T2MHA2	Bifunctional aminoacyl-tRNA synthetase (Fragment) OS=Hydra vulgaris	1	1
T2MHF1	Elongation factor 2 OS=Hydra vulgaris	3.3	2
T2MHH5	Myosin-6 OS=Hydra vulgaris	2.6	4
T2MHI3	Flotillin-1 (Fragment) OS=Hydra vulgaris	3.4	1
T2MHI5	Alpha-actinin-1 OS=Hydra vulgaris	5.1	5
T2MHI8	Ras-related protein Ral-A OS=Hydra vulgaris	5.6	1

T2MHJ7	60 kDa heat shock protein,mitochondrial (Fragment) OS=Hydra vulgaris	2	1
T2MHN7	Citrate synthase OS=Hydra vulgaris	2.6	1
T2MHT5	Heat shock protein HSP 90-alpha OS=Hydra vulgaris	9.8	9
T2MIB9	AP-2 complex subunit alpha OS=Hydra vulgaris	1	1
T2MIQ9	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial (Fragment) OS=Hydra vulgaris	1.8	1
W8PTQ2	Peroxisredoxin 4 OS=Cyanea capillata	22.7	5
W8Q1J8	Glyceraldehyde-3-phosphate dehydrogenase OS=Cyanea capillata	9.6	2

1.2 Identification of protein from nematocyst

Table G-2. List of proteins identified (452 proteins) from nematocyst of highly venomous jellyfish by using extraction of SDS coupled with sonication. The proteins were derived from in-gel digestion experiment. Database of taxonomy Cnidaria (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptide
A0A3M6UR37	Eukaryotic translation initiation factor 3 subunit I OS=Pocillopora damicornis	3.8	1
T2MCI6	Transmembrane emp24 domain-containing protein 2 OS=Hydra vulgaris	4.6	1
E5F7D0	Non-muscle actin II OS=Hydractinia echinata	49.7	17
T2MGY6	Sodium/potassium-transporting ATPase subunit alpha OS=Hydra vulgaris	7.8	5
T2MGR0	60S ribosomal protein L17 OS=Hydra vulgaris	8.7	1
P38984	40S ribosomal protein SA OS=Hydra viridissima	4.1	1
P41113	Actin-3 OS=Podocoryna carnea	47.6	16
P51539	Ras-like protein RAS1 OS=Hydra vulgaris	19.1	4
P62184	Calmodulin OS=Renilla reniformis	58.4	4
A7S9A5	Predicted protein OS=Nematostella vectensis	3.8	1
B1PM92	Calmodulin OS=Acropora muricata	58.4	4
A0A069DM56	Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Clytia hemisphaerica	4	1
A0A069DMJ2	Glutamate deshydrogenase (Fragment) OS=Clytia hemisphaerica	6.5	3
A0A0C2I839	Cytosol aminopeptidase OS=Thelohanellus kitauei	2.4	1
A7SRV8	40S ribosomal protein S4 OS=Nematostella vectensis	4.6	2
A0A0C2ISA3	Serine/threonine-protein phosphatase OS=Thelohanellus kitauei	5.7	1
A0A0C2IZS4	Outer membrane protein TolC OS=Thelohanellus kitauei	3.8	1
T2MF79	Transforming protein RhoA OS=Hydra vulgaris	16.7	3
A0A0C2JBA7	40S ribosomal protein S23 OS=Thelohanellus kitauei	8.4	1
A0A0C2JEY5	6-phosphogluconate dehydrogenase, decarboxylating OS=Thelohanellus kitauei	7	3
D1FNZ6	Ribosomal protein L16p/L10e (Fragment) OS=Carukia barnesi	5.4	1
A0A0C2M5P0	Outer membrane protein A OS=Thelohanellus kitauei	5.6	2
A0A0C2MCV7	60S ribosomal protein L34 OS=Thelohanellus kitauei	7.4	1
A0A0C2MNQ3	Myosin-10 OS=Thelohanellus kitauei	4.1	3
A0A0C2MS24	Methylmalonyl-CoA mutase, mitochondrial OS=Thelohanellus kitauei	7.2	1
A0A0C2MT43	Heat shock protein HSP 90-alpha 1 OS=Thelohanellus kitauei	1.7	1

A0A0C2MUS2	60 kDa chaperonin OS=Thelohanellus kitauei	4.7	1
A0A0C2N200	Ras-related protein RABA2a OS=Thelohanellus kitauei	5.3	1
A0A0C2N354	ATP synthase subunit beta OS=Thelohanellus kitauei	9	3
A0A0C2N442	Ras-related protein Rab-11A OS=Thelohanellus kitauei	5.3	1
A0A0C4VZ14	78 kDa glucose-regulated protein (Fragment) OS=Capnella imbricata	11.9	3
A0A2B4STX3	Heat shock protein 70 B2 OS=Stylophora pistillata	6.1	3
A0A0U2JZC1	Gs protein alpha subunit OS=Tripedalia cystophora	8.6	3
A0A169Q0T5	Glyceraldehyde-3-phosphate dehydrogenase OS=Aurelia sp. SETO	6.8	2
A0A2Z5WH77	Actin-1 OS=Aurelia sp. 2017-HT	50.3	18
A0A1V0IGH5	Histone H2B OS=Hydra vulgaris	17.9	2
A0A1B3IQX8	Histone H2A OS=Hydractinia echinata	29	2
A0A1L2A726	Superoxide dismutase [Cu-Zn] OS=Cyanea capillata	24	3
A0A1U9XQR0	Fructose-bisphosphate aldolase OS=Aurelia sp. 1 GW-2014	10	4
A0A288W1V0	Mitogen-activated protein kinase OS=Aurelia aurita	13.6	3
A0A288W1V6	Mitogen-activated protein kinase OS=Aurelia aurita	8.5	2
A0A2B4R364	GTP-binding protein TypA/BipA-like OS=Stylophora pistillata	4.5	1
A0A2B4R6Q9	Fumarate hydratase class II OS=Stylophora pistillata	1.6	1
A0A2B4R9G5	Histone H2B OS=Stylophora pistillata	7.3	2
A0A2B4R9Q9	Histone H4 OS=Stylophora pistillata	44.3	16
A0A2B4R9T9	Chaperone protein DnaK OS=Stylophora pistillata	2.3	1
A0A2B4RAR4	60S ribosomal protein L4 (Fragment) OS=Stylophora pistillata	7.4	2
A7RQD8	Predicted protein OS=Nematostella vectensis	39.8	4
A0A3M6TT35	Uncharacterized protein OS=Pocillopora damicornis	5.7	4
T2MHV0	Aldehyde dehydrogenase, mitochondrial OS=Hydra vulgaris	2.3	1
A7SWU4	Predicted protein (Fragment) OS=Nematostella vectensis	8	2
T2MEZ1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial (Fragment) OS=Hydra vulgaris	3.6	2
A0A2B4RHG2	V-type proton ATPase catalytic subunit A OS=Stylophora pistillata	21.7	9
A0A2B4RHH5	Enoyl-CoA hydratase, mitochondrial OS=Stylophora pistillata	11.9	2
A0A2B4RI23	GTP-binding protein SAR1 OS=Stylophora pistillata	6.8	1
A0A3M6V529	Ribosomal_L23eN domain-containing protein (Fragment) OS=Pocillopora damicornis	13.3	2
A0A2B4RJH1	Tubulin beta chain OS=Stylophora pistillata	61.5	24
A0A3M6TIL0	Uncharacterized protein OS=Pocillopora damicornis	6.5	1
A0A3M6U938	Kinesin motor domain-containing protein OS=Pocillopora damicornis	2.3	1
A0A2B4RKG6	U6 snRNA-associated Sm-like protein LSm8 OS=Stylophora pistillata	21.3	1
A0A2B4RKT3	26S proteasome non-ATPase regulatory subunit 2 OS=Stylophora pistillata	1.7	1
A0A2B4RKT5	Actin-related protein 2 OS=Stylophora pistillata	6.5	2
A7RRD6	Predicted protein OS=Nematostella vectensis	1.7	1
A0A3M6T5M4	Glucose-6-phosphate 1-dehydrogenase OS=Pocillopora damicornis	1.9	1
A0A2B4RLP4	Early endosome antigen 1 OS=Stylophora pistillata	0.7	1
A0A3M6V3V6	Uncharacterized protein OS=Pocillopora damicornis	13.1	3
A0A2B4RPA9	Clathrin heavy chain OS=Stylophora pistillata	8.3	12
A7T120	F-actin-capping protein subunit beta (Fragment) OS=Nematostella vectensis	13.3	2
A0A2B4RPD3	Endoplasmic reticulum chaperone OS=Stylophora pistillata	2.7	2

A7SQS1	Malate dehydrogenase OS=Nematostella vectensis	4.7	1
A0A3M6V4M9	Uncharacterized protein OS=Pocillopora damicornis	9.5	3
A0A3M6U9J9	Uncharacterized protein OS=Pocillopora damicornis	4.2	2
A0A3M6TQ41	Catalase OS=Pocillopora damicornis	8.3	3
Q93116	Ub52 OS=Acropora millepora	36.4	4
A0A2B4RSF5	Mucin-4 OS=Stylophora pistillata	0.2	1
A0A2B4RSK7	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Stylophora pistillata	2.3	1
A0A2B4RTD9	Catenin alpha-2 OS=Stylophora pistillata	1.8	2
A0A2B4RU80	Coatomer subunit beta OS=Stylophora pistillata	3	2
Q2F6G0	Prohibitin (Fragment) OS=Anthopleura elegantissima	10	1
A0A2B4RVD0	Ribonuclease UK114 OS=Stylophora pistillata	13.7	1
A0A2B4RWB5	Elongation factor 1-gamma OS=Stylophora pistillata	2.6	1
A0A3M6UGY3	UBIQUITIN_CONJUGAT_2 domain-containing protein OS=Pocillopora damicornis	16.4	2
A0A2B4RXI4	Ras-related protein Rab-5B OS=Stylophora pistillata	16.2	3
A7S494	40S ribosomal protein S27 OS=Nematostella vectensis	25	2
A0A2B4RYR5	60S ribosomal protein L5 (Fragment) OS=Stylophora pistillata	11.9	2
A7RTW3	Predicted protein OS=Nematostella vectensis	2.6	1
A0A3M6THY8	Uncharacterized protein OS=Pocillopora damicornis	1.7	1
A0A3M6TNT3	Coatomer subunit delta OS=Pocillopora damicornis	2.4	1
A0A2B4S092	Multifunctional fusion protein OS=Stylophora pistillata	0.7	2
A0A2B4S0G4	T-complex protein 1 subunit zeta OS=Stylophora pistillata	4.9	1
A7SGM6	Predicted protein OS=Nematostella vectensis	4.8	2
A0A2B4S129	Peroxiredoxin-1 OS=Stylophora pistillata	4	1
Q6YCHO	Ribosomal protein S3 (Fragment) OS=Hydra vulgaris	14.3	3
A7RUL8	Predicted protein (Fragment) OS=Nematostella vectensis	3.9	2
A0A2B4S2V2	Cathepsin B OS=Stylophora pistillata	5.7	1
A7SWV8	Predicted protein OS=Nematostella vectensis	3.9	1
E0YPA3	Heat shock protein 70 OS=Seriatopora hystrix	3.6	2
A0A3M6UK04	Uncharacterized protein OS=Pocillopora damicornis	0.8	2
T2MEG1	Cell division control protein 42 homolog OS=Hydra vulgaris	27.2	4
A0A2B4S569	RuvB-like helicase OS=Stylophora pistillata	9.8	3
A0A2B4S5E4	ADP-ribosylation factor 6 OS=Stylophora pistillata	8.6	1
A0A2B4S5N4	Alanine--tRNA ligase, cytoplasmic OS=Stylophora pistillata	1.4	1
A0A3M6UGG9	Uncharacterized protein OS=Pocillopora damicornis	18.3	11
A0A2B4S643	Doublesex-and mab-3-related transcription factor A2 OS=Stylophora pistillata	3.3	1
A0A2B4S6M0	Tubulin alpha-1D chain OS=Stylophora pistillata	44.7	19
A7SHC3	Predicted protein (Fragment) OS=Nematostella vectensis	3.3	1
A0A2B4S6V6	Filamin-A OS=Stylophora pistillata	0.8	3
A0A2B4S736	Vacuolar proton pump subunit B OS=Stylophora pistillata	10.3	3
A0A3M6TMR5	Uncharacterized protein OS=Pocillopora damicornis	10.4	3
A0A2B4S8M8	Aminopeptidase OS=Stylophora pistillata	1.2	1
A0A3M6TK98	Uncharacterized protein OS=Pocillopora damicornis	4.2	2
A7RIX7	Proteasome subunit alpha type OS=Nematostella vectensis	4.1	1

A7SU78	Predicted protein OS=Nematostella vectensis	5.2	2
T2MEK8	Ras-related protein Rab-1A OS=Hydra vulgaris	31.7	5
Q9Y208	G protein a subunit 2 (Fragment) OS=Hydra vulgaris	5.2	1
A0A2B4SBE9	Alpha-mannosidase OS=Stylophora pistillata	1.7	1
A0A3M6UX22	AMP-binding domain-containing protein OS=Pocillopora damicornis	2.1	1
A0A2B4SCP3	Peptidylprolyl isomerase OS=Stylophora pistillata	10.6	2
J3T9N7	PL10 OS=Euphyllia ancora	5.2	3
T2M856	Dynein light chain OS=Hydra vulgaris	24.7	2
A0A3M6T7R7	Small nuclear ribonucleoprotein Sm D2 OS=Pocillopora damicornis	24.6	3
A7RFJ1	Predicted protein OS=Nematostella vectensis	7.7	1
A0A2B4SH13	Mechanosensory protein 2 OS=Stylophora pistillata	11.6	3
A0A2B4SE68	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Stylophora pistillata	3	1
A7T1P0	Ribosomal protein L19 OS=Nematostella vectensis	4.6	1
A0A3M6U2E3	40S ribosomal protein S8 OS=Pocillopora damicornis	7.7	1
A7RKK8	Predicted protein (Fragment) OS=Nematostella vectensis	4.7	1
T2M8Q9	Probable aminopeptidase NPEPL1 OS=Hydra vulgaris	2.6	1
A7RRK9	Predicted protein (Fragment) OS=Nematostella vectensis	3.7	1
A0A3M6UEF8	Histone deacetylase OS=Pocillopora damicornis	5	2
A7RK04	Predicted protein OS=Nematostella vectensis	6.7	1
A0A3M6TKN8	Transaldolase OS=Pocillopora damicornis	3.4	2
A0A3M6TSM5	Uncharacterized protein OS=Pocillopora damicornis	1.5	1
A7SPP0	ATP synthase subunit beta OS=Nematostella vectensis	19.7	6
A0A3M6TT74	Uncharacterized protein OS=Pocillopora damicornis	1	1
A0A3M6TT70	V-type proton ATPase proteolipid subunit OS=Pocillopora damicornis	11.7	1
Q58I86	Leonardo protein (Fragment) OS=Hydractinia echinata	26.3	2
A7RV73	Vacuolar protein sorting-associated protein 29 OS=Nematostella vectensis	12.6	2
A0A2B4SPX6	Plastin-3 OS=Stylophora pistillata	1	2
A7SI51	Proteasome subunit alpha type (Fragment) OS=Nematostella vectensis	6.5	1
A7SMW8	Predicted protein OS=Nematostella vectensis	5.4	1
A7SKL5	Predicted protein (Fragment) OS=Nematostella vectensis	3	1
A7SHU3	Predicted protein OS=Nematostella vectensis	33.5	6
A7SMT0	Predicted protein OS=Nematostella vectensis	4.6	1
A0A2B4SR64	Glutamate dehydrogenase OS=Stylophora pistillata	7.3	3
T2MFM0	Tricarboxylate transport protein, mitochondrial OS=Hydra vulgaris	7.3	2
A0A3M6TAX3	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Pocillopora damicornis	4	2
A0A2B4SSG5	Putative E3 ubiquitin-protein ligase hula OS=Stylophora pistillata	1.4	1
A0A2B4SSG8	Actin, cytoplasmic OS=Stylophora pistillata	20.6	4
A0A3M6V2N5	Adenosylhomocysteinase OS=Pocillopora damicornis	2.8	1
A7T2Q5	Serine/threonine-protein phosphatase OS=Nematostella vectensis	9.4	2
A0A2B4ST58	Dickkopf-related protein 3 OS=Stylophora pistillata	7.5	1
A0A3M6TL03	Phospholipid scramblase OS=Pocillopora damicornis	6.8	1
T2MBK6	Integrator complex subunit 11 (Fragment) OS=Hydra vulgaris	3	1
A0A2B4STP6	Kinesin-like protein KIF28P OS=Stylophora pistillata	1.4	1

A0A2B4SU74	G protein-coupled receptor kinase OS=Stylophora pistillata	5.5	2
A0A3M6TUZ8	Isocitrate dehydrogenase [NADP] OS=Pocillopora damicornis	5.4	2
A0A2B4SV07	Tubulin beta chain OS=Stylophora pistillata	59.4	24
A7SQP1	Predicted protein OS=Nematostella vectensis	15.2	3
A0A3M6TU98	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	9.9	1
A7RID7	Predicted protein OS=Nematostella vectensis	5.9	1
A0A2B4SW93	Dynein heavy chain 5, axonemal OS=Stylophora pistillata	0.6	2
A0A3M6TM92	Proteasome subunit alpha type OS=Pocillopora damicornis	16	2
A0A3M6TPE2	Uncharacterized protein OS=Pocillopora damicornis	4.1	1
A0A3M6U4Q7	Uncharacterized protein OS=Pocillopora damicornis	6.6	1
A7T2C3	Predicted protein OS=Nematostella vectensis	1.1	1
A0A3M6TLP2	Uncharacterized protein OS=Pocillopora damicornis	12.6	1
A0A2B4SZV5	Ras GTPase-activating-like protein IQGAP1 OS=Stylophora pistillata	1.4	2
A7RFF5	Predicted protein OS=Nematostella vectensis	1.4	1
A0A2B4T1C4	ATP synthase subunit alpha OS=Stylophora pistillata	16.3	8
A7S5C8	Predicted protein (Fragment) OS=Nematostella vectensis	2.1	1
A7SBR9	Predicted protein OS=Nematostella vectensis	4.9	2
A7T1M0	RNA-binding protein 8A (Fragment) OS=Nematostella vectensis	12.5	1
A0A2Z5WH73	Myosin heavy chain OS=Aurelia sp. 2017-HT	12.6	30
A0A2Z5WH78	Ser-Thr kinase OS=Aurelia sp. 2017-HT	3.6	2
A0A2Z5WH80	Myosin regulatory light chain OS=Aurelia sp. 2017-HT	50.3	6
A0A2Z5WH81	Myosin essential light chain OS=Aurelia sp. 2017-HT	7.3	1
A0A2Z5WH82	Tropomyosin-1 OS=Aurelia sp. 2017-HT	10.7	2
A7S2J5	Predicted protein OS=Nematostella vectensis	31.4	5
A0A3M6T8X3	Calcium-transporting ATPase OS=Pocillopora damicornis	3.1	2
A7S1T2	Predicted protein OS=Nematostella vectensis	5.5	2
A0A3M6TA99	Uncharacterized protein OS=Pocillopora damicornis	14.2	1
A7SXV0	Predicted protein OS=Nematostella vectensis	3	1
A0A3M6TIF8	Uncharacterized protein OS=Pocillopora damicornis	5.1	1
A0A3M6TL25	Profilin OS=Pocillopora damicornis	10	1
A0A3M6TLD9	Uncharacterized protein OS=Pocillopora damicornis	10.6	2
A0A3M6TLS3	Uncharacterized protein OS=Pocillopora damicornis	2.3	1
A7S2G4	Predicted protein (Fragment) OS=Nematostella vectensis	16.5	2
A0A3M6TVL9	Uncharacterized protein OS=Pocillopora damicornis	2.1	1
A0A3M6TVV7	Hcy-binding domain-containing protein OS=Pocillopora damicornis	4.4	1
A0A3M6U1Z2	Uncharacterized protein OS=Pocillopora damicornis	2.7	1
A0A3M6U269	Uncharacterized protein OS=Pocillopora damicornis	4.1	2
A0A3M6U454	Histone H2A OS=Pocillopora damicornis	17.4	2
A0A3M6U4P1	Uncharacterized protein OS=Pocillopora damicornis	6.7	2
A0A3M6U507	Calponin-homology (CH) domain-containing protein OS=Pocillopora damicornis	5.4	1
A0A3M6U6D1	UBR-type domain-containing protein OS=Pocillopora damicornis	0.3	1
A7S690	Predicted protein (Fragment) OS=Nematostella vectensis	10.5	1
A0A3M6U901	EF-hand domain-containing protein OS=Pocillopora damicornis	2.8	2

A0A3M6UD47	Metalloendopeptidase (Fragment) OS=Pocillopora damicornis	2.3	1
A0A3M6UEC5	Serine/threonine-protein phosphatase OS=Pocillopora damicornis	10.6	4
A0A3M6UGM1	V-type proton ATPase subunit a OS=Pocillopora damicornis	4.4	1
A0A3M6UH10	Par3_HAL_N_term domain-containing protein OS=Pocillopora damicornis	1.5	1
A0A3M6UH78	S4 RNA-binding domain-containing protein OS=Pocillopora damicornis	14.1	4
T2M3D0	Nucleolar protein 58 OS=Hydra vulgaris	5.7	2
A0A3M6UKT7	Uncharacterized protein OS=Pocillopora damicornis	6.5	4
A0A3M6UMV8	Aconitate hydratase, mitochondrial OS=Pocillopora damicornis	3	1
A0A3M6UP81	Uncharacterized protein OS=Pocillopora damicornis	46.3	14
A0A3M6UPZ4	Uncharacterized protein OS=Pocillopora damicornis	4.5	3
A7SKY1	40S ribosomal protein S25 OS=Nematostella vectensis	8.6	1
A0A3M6UUU1	Uncharacterized protein OS=Pocillopora damicornis	3.5	1
A0A3M6UYC1	cGMP-dependent protein kinase OS=Pocillopora damicornis	1.7	1
A0A3M6UZ63	Annexin OS=Pocillopora damicornis	11.4	7
A0A3M6V0Z0	Uncharacterized protein OS=Pocillopora damicornis	1.5	2
A0A411JKF8	Beta-catenin OS=Dynamena pumila	7.7	5
A0A515L5S5	Beta-tubulin (Fragment) OS=Porites lutea	52.3	5
T2MEW7	Ras-related protein Rab-10 OS=Hydra vulgaris	16.3	3
A3F9E8	Histone H2B (Fragment) OS=Anacropora matthai	17.1	2
A4UAH1	Beta-catenin OS=Podocoryna carnea	8.7	5
A7REV0	Anoctamin (Fragment) OS=Nematostella vectensis	1.6	1
A7RFS1	Predicted protein OS=Nematostella vectensis	6.7	1
A7RG06	Inosine-5-monophosphate dehydrogenase OS=Nematostella vectensis	2.1	1
A7RGP3	Predicted protein (Fragment) OS=Nematostella vectensis	13.4	1
A7RH22	Predicted protein OS=Nematostella vectensis	0.6	1
A7RHS7	Predicted protein OS=Nematostella vectensis	5.8	4
A7RIF0	T-complex protein 1 subunit eta OS=Nematostella vectensis	4.8	2
A7TAM5	Predicted protein (Fragment) OS=Nematostella vectensis	6.3	1
A7RIZ6	Predicted protein (Fragment) OS=Nematostella vectensis	1.7	1
A7RJ25	Predicted protein OS=Nematostella vectensis	35.7	5
A7RL77	Coatomer subunit beta OS=Nematostella vectensis	2.3	2
A7RMQ8	Proteasome subunit alpha type OS=Nematostella vectensis	9	2
A7RN38	Predicted protein OS=Nematostella vectensis	16.4	6
A7RNE1	Predicted protein OS=Nematostella vectensis	3	1
A7RNH9	Predicted protein OS=Nematostella vectensis	4.3	2
A7RQD2	Predicted protein OS=Nematostella vectensis	3.1	2
A7RQF7	Predicted protein OS=Nematostella vectensis	8.7	2
A7RQR3	10-formyltetrahydrofolate dehydrogenase OS=Nematostella vectensis	1.4	1
T2MGG2	Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment) OS=Hydra vulgaris	9.6	2
A7RRG4	Actin-related protein 2/3 complex subunit 4 OS=Nematostella vectensis	4.8	1
A7RTG8	Predicted protein OS=Nematostella vectensis	2.1	1
A7RU93	Predicted protein OS=Nematostella vectensis	12	2
A7RUF9	Predicted protein (Fragment) OS=Nematostella vectensis	8.9	2

A7RUT1	Tubulin alpha chain OS=Nematostella vectensis	54.2	19
A7RVC0	Clathrin heavy chain OS=Nematostella vectensis	8.5	12
A7RVD9	Tubulin alpha chain OS=Nematostella vectensis	48.2	16
A7RXA1	Predicted protein OS=Nematostella vectensis	1.8	8
A7S018	Obg-like ATPase 1 OS=Nematostella vectensis	3.8	1
A7S0L1	Vacuolar proton pump subunit B OS=Nematostella vectensis	13.2	4
A7S183	Predicted protein OS=Nematostella vectensis	4.2	1
A7S1I1	Predicted protein OS=Nematostella vectensis	1.6	1
A7S214	Predicted protein OS=Nematostella vectensis	37.6	5
A7S269	AP complex subunit sigma (Fragment) OS=Nematostella vectensis	10.6	1
A7S289	Predicted protein OS=Nematostella vectensis	17.9	1
A7S335	Predicted protein OS=Nematostella vectensis	3.5	6
A7S469	Predicted protein OS=Nematostella vectensis	6.9	1
A7S4X0	Predicted protein OS=Nematostella vectensis	2.7	2
T2MEK4	60S ribosomal protein L8 OS=Hydra vulgaris	3.9	1
A7S5Z0	Predicted protein OS=Nematostella vectensis	11.3	4
A7S616	Predicted protein OS=Nematostella vectensis	12	1
A7T9G3	Predicted protein OS=Nematostella vectensis	16.2	1
A7S7K4	Predicted protein OS=Nematostella vectensis	7.9	2
A7S837	Predicted protein OS=Nematostella vectensis	16.4	1
A7S8H2	Predicted protein OS=Nematostella vectensis	2.5	1
A7S8Z2	RuvB-like helicase OS=Nematostella vectensis	9.9	4
A7SAS6	Predicted protein OS=Nematostella vectensis	11.5	2
A7SCK6	Predicted protein OS=Nematostella vectensis	11.3	2
A7SD28	Predicted protein OS=Nematostella vectensis	7.1	1
A7SDY3	Tubulin alpha chain OS=Nematostella vectensis	51	19
A7T660	Glutamate dehydrogenase OS=Nematostella vectensis	11.3	3
A7SEN4	Predicted protein OS=Nematostella vectensis	3.7	2
A7SFJ3	Predicted protein OS=Nematostella vectensis	10.4	3
A7SFJ6	Predicted protein OS=Nematostella vectensis	1	1
A7SG05	GTP-binding nuclear protein OS=Nematostella vectensis	18.4	4
A7SGG1	Predicted protein OS=Nematostella vectensis	0.7	1
A7SHH5	Protein disulfide-isomerase (Fragment) OS=Nematostella vectensis	2.5	1
A7SJR5	Predicted protein OS=Nematostella vectensis	1.2	1
A7SMZ7	Dynein light chain roadblock OS=Nematostella vectensis	12.5	1
A7SP62	V-type proton ATPase subunit G OS=Nematostella vectensis	14.5	1
A7SPM9	Predicted protein (Fragment) OS=Nematostella vectensis	2.3	1
A7SPQ4	Predicted protein OS=Nematostella vectensis	16.5	3
A7SQ60	Predicted protein OS=Nematostella vectensis	5.9	2
A7SQV3	Proteasome subunit beta OS=Nematostella vectensis	15.4	4
A7SRK8	Adenosylhomocysteinase OS=Nematostella vectensis	5.4	2
A7SSL5	Predicted protein OS=Nematostella vectensis	6.3	4
A7SSV8	Polyadenylate-binding protein OS=Nematostella vectensis	4.5	2
A7SVC4	Predicted protein OS=Nematostella vectensis	5.5	1

A7SW17	Predicted protein (Fragment) OS=Nematostella vectensis	2.6	1
A7SWC2	Predicted protein OS=Nematostella vectensis	3.1	2
A7SWR9	Predicted protein OS=Nematostella vectensis	8.6	2
A7SXN2	Peptidyl-prolyl cis-trans isomerase OS=Nematostella vectensis	25.2	2
A7SYP4	Predicted protein OS=Nematostella vectensis	6.6	2
A7T1L2	Histone H2B OS=Nematostella vectensis	31.2	3
A7T5A3	Predicted protein OS=Nematostella vectensis	2.7	1
A7TCL7	Histone H2A OS=Nematostella vectensis	42.2	14
A7TDI1	Predicted protein OS=Nematostella vectensis	8.7	1
A8DRV3	Vacuolar ATP synthase subunit B (Fragment) OS=Urticina eques	20.7	2
A8DX89	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Urticina eques	10.7	3
B2KTD5	Dickkopf protein 3 OS=Clytia hemisphaerica	18.3	2
B3EZK6	Ribosomal protein S5 (Fragment) OS=Cyanea capillata	21.6	4
B5MG02	Beta tubulin (Fragment) OS=Cirrhopathes sp. TW24	48.6	6
C1IS27	Clathrin heavy chain (Fragment) OS=Carukia barnesi	12.8	2
C1IS28	Clathrin heavy chain (Fragment) OS=Carukia barnesi	24.8	5
C7SP37	Glyceraldehyde 3-phosphate dehydrogenase (Fragment) OS=Anemonia sulcata	21.9	4
C7SP38	Glyceraldehyde 3-phosphate dehydrogenase (Fragment) OS=Metridium senile	23.5	3
G3LIV9	Heat shock cognate protein 71 OS=Hydractinia echinata	6.9	5
G8DM04	Cytochrome c oxidase subunit 2 OS=Chrysaora quinquecirrha	6.9	1
G9ISY6	NADH-ubiquinone oxidoreductase chain 1 OS=Pelagia noctiluca	6.2	2
G9ISX7	Cytochrome c oxidase subunit 2 OS=Pelagia noctiluca	8.1	1
I2G9E9	Myosin II heavy chain, smooth/non-muscle-type (Fragment) OS=Clytia hemisphaerica	3.4	1
K0A063	Beta-actin (Fragment) OS=Chrysaora quinquecirrha	57.1	17
M1E2A8	Calmodulin (Fragment) OS=Rhizostoma octopus	42.6	3
M1G2E5	Ras2 (Fragment) OS=Hydractinia echinata	17.7	2
O44222	Voltage-gated calcium channel beta subunit OS=Cyanea capillata	6.1	2
Q0H8V3	Heat shock protein 70 (Fragment) OS=Cnidaria environmental sample	12.2	2
Q6B4R5	Elongation factor 1-alpha OS=Scleronephtya gracillimum	9.8	4
Q2XWU1	Rab11 protein OS=Aiptasia pulchella	18.8	4
Q56GW1	60S ribosomal protein L12 (Fragment) OS=Hydractinia echinata	16.5	1
Q56GW5	40S ribosomal protein S4 (Fragment) OS=Hydractinia echinata	14.3	1
Q5EN91	Putative 3-hydroxyacyl-Coenzyme A dehydrogenase (Fragment) OS=Aurelia aurita	32.6	4
Q5XPR4	NaK-ATPase alpha subunit (Fragment) OS=Hydractinia echinata	6.6	1
Q6PTK3	Triosephosphate isomerase (Fragment) OS=Obelia sp. KJP-2004	11.8	2
Q7YZI4	90-kDa heat-shock protein (Fragment) OS=Aurelia aurita	11.9	3
Q7YZJ5	Elongation factor 2 (Fragment) OS=Aurelia aurita	19	3
Q7YZK4	Tubulin beta chain (Fragment) OS=Aurelia aurita	66.4	23
Q8I8C6	Putative beta-actin (Fragment) OS=Myxobolus insidiosus	21.7	1
Q967H6	Nucleoside diphosphate kinase OS=Hydra vulgaris	6	1
Q9GUZ6	PL10-related protein CnPL10 (Fragment) OS=Sandaria malayensis	32.8	3
Q9NDL6	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Sandaria malayensis	55	2
R9S2M2	Elongation factor 1-alpha OS=Aurelia aurita	14.7	6

T2M278	Hypoxia up-regulated protein 1 OS=Hydra vulgaris	1.6	1
T2M2P0	Coatomer subunit gamma (Fragment) OS=Hydra vulgaris	2.4	2
T2M2P5	RuvB-like helicase OS=Hydra vulgaris	10.8	4
T2M2W2	Talin-2 OS=Hydra vulgaris	2.2	3
T2M2X1	Adenylate kinase isoenzyme 5 OS=Hydra vulgaris	1.4	1
T2M388	Calcium/calmodulin-dependent protein kinase type II subunit alpha OS=Hydra vulgaris	6.9	3
T2M399	Pre-mRNA branch site protein p14 OS=Hydra vulgaris	11.4	1
T2M3D1	Eukaryotic translation initiation factor 3 subunit L OS=Hydra vulgaris	2.5	1
T2M3E6	Myosin-Ia (Fragment) OS=Hydra vulgaris	0.5	1
T2M3I7	RuvB-like helicase OS=Hydra vulgaris	6.6	2
T2M3U5	Sarcosine dehydrogenase,mitochondrial (Fragment) OS=Hydra vulgaris	1	1
T2M4B6	Vacuolar protein sorting-associated protein 45 OS=Hydra vulgaris	3.8	2
T2M4D5	Leucyl-tRNA synthetase,cytoplasmic (Fragment) OS=Hydra vulgaris	1.6	1
T2M4N0	Ras-related GTP-binding protein C OS=Hydra vulgaris	3.7	1
T2M4N6	Guanine nucleotide-binding protein subunit beta-4 (Fragment) OS=Hydra vulgaris	13.7	4
T2M5D3	Protein transport protein Sec61 subunit alpha isoform 2 OS=Hydra vulgaris	4.2	2
T2M644	Microtubule-associated proteins 1A/1B light chain 3C OS=Hydra vulgaris	32.8	3
T2M6B6	Ethanolamine-phosphate cytidyltransferase OS=Hydra vulgaris	3.5	1
T2M6G7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Hydra vulgaris	1.4	1
T2M6Z7	26S proteasome non-ATPase regulatory subunit 1 (Fragment) OS=Hydra vulgaris	1.5	1
T2M7H2	Adenosylhomocysteinase OS=Hydra vulgaris	4.2	2
T2M7J1	Vacuolar protein sorting-associated protein 35 (Fragment) OS=Hydra vulgaris	2.4	2
T2M7Z5	Ras-related protein Rab-3C OS=Hydra vulgaris	4.7	1
T2M8F7	Actin-related protein 2/3 complex subunit 1A (Fragment) OS=Hydra vulgaris	3.8	1
T2MA69	WD repeat-containing protein 69 OS=Hydra vulgaris	6.7	2
T2MAB0	Staphylococcal nuclease domain-containing protein OS=Hydra vulgaris	2.6	2
T2MAB9	Tubulin alpha-1A chain (Fragment) OS=Hydra vulgaris	22.6	14
T2MBN1	Kynurenine--oxoglutarate transaminase 3 OS=Hydra vulgaris	2.9	1
T2MCN2	26S proteasome non-ATPase regulatory subunit 6 (Fragment) OS=Hydra vulgaris	3.3	1
T2MCX1	10-formyltetrahydrofolate dehydrogenase OS=Hydra vulgaris	1.3	1
T2MCX5	Vacuolar protein sorting-associated protein 26B (Fragment) OS=Hydra vulgaris	7.4	2
T2MD34	Serine/threonine protein phosphatase 2A regulatory subunit OS=Hydra vulgaris	2.8	1
T2MD44	Major vault protein OS=Hydra vulgaris	4.4	4
T2MD57	Calcium-transporting ATPase OS=Hydra vulgaris	3.5	4
T2MDB0	Eukaryotic initiation factor 4A-II OS=Hydra vulgaris	3.4	1
T2MDF0	Histone-binding protein RBBP4 OS=Hydra vulgaris	3	1
T2MDG4	Flotillin-2 OS=Hydra vulgaris	11.2	4
T2MDI5	Septin-6 (Fragment) OS=Hydra vulgaris	3.7	1
T2MDK8	Spliceosome RNA helicase DDX39B OS=Hydra vulgaris	10.4	4
T2MDT0	Cytoplasmic dynein 1 heavy chain 1 OS=Hydra vulgaris	2.4	9
T2ME66	Ras-related protein Rab-11A OS=Hydra vulgaris	16.5	3
T2ME76	Small nuclear ribonucleoprotein G OS=Hydra vulgaris	17.1	1

T2MEA3	Myosin-1e (Fragment) OS=Hydra vulgaris	3	2
T2MEB5	ADP-ribosylation factor 1 OS=Hydra vulgaris	37.6	5
T2MEC1	Serine/threonine-protein phosphatase OS=Hydra vulgaris	7.3	3
T2MEH3	Casein kinase II subunit alpha OS=Hydra vulgaris	5.1	2
T2MEI1	AP-2 complex subunit beta (Fragment) OS=Hydra vulgaris	11.2	7
T2MEI3	40S ribosomal protein S21 (Fragment) OS=Hydra vulgaris	28.6	2
T2MEN2	40S ribosomal protein S6 OS=Hydra vulgaris	4.8	1
T2MEN5	Clathrin heavy chain OS=Hydra vulgaris	10.7	15
T2MEP0	26S protease regulatory subunit 10B OS=Hydra vulgaris	5.4	2
T2MEP2	40S ribosomal protein S18 OS=Hydra vulgaris	11.6	2
T2MEQ7	26S protease regulatory subunit 4 OS=Hydra vulgaris	5.7	2
T2MES1	40S ribosomal protein S15a OS=Hydra vulgaris	10.8	1
T2MET6	Ras-related protein Rap-1b OS=Hydra vulgaris	19.7	3
T2MET8	WD repeat-containing protein 5 OS=Hydra vulgaris	7.9	2
T2MEV1	Tubulin beta chain (Fragment) OS=Hydra vulgaris	33.8	16
T2MEW2	Actin-related protein 3 OS=Hydra vulgaris	15.1	3
T2MEW9	Calcineurin subunit B type 1 OS=Hydra vulgaris	5.9	1
T2MEY1	60S ribosomal protein L11 (Fragment) OS=Hydra vulgaris	7.2	1
T2MF38	Adenylate kinase OS=Hydra vulgaris	4.1	2
T2MF60	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Hydra vulgaris	4.8	1
T2MF93	Ras-related protein Rab-14 (Fragment) OS=Hydra vulgaris	28.4	5
T2MFD2	60S ribosomal protein L26 OS=Hydra vulgaris	6.2	1
T2MFH7	Poly(RC)-binding protein 3 (Fragment) OS=Hydra vulgaris	4.1	1
T2MFI1	T-complex protein 1 subunit gamma OS=Hydra vulgaris	2	1
T2MFJ1	Stress-70 protein, mitochondrial (Fragment) OS=Hydra vulgaris	8.2	3
T2MFJ6	AP complex subunit sigma (Fragment) OS=Hydra vulgaris	5.3	1
T2MFM1	Transitional endoplasmic reticulum ATPase (Fragment) OS=Hydra vulgaris	14.4	8
T2MGC9	Tyrosine-protein kinase (Fragment) OS=Hydra vulgaris	1.6	1
T2MFR8	Ras-related protein Rab-7a OS=Hydra vulgaris	44.2	9
T2MFU3	Guanine nucleotide-binding protein G(Q) subunit alpha OS=Hydra vulgaris	13.3	4
T2MFU6	26S proteasome non-ATPase regulatory subunit 7 OS=Hydra vulgaris	5.2	1
T2MFU8	Rab GDP dissociation inhibitor (Fragment) OS=Hydra vulgaris	6.3	2
T2MFV4	Isoleucyl-tRNA synthetase,cytoplasmic (Fragment) OS=Hydra vulgaris	1.7	2
T2MFY6	Hippocalcin-like protein 1 OS=Hydra vulgaris	21.5	4
T2MFZ8	V-type proton ATPase catalytic subunit A OS=Hydra vulgaris	8	3
T2MG06	Transaldolase OS=Hydra vulgaris	6.2	2
T2MG36	Myosin-10 OS=Hydra vulgaris	3	6
T2MG47	Radixin OS=Hydra vulgaris	4.3	2
T2MG68	Proteasome subunit beta OS=Hydra vulgaris	6.2	1
T2MGA3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Hydra vulgaris	5.8	3
T2MGD8	Eukaryotic initiation factor 4A-III (Fragment) OS=Hydra vulgaris	2.6	1
T2MGF7	Malate dehydrogenase,mitochondrial OS=Hydra vulgaris	10.2	2
T2MGG5	Proteasome subunit alpha type OS=Hydra vulgaris	9.6	2

T2MGG7	ADP-ribosylation factor-like protein 3 OS=Hydra vulgaris	6.1	1
T2MGH4	Proteasome subunit alpha type OS=Hydra vulgaris	4	2
T2MGI5	Cystathionine beta-synthase OS=Hydra vulgaris	1.7	1
T2MGL9	40S ribosomal protein S17-like OS=Hydra vulgaris	9	1
T2MGN9	Fructose-1,6-bisphosphatase 1 (Fragment) OS=Hydra vulgaris	3.2	1
T2MGQ4	ER lumen protein retaining receptor 2 OS=Hydra vulgaris	12.6	2
T2MGR5	60S ribosomal protein L7 (Fragment) OS=Hydra vulgaris	9.2	2
T2MGS3	cAMP-dependent protein kinase catalytic subunit alpha OS=Hydra vulgaris	8.3	2
T2MGT2	Transketolase OS=Hydra vulgaris	3.5	2
T2MGW9	Small nuclear ribonucleoprotein-associated proteins B and B (Fragment) OS=Hydra vulgaris	7.8	1
T2MGX7	60S ribosomal protein L13 (Fragment) OS=Hydra vulgaris	4.7	1
T2MGZ6	ATP synthase subunit alpha OS=Hydra vulgaris	20.2	9
T2MH23	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial (Fragment) OS=Hydra vulgaris	2.5	1
T2MH41	78 kDa glucose-regulated protein OS=Hydra vulgaris	5.9	4
T2MH44	Vacuolar proton pump subunit B (Fragment) OS=Hydra vulgaris	10.2	3
T2MH46	Filamin-A OS=Hydra vulgaris	0.9	3
T2MH95	Vinculin OS=Hydra vulgaris	1	1
T2MHA2	Bifunctional aminoacyl-tRNA synthetase (Fragment) OS=Hydra vulgaris	1	1
T2MHA5	X-box-binding protein 1 OS=Hydra vulgaris	3.9	1
T2MHC8	Epsin-2 OS=Hydra vulgaris	3.5	1
T2MHD4	Eukaryotic translation initiation factor 2 subunit 1 OS=Hydra vulgaris	3.9	1
T2MHE8	Aspartyl-tRNA synthetase, cytoplasmic OS=Hydra vulgaris	4	2
T2MHH5	Myosin-6 OS=Hydra vulgaris	3.1	6
T2MHI3	Flotillin-1 (Fragment) OS=Hydra vulgaris	3.4	1
T2MHI5	Alpha-actinin-1 OS=Hydra vulgaris	6.6	6
T2MHJ0	Non-specific serine/threonine protein kinase OS=Hydra vulgaris	3.5	1
T2MHJ7	60 kDa heat shock protein, mitochondrial (Fragment) OS=Hydra vulgaris	3.5	2
T2MHN7	Citrate synthase OS=Hydra vulgaris	2.6	1
T2MHT5	Heat shock protein HSP 90-alpha OS=Hydra vulgaris	9.8	9
T2MHY4	Argininosuccinate synthase (Fragment) OS=Hydra vulgaris	4.6	2
T2MIB9	AP-2 complex subunit alpha OS=Hydra vulgaris	2.9	2
T2MIF5	Endothelin-converting enzyme 2 OS=Hydra vulgaris	3.1	1
T2MIJ7	Dysferlin OS=Hydra vulgaris	0.9	2
T2MIR7	WD repeat-containing protein 1 OS=Hydra vulgaris	1.6	1
T2MJ45	Calpain-9 (Fragment) OS=Hydra vulgaris	2	1
T2MJJ5	Myosin regulatory light chain 12B OS=Hydra vulgaris	32.4	4
T2MK25	CCR4-NOT transcription complex subunit 1 (Fragment) OS=Hydra vulgaris	0.6	1
T2MK48	Fucose mutarotase OS=Hydra vulgaris	13.6	1
W8PTQ2	Peroxiredoxin 4 OS=Cyanea capillata	23.1	5

Table G-3. List of proteins identified (473 proteins) from nematocyst of highly venomous jellyfish by using extraction of PBS buffer coupled with ultrasonication.

The proteins were derived from in-gel digestion experiment. Database of taxonomy Cnidaria (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
A0A3M6UR37	Eukaryotic translation initiation factor 3 subunit I OS=Pocillopora damicornis	3.8	1
A0A3M6V5T4	Uncharacterized protein OS=Pocillopora damicornis	0.7	1
T2MCI6	Transmembrane emp24 domain-containing protein 2 OS=Hydra vulgaris	4.6	1
A7RFY7	Predicted protein OS=Nematostella vectensis	3.6	1
T2MGY6	Sodium/potassium-transporting ATPase subunit alpha OS=Hydra vulgaris	5.5	4
M1G2E5	Ras2 (Fragment) OS=Hydractinia echinata	9.9	1
P38984	40S ribosomal protein SA OS=Hydra viridissima	4.1	1
P41113	Actin-3 OS=Podocoryna carnea	52.7	17
M1G4Y4	Ras1 (Fragment) OS=Hydractinia echinata	6.2	1
P62184	Calmodulin OS=Renilla reniformis	58.4	4
B1PM92	Calmodulin OS=Acropora muricata	58.4	4
A0A069DMJ2	Glutamate deshydrogenase (Fragment) OS=Clytia hemisphaerica	2.1	1
A0A0A7KS39	Elongation factor 2 (Fragment) OS=Ceratomyxa verudensis	7.6	2
A0A0C2I839	Cytosol aminopeptidase OS=Thelohanellus kitauei	2.4	1
A0A0C2I8G7	Eukaryotic initiation factor 4A-III OS=Thelohanellus kitauei	4.6	1
A7SRV8	40S ribosomal protein S4 OS=Nematostella vectensis	4.6	2
A0A1V0IGH5	Histone H2B OS=Hydra vulgaris	11.2	1
A0A0C2J3J1	60 kDa heat shock protein, mitochondrial OS=Thelohanellus kitauei	2.6	3
A7TBQ1	Predicted protein (Fragment) OS=Nematostella vectensis	3	1
T2MF79	Transforming protein RhoA OS=Hydra vulgaris	7.8	2
A0A0C2JEY5	6-phosphogluconate dehydrogenase, decarboxylating OS=Thelohanellus kitauei	7	3
D1FNZ6	Ribosomal protein L16p/L10e (Fragment) OS=Carukia barnesi	5.4	1
A0A0C2JSP7	Peptidyl-prolyl cis-trans isomerase OS=Thelohanellus kitauei	8.7	1
A0A0C2JSW9	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 OS=Thelohanellus kitauei	1.9	1
A0A0C2M5P0	Outer membrane protein A OS=Thelohanellus kitauei	2.5	1
A0A0C2M9V2	Arginine--tRNA ligase, cytoplasmic OS=Thelohanellus kitauei	1.8	1
A0A0C2MCV7	60S ribosomal protein L34 OS=Thelohanellus kitauei	7.4	1
A0A0C2MNQ3	Myosin-10 OS=Thelohanellus kitauei	4.1	3
A0A0C2MS24	Methylmalonyl-CoA mutase, mitochondrial OS=Thelohanellus kitauei	7.2	1
A0A0C2MT43	Heat shock protein HSP 90-alpha 1 OS=Thelohanellus kitauei	1.7	1
A0A0C2MUS2	60 kDa chaperonin OS=Thelohanellus kitauei	4.7	1
A0A0C2MZD7	Uncharacterized protein OS=Thelohanellus kitauei	11.6	1
A0A0C2N1W8	Calcium-transporting ATPase OS=Thelohanellus kitauei	1	1
A0A0C2N200	Ras-related protein RABA2a OS=Thelohanellus kitauei	5.3	1
A0A0C2N354	ATP synthase subunit beta OS=Thelohanellus kitauei	9	3
A0A0C2N442	Ras-related protein Rab-11A OS=Thelohanellus kitauei	5.3	1
A0A0C2N916	Casein kinase I isoform gamma-1 OS=Thelohanellus kitauei	3.9	1
A0A0C2NF10	60S ribosomal protein L28 OS=Thelohanellus kitauei	7.2	1
A0A0C4VZ14	78 kDa glycose-regulated protein (Fragment) OS=Capnella imbricata	16.1	4

A0A2B4STX3	Heat shock protein 70 B2 OS=Stylophora pistillata	6.1	3
A0A0U2JZC1	Gs protein alpha subunit OS=Tripedalia cystophora	5.4	2
A0A142I2D1	Cytochrome c oxidase subunit 3 (Fragment) OS=Phyllorhiza punctata	6.2	1
A0A169Q0T5	Glyceraldehyde-3-phosphate dehydrogenase OS=Aurelia sp. SETO	4.5	1
A0A2Z5WH77	Actin-1 OS=Aurelia sp. 2017-HT	61.2	22
A0A1L2A726	Superoxide dismutase [Cu-Zn] OS=Cyanea capillata	18.2	2
A0A1U9XQR0	Fructose-bisphosphate aldolase OS=Aurelia sp. 1 GW-2014	3.9	1
A0A288W1V0	Mitogen-activated protein kinase OS=Aurelia aurita	7.3	2
A0A288W1V6	Mitogen-activated protein kinase OS=Aurelia aurita	3.9	1
A0A2B4R364	GTP-binding protein TypA/BipA-like OS=Stylophora pistillata	4.5	1
A0A2B4R9G5	Histone H2B OS=Stylophora pistillata	7.3	2
A0A2B4R9Q9	Histone H4 OS=Stylophora pistillata	38.7	12
A0A2B4R9T9	Chaperone protein DnaK OS=Stylophora pistillata	2.3	1
A0A2B4RAR4	60S ribosomal protein L4 (Fragment) OS=Stylophora pistillata	3.2	1
A7RQD8	Predicted protein OS=Nematostella vectensis	39.8	3
T2MHV0	Aldehyde dehydrogenase,mitochondrial OS=Hydra vulgaris	2.3	1
A7SWU4	Predicted protein (Fragment) OS=Nematostella vectensis	8	2
A0A2B4RG26	Dual specificity protein kinase shkC OS=Stylophora pistillata	1.4	1
A0A2B4RGN0	Serine/threonine-protein kinase TOR (Fragment) OS=Stylophora pistillata	1	1
A7S2T7	Predicted protein OS=Nematostella vectensis	1.5	1
A0A2B4RHG2	V-type proton ATPase catalytic subunit A OS=Stylophora pistillata	16.7	7
A0A2B4RHH5	Enoyl-CoA hydratase, mitochondrial OS=Stylophora pistillata	6	1
A0A2B4RHS6	Glutamine--tRNA ligase OS=Stylophora pistillata	1.5	1
A0A2B4RI23	GTP-binding protein SAR1 OS=Stylophora pistillata	6.8	1
A0A3M6TI71	Glutamate dehydrogenase OS=Pocillopora damicornis	4.9	1
A0A3M6V529	Ribosomal_L23eN domain-containing protein (Fragment) OS=Pocillopora damicornis	13.3	2
A0A2B4RIF3	Retrovirus-related Pol polyprotein OS=Stylophora pistillata	3.2	1
A0A3M6TVK8	6PF2K domain-containing protein OS=Pocillopora damicornis	2.4	1
A0A2B4RJH1	Tubulin beta chain OS=Stylophora pistillata	69.6	26
A0A3M6U938	Kinesin motor domain-containing protein OS=Pocillopora damicornis	2.5	2
A0A2B4RKT3	26S proteasome non-ATPase regulatory subunit 2 OS=Stylophora pistillata	3.3	2
A0A2B4RKT5	Actin-related protein 2 OS=Stylophora pistillata	11.7	4
A7RRD6	Predicted protein OS=Nematostella vectensis	1.7	1
A0A3M6T5M4	Glucose-6-phosphate 1-dehydrogenase OS=Pocillopora damicornis	1.9	1
A0A3M6V3V6	Uncharacterized protein OS=Pocillopora damicornis	12.4	2
A0A2B4RPA9	Clathrin heavy chain OS=Stylophora pistillata	6.2	8
A7T120	F-actin-capping protein subunit beta (Fragment) OS=Nematostella vectensis	6.7	1
A0A2B4RPD3	Endoplasmic reticulum chaperone protein OS=Stylophora pistillata	2.7	2
A7SQS1	Malate dehydrogenase OS=Nematostella vectensis	4.7	1
A0A3M6V4M9	Uncharacterized protein OS=Pocillopora damicornis	9.5	3
A0A3M6U9J9	Uncharacterized protein OS=Pocillopora damicornis	2	1
A0A3M6TQ41	Catalase OS=Pocillopora damicornis	5.5	2
Q93116	Ub52 OS=Acropora millepora	36.4	4

A0A3M6UUF7	Uncharacterized protein OS=Pocillopora damicornis	2.7	1
A0A2B4RSK7	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Stylophora pistillata	2.3	1
A0A2B4RSU6	Multidrug resistance-associated protein 4 OS=Stylophora pistillata	2	2
A0A2B4RTD9	Catenin alpha-2 OS=Stylophora pistillata	1.8	2
A0A3M6TM54	Coatomer subunit beta OS=Pocillopora damicornis	1.7	1
I2G9E1	Serine/threonine-protein phosphatase (Fragment) OS=Clytia hemisphaerica	6.7	3
Q2F6G0	Prohibitin (Fragment) OS=Anthopleura elegantissima	10	1
T2M3D0	Nucleolar protein 58 OS=Hydra vulgaris	2.6	1
A0A2B4RVA0	Tubulin alpha chain OS=Stylophora pistillata	21.7	8
A0A2B4RVD0	Ribonuclease UK114 OS=Stylophora pistillata	13.7	1
A0A2B4RWB5	Elongation factor 1-gamma OS=Stylophora pistillata	2.6	1
A0A3M6U3P0	Uncharacterized protein OS=Pocillopora damicornis	1.5	1
A0A3M6UGY3	UBIQUITIN_CONJUGAT_2 domain-containing protein OS=Pocillopora damicornis	16.4	2
A0A2B4RXI4	Ras-related protein Rab-5B OS=Stylophora pistillata	10.6	2
A0A2B4RXU3	Peptidyl-prolyl cis-trans isomerase OS=Stylophora pistillata	5.5	1
A7S494	40S ribosomal protein S27 OS=Nematostella vectensis	15.5	1
A0A2B4RYR5	60S ribosomal protein L5 (Fragment) OS=Stylophora pistillata	7.7	1
A7RTW3	Predicted protein OS=Nematostella vectensis	2.6	1
A0A3M6U8S0	Uncharacterized protein OS=Pocillopora damicornis	0.4	1
A0A2B4RZN2	Tubulin beta chain OS=Stylophora pistillata	37.1	18
A0A2B4S0G4	T-complex protein 1 subunit zeta OS=Stylophora pistillata	4.9	1
L0AUB3	Alpha q G protein OS=Acropora palmata	7.6	2
A0A3M6V6P2	FAA_hydrolase domain-containing protein OS=Pocillopora damicornis	3.2	1
A0A2B4S129	Peroxisome oxidoreductin-1 OS=Stylophora pistillata	4	1
A0A3M6T6R6	Uncharacterized protein OS=Pocillopora damicornis	4.6	2
T2MERO	40S ribosomal protein S14 OS=Hydra vulgaris	17.9	4
A7RN37	Predicted protein OS=Nematostella vectensis	3	1
Q6YCHO	Ribosomal protein S3 (Fragment) OS=Hydra vulgaris	9.2	2
A7RUL8	Predicted protein (Fragment) OS=Nematostella vectensis	3.9	2
A0A2B4S2W7	Major vault protein OS=Stylophora pistillata	3.9	3
A7SWV8	Predicted protein OS=Nematostella vectensis	3.9	1
E0YPA3	Heat shock protein 70 OS=Seriatopora hystrix	3.6	2
A0A3M6UK04	Uncharacterized protein OS=Pocillopora damicornis	0.8	2
T2MEG1	Cell division control protein 42 homolog OS=Hydra vulgaris	14.7	2
A7T9Z8	Predicted protein (Fragment) OS=Nematostella vectensis	13.8	1
A0A2B4S811	ADP-ribosylation factor 3 OS=Stylophora pistillata	6.4	1
A0A2B4S5N4	Alanine--tRNA ligase, cytoplasmic OS=Stylophora pistillata	1.4	1
A0A2B4S5Q6	RNA-dependent RNA polymerase 2 OS=Stylophora pistillata	1.5	1
A7SJ61	Predicted protein OS=Nematostella vectensis	10.9	8
A7T5I4	6-phosphogluconate dehydrogenase, decarboxylating (Fragment) OS=Nematostella vectensis	3.6	1
A0A3M6UAV3	Uncharacterized protein OS=Pocillopora damicornis	1.7	1
A0A3M6UQS3	UBA_e1_C domain-containing protein OS=Pocillopora damicornis	1.4	1
A0A2B4S6M0	Tubulin alpha-1D chain OS=Stylophora pistillata	44.7	19

A7SHC3	Predicted protein (Fragment) OS=Nematostella vectensis	3.3	1
A0A2B4S6V6	Filamin-A OS=Stylophora pistillata	0.8	3
A0A2B4S736	Vacuolar proton pump subunit B OS=Stylophora pistillata	18.1	6
A0A3M6TMR5	Uncharacterized protein OS=Pocillopora damicornis	3	1
A0A2B4S7M6	Phospholipid-transporting ATPase OS=Stylophora pistillata	1.1	1
A0A2B4S8M8	Aminopeptidase OS=Stylophora pistillata	1.2	1
A0A3M6TIH2	TRANSKETOLASE_1 domain-containing protein OS=Pocillopora damicornis	1.4	1
T2MG46	T-complex protein 1 subunit epsilon OS=Hydra vulgaris	1.8	1
A7SIB3	Predicted protein OS=Nematostella vectensis	1.4	1
A7SU78	Predicted protein OS=Nematostella vectensis	5.2	2
A7S3B3	Predicted protein OS=Nematostella vectensis	7.9	2
J3T9N7	PL10 OS=Euphyllia ancora	5.2	3
T2M856	Dynein light chain OS=Hydra vulgaris	24.7	2
A0A3M6T7R7	Small nuclear ribonucleoprotein Sm D2 OS=Pocillopora damicornis	16.1	2
A7RFJ1	Predicted protein OS=Nematostella vectensis	7.7	1
A7SS49	Predicted protein OS=Nematostella vectensis	10	3
A0A2B4SD19	ATP-citrate synthase OS=Stylophora pistillata	1.5	1
A7SLQ2	Predicted protein OS=Nematostella vectensis	9.9	3
A0A3M6U2E3	40S ribosomal protein S8 OS=Pocillopora damicornis	7.7	1
A7RKK8	Predicted protein (Fragment) OS=Nematostella vectensis	4.7	1
A0A2B4SGK7	T-complex protein 1 subunit alpha OS=Stylophora pistillata	2.4	1
T2M8Q9	Probable aminopeptidase NPEPL1 OS=Hydra vulgaris	2.6	1
A0A3M6TAD6	Uncharacterized protein OS=Pocillopora damicornis	1.4	1
A0A2B4SH13	Mechanosensory protein 2 OS=Stylophora pistillata	11	3
A0A3M6U381	Uncharacterized protein OS=Pocillopora damicornis	7	1
A0A3M6U8V1	E3 ubiquitin-protein ligase OS=Pocillopora damicornis	1.5	1
A0A3M6TKN8	Transaldolase OS=Pocillopora damicornis	6.5	2
A0A3M6TSM5	Uncharacterized protein OS=Pocillopora damicornis	2.3	2
A7SPP0	ATP synthase subunit beta OS=Nematostella vectensis	17.3	5
A0A2B4SJU8	Protein transport protein Sec61 subunit beta OS=Stylophora pistillata	10.6	1
A0A3M6T7K7	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	3.3	1
A0A3M6TT74	Uncharacterized protein OS=Pocillopora damicornis	1	1
A0A3M6VAC5	Uncharacterized protein OS=Pocillopora damicornis	2.8	1
A0A3M6TT70	V-type proton ATPase proteolipid subunit OS=Pocillopora damicornis	11.7	1
Q58I86	Leonardo protein (Fragment) OS=Hydractinia echinata	26.3	2
A7RV73	Vacuolar protein sorting-associated protein 29 OS=Nematostella vectensis	7.1	1
A0A2B4SPX6	Plastin-3 OS=Stylophora pistillata	1	2
A7SMW8	Predicted protein OS=Nematostella vectensis	5.4	1
A7SKL5	Predicted protein (Fragment) OS=Nematostella vectensis	3	1
A7SHU3	Predicted protein OS=Nematostella vectensis	33.5	6
A0A3M6TRH7	Uncharacterized protein OS=Pocillopora damicornis	2.7	11
A0A3M6UD35	Coatomer subunit alpha OS=Pocillopora damicornis	2.1	2
A0A2B4SR60	AP-2 complex subunit alpha OS=Stylophora pistillata	4.5	2
A0A2B4SRE9	AP complex subunit beta OS=Stylophora pistillata	3.7	3

T2MFM0	Tricarboxylate transport protein,mitochondrial OS=Hydra vulgaris	3.5	1
A0A3M6V2N5	Adenosylhomocysteinase OS=Pocillopora damicornis	2.8	1
A7T2Q5	Serine/threonine-protein phosphatase OS=Nematostella vectensis	9.4	2
A0A3M6V0Z0	Uncharacterized protein OS=Pocillopora damicornis	0.7	1
A0A3M6TL03	Phospholipid scramblase OS=Pocillopora damicornis	6.8	1
A0A2B4STP6	Kinesin-like protein KIF28P OS=Stylophora pistillata	1.4	1
A0A2B4STS3	Guanylate cyclase OS=Stylophora pistillata	1.2	1
A0A2B4STV7	Dihydropyrimidine dehydrogenase [NADP(+)] OS=Stylophora pistillata	1.7	1
A0A2B4SU54	Collagen alpha-1(XIV) chain OS=Stylophora pistillata	0.6	1
A0A2B4SV07	Tubulin beta chain OS=Stylophora pistillata	60.3	25
A7SQP1	Predicted protein OS=Nematostella vectensis	8.6	2
A0A2B4SVH3	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial OS=Stylophora pistillata	3.9	1
A0A3M6TL78	Uncharacterized protein OS=Pocillopora damicornis	2.5	2
A7RID7	Predicted protein OS=Nematostella vectensis	5.9	1
A0A3M6TGT9	Uncharacterized protein OS=Pocillopora damicornis	2	1
A0A2B4SW93	Dynein heavy chain 5, axonemal OS=Stylophora pistillata	0.4	1
A0A3M6TM92	Proteasome subunit alpha type OS=Pocillopora damicornis	16	2
A0A3M6TPE2	Uncharacterized protein OS=Pocillopora damicornis	4.1	1
A0A3M6U4Q7	Uncharacterized protein OS=Pocillopora damicornis	6.6	1
A7T2C3	Predicted protein OS=Nematostella vectensis	1.1	1
A0A2B4SZV5	Ras GTPase-activating-like protein IQGAP1 OS=Stylophora pistillata	1.4	2
A0A2B4T1C4	ATP synthase subunit alpha OS=Stylophora pistillata	16.3	8
A7T1M0	RNA-binding protein 8A (Fragment) OS=Nematostella vectensis	12.5	1
A0A2Z5WH73	Myosin heavy chain OS=Aurelia sp. 2017-HT	11.3	26
A0A2Z5WH78	Ser-Thr kinase OS=Aurelia sp. 2017-HT	3.6	2
A0A2Z5WH80	Myosin regulatory light chain OS=Aurelia sp. 2017-HT	56.7	9
A0A2Z5WH81	Myosin essential light chain OS=Aurelia sp. 2017-HT	7.3	1
A0A2Z5WH82	Tropomyosin-1 OS=Aurelia sp. 2017-HT	10.7	2
A0A3M6T5Z9	Uncharacterized protein OS=Pocillopora damicornis	0.7	1
A0A3M6T656	Uncharacterized protein OS=Pocillopora damicornis	0.2	1
A0A3M6TA99	Uncharacterized protein OS=Pocillopora damicornis	14.2	1
A0A3M6TAB1	Cation_ATPase_N domain-containing protein OS=Pocillopora damicornis	4	4
A0A3M6TCL4	TIP120 domain-containing protein (Fragment) OS=Pocillopora damicornis	2.9	3
A0A3M6TE02	Uncharacterized protein OS=Pocillopora damicornis	0.3	1
A0A3M6TE61	Uncharacterized protein OS=Pocillopora damicornis	1.8	1
A7RR97	Lysine--tRNA ligase OS=Nematostella vectensis	1.6	1
A0A3M6TIE8	Non-specific serine/threonine protein kinase OS=Pocillopora damicornis	0.8	1
A0A3M6TIL3	BPTI/Kunitz inhibitor domain-containing protein OS=Pocillopora damicornis	3.8	1
A0A3M6TJC0	Uncharacterized protein OS=Pocillopora damicornis	3.9	2
A0A3M6TLD9	Uncharacterized protein OS=Pocillopora damicornis	10.6	2
A0A3M6TLS3	Uncharacterized protein OS=Pocillopora damicornis	2.3	1
A7S752	Predicted protein (Fragment) OS=Nematostella vectensis	1.2	1
A0S5V7	Mitochondrial succinate dehydrogenase flavoprotein subunit (Fragment) OS=Hydra vulgaris	6.9	2

A0A3M6TST2	Uncharacterized protein OS=Pocillopora damicornis	5.4	1
A0A3M6TT35	Uncharacterized protein OS=Pocillopora damicornis	5.8	4
A0A3M6TU20	Uncharacterized protein OS=Pocillopora damicornis	1.9	1
A0A3M6TVV7	Hcy-binding domain-containing protein OS=Pocillopora damicornis	4.4	1
A0A3M6TW59	Ubiquitin carboxyl-terminal hydrolase OS=Pocillopora damicornis	2.3	1
A7RSB9	Predicted protein OS=Nematostella vectensis	2.4	2
A7T9A3	Predicted protein (Fragment) OS=Nematostella vectensis	5.9	1
A0A3M6U1Z2	Uncharacterized protein OS=Pocillopora damicornis	2.7	1
A0A3M6U454	Histone H2A OS=Pocillopora damicornis	17.4	2
A0A3M6U507	Calponin-homology (CH) domain-containing protein OS=Pocillopora damicornis	5.4	1
A0A3M6U7U8	Uncharacterized protein OS=Pocillopora damicornis	5	2
A7S690	Predicted protein (Fragment) OS=Nematostella vectensis	10.5	1
A0A3M6UAY9	AAA domain-containing protein OS=Pocillopora damicornis	8	3
A0A3M6UEC5	Serine/threonine-protein phosphatase OS=Pocillopora damicornis	13.4	5
A0A3M6UGM1	V-type proton ATPase subunit a OS=Pocillopora damicornis	4.4	1
A0A3M6UGH9	Uncharacterized protein OS=Pocillopora damicornis	9.3	1
A0A3M6UH10	Par3_HAL_N_term domain-containing protein OS=Pocillopora damicornis	1.5	1
A0A3M6UKT7	Uncharacterized protein OS=Pocillopora damicornis	7.2	5
A0A3M6UMV8	Aconitate hydratase, mitochondrial OS=Pocillopora damicornis	5.2	2
A0A3M6UP43	Uncharacterized protein OS=Pocillopora damicornis	42.6	17
A0A3M6UP81	Uncharacterized protein OS=Pocillopora damicornis	46.8	16
A0A3M6UPR6	Uncharacterized protein OS=Pocillopora damicornis	2.9	2
A0A3M6UPZ4	Uncharacterized protein OS=Pocillopora damicornis	4.3	2
A7SKY1	ribosomal protein S25 OS=Nematostella vectensis	8.6	1
A0A3M6UUU1	Uncharacterized protein OS=Pocillopora damicornis	3.5	1
A0A3M6UXC6	Uncharacterized protein OS=Pocillopora damicornis	3.3	1
A0A3M6UYC1	cGMP-dependent protein kinase OS=Pocillopora damicornis	1.7	1
A0A3M6UZ63	Annexin OS=Pocillopora damicornis	11.2	6
A0A3M6V116	Uncharacterized protein OS=Pocillopora damicornis	0.7	1
A0A3M6V4Z5	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	0.2	1
A0A411JKF8	Beta-catenin OS=Dynamena pumila	7.7	5
A0A515L5S5	Beta-tubulin (Fragment) OS=Porites lutea	52.3	5
A4UAH1	Beta-catenin OS=Podocoryna carnea	8.7	5
A7REV0	Anoctamin (Fragment) OS=Nematostella vectensis	3.5	2
A7RGP3	Predicted protein (Fragment) OS=Nematostella vectensis	13.4	1
A7RGV0	Predicted protein OS=Nematostella vectensis	3.5	1
A7RH22	Predicted protein OS=Nematostella vectensis	0.6	1
A7RHF7	Eukaryotic translation initiation factor 6 OS=Nematostella vectensis	10.2	1
A7RIF0	T-complex protein 1 subunit eta OS=Nematostella vectensis	7	3
A7RIZ6	Predicted protein (Fragment) OS=Nematostella vectensis	1.7	1
A7RJD9	Predicted protein OS=Nematostella vectensis	19	2
A7RKR4	Predicted protein OS=Nematostella vectensis	3.8	2
A7RL77	Coatomer subunit beta OS=Nematostella vectensis	1	1

A7RMQ8	Proteasome subunit alpha type OS=Nematostella vectensis	8.6	1
A7RMZ4	Predicted protein OS=Nematostella vectensis	5.4	1
A7RNE1	Predicted protein OS=Nematostella vectensis	6.6	2
A7RNH9	Predicted protein OS=Nematostella vectensis	4.3	2
A7RQF7	Predicted protein OS=Nematostella vectensis	8.7	2
A7RQH5	Adenylyl cyclase-associated protein OS=Nematostella vectensis	2.2	1
A7RQR3	10-formyltetrahydrofolate dehydrogenase OS=Nematostella vectensis	1.4	1
A7RRG4	Actin-related protein 2/3 complex subunit 4 OS=Nematostella vectensis	4.8	1
A7T836	Predicted protein (Fragment) OS=Nematostella vectensis	3.3	2
A7RT97	Predicted protein OS=Nematostella vectensis	3.3	3
A7RUF9	Predicted protein (Fragment) OS=Nematostella vectensis	8.9	2
A7RUT1	Tubulin alpha chain OS=Nematostella vectensis	54.2	19
A7RVC0	Clathrin heavy chain OS=Nematostella vectensis	7.1	9
A7RVD9	Tubulin alpha chain OS=Nematostella vectensis	48.4	17
A7RVT1	Predicted protein OS=Nematostella vectensis	1.2	1
A7RZC0	Predicted protein OS=Nematostella vectensis	2.1	1
A7S018	Obg-like ATPase 1 OS=Nematostella vectensis	3.8	1
A7S0L1	Vacuolar proton pump subunit B OS=Nematostella vectensis	12	4
A7S183	Predicted protein OS=Nematostella vectensis	4.2	1
A7S1I1	Predicted protein OS=Nematostella vectensis	2.7	2
A7S1L7	Prohibitin OS=Nematostella vectensis	3.7	1
A7S214	Predicted protein OS=Nematostella vectensis	37.6	6
A7S335	Predicted protein OS=Nematostella vectensis	1.9	3
A7S394	Aminopeptidase (Fragment) OS=Nematostella vectensis	1.4	1
A7S3I0	Predicted protein (Fragment) OS=Nematostella vectensis	4.4	4
A7S473	Coronin OS=Nematostella vectensis	1.8	1
T2MEK4	60S ribosomal protein L8 OS=Hydra vulgaris	3.9	1
A7S5Z0	Predicted protein OS=Nematostella vectensis	7.8	2
A7T9G3	Predicted protein OS=Nematostella vectensis	16.2	1
A7S7H8	Predicted protein OS=Nematostella vectensis	2.1	2
A7S7K4	Predicted protein OS=Nematostella vectensis	7.9	2
Q7YZK5	Tubulin beta chain (Fragment) OS=Nematostella vectensis	75.5	25
A7S8Z2	RuvB-like helicase OS=Nematostella vectensis	9.9	4
A7SAZ3	Acetyl-coenzyme A synthetase OS=Nematostella vectensis	2	1
A7T7R5	Predicted protein OS=Nematostella vectensis	7.6	2
A7SCK6	Predicted protein OS=Nematostella vectensis	11.3	2
A7SD28	Predicted protein OS=Nematostella vectensis	7.1	1
A7SDY3	Tubulin alpha chain OS=Nematostella vectensis	51	19
A7SF39	Predicted protein OS=Nematostella vectensis	3.3	1
A7SFJ3	Predicted protein OS=Nematostella vectensis	7.6	2
A7SG05	GTP-binding nuclear protein OS=Nematostella vectensis	19.8	4
A7SHH5	Protein disulfide-isomerase (Fragment) OS=Nematostella vectensis	4	2
A7SJR5	Predicted protein OS=Nematostella vectensis	1.2	1
A7SKV7	Predicted protein OS=Nematostella vectensis	1	2

A7SMT0	Predicted protein OS=Nematostella vectensis	13.4	2
A7SMZ7	Dynein light chain roadblock OS=Nematostella vectensis	12.5	1
A7SPM9	Predicted protein (Fragment) OS=Nematostella vectensis	2.3	1
A7SPQ4	Predicted protein OS=Nematostella vectensis	16.5	2
A7SQ60	Predicted protein OS=Nematostella vectensis	11.5	3
A7SQV3	Proteasome subunit beta OS=Nematostella vectensis	9.7	2
A7SUX1	Predicted protein OS=Nematostella vectensis	1.5	1
A7SVC4	Predicted protein OS=Nematostella vectensis	5.5	1
A7SVT6	Predicted protein OS=Nematostella vectensis	2.4	2
A7SW17	Predicted protein (Fragment) OS=Nematostella vectensis	2.6	1
A7SWC2	Predicted protein OS=Nematostella vectensis	3.1	2
A7SWR9	Predicted protein OS=Nematostella vectensis	8.6	2
A7SXD7	Protein disulfide-isomerase OS=Nematostella vectensis	2.7	1
A7SXN2	Peptidyl-prolyl cis-trans isomerase OS=Nematostella vectensis	25.2	2
A7T3D9	Predicted protein OS=Nematostella vectensis	5.7	2
A7T5A3	Predicted protein OS=Nematostella vectensis	2.7	1
A7TCL7	Histone H2A OS=Nematostella vectensis	35.6	10
A8DRV3	Vacuolar ATP synthase subunit B (Fragment) OS=Urticina eques	20.7	2
B3EZK6	Ribosomal protein S5 (Fragment) OS=Cyanea capillata	13.5	2
B5MG02	Beta tubulin (Fragment) OS=Cirripathes sp. TW24	48.6	6
C1IS27	Clathrin heavy chain (Fragment) OS=Carukia barnesi	8.8	1
C1IS28	Clathrin heavy chain (Fragment) OS=Carukia barnesi	24.8	5
C7SP37	Glyceraldehyde 3-phosphate dehydrogenase (Fragment) OS=Anemonia sulcata	17.9	2
G3LIV9	Heat shock cognate protein 71 OS=Hydractinia echinata	6.9	5
G8DM04	Cytochrome c oxidase subunit 2 OS=Chrysaora quinquecirrha	6.9	1
G9ISY6	NADH-ubiquinone oxidoreductase chain 1 OS=Pelagia noctiluca	6.2	2
G9ISX7	Cytochrome c oxidase subunit 2 OS=Pelagia noctiluca	8.1	1
Q8I822	14-3-3 protein A OS=Hydra vulgaris	7.2	2
K0A063	Beta-actin (Fragment) OS=Chrysaora quinquecirrha	66.3	20
M1E2A8	Calmodulin (Fragment) OS=Rhizostoma octopus	42.6	3
Q0H8V3	Heat shock protein 70 (Fragment) OS=Cnidaria environmental sample	12.2	2
Q6B4R5	Elongation factor 1-alpha OS=Scleronephthya gracillimum	7.8	3
Q2XWU1	Rab11 protein OS=Aiptasia pulchella	22.5	5
Q56GW1	60S ribosomal protein L12 (Fragment) OS=Hydractinia echinata	16.5	1
Q56GW5	40S ribosomal protein S4 (Fragment) OS=Hydractinia echinata	14.3	1
Q5EN87	Putative tyrosine-rich heat shock protein (Fragment) OS=Aurelia aurita	4.5	1
Q5EN88	Actin-related protein 2/3 complex subunit 5 OS=Aurelia aurita	7.3	1
Q5EN91	Putative 3-hydroxyacyl-Coenzyme A dehydrogenase (Fragment) OS=Aurelia aurita	32.6	4
Q5XPR4	NaK-ATPase alpha subunit (Fragment) OS=Hydractinia echinata	6.6	1
Q6PTK3	Triosephosphate isomerase (Fragment) OS=Obelia sp. KJP-2004	11.8	2
Q7YZI4	90-kDa heat-shock protein (Fragment) OS=Aurelia aurita	15.7	4
Q8I8B9	Putative beta-actin (Fragment) OS=Kudoa ovivora	70	2
Q8MUA5	Protein kinase B OS=Hydra vulgaris	2.8	1

Q8MV93	Myosin heavy chain type II (Fragment) OS=Podocoryna carnea	5.7	1
Q8WP37	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Dendronephthya klunzingeri	4.3	1
Q967E1	Heat shock protein 90 OS=Dendronephthya klunzingeri	6.5	4
Q967H6	Nucleoside diphosphate kinase OS=Hydra vulgaris	6	1
Q9GUZ6	PL10-related protein CnPL10 (Fragment) OS=Sandaria malayensis	18	2
Q9NDL6	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Sandaria malayensis	55	2
Q9XZE9	IQGAP (Fragment) OS=Hydra vulgaris	1.2	2
R9S2M2	Elongation factor 1-alpha OS=Aurelia aurita	13.1	6
T2M278	Hypoxia up-regulated protein 1 OS=Hydra vulgaris	1.6	1
T2M2P0	Coatomer subunit gamma (Fragment) OS=Hydra vulgaris	2.4	2
T2M2P5	RuvB-like helicase OS=Hydra vulgaris	10.8	4
T2M2X1	Adenylate kinase isoenzyme 5 OS=Hydra vulgaris	3.3	2
T2M388	Calcium/calmodulin-dependent protein kinase type II subunit alpha OS=Hydra vulgaris	6.9	3
T2M3D1	Eukaryotic translation initiation factor 3 subunit L OS=Hydra vulgaris	2.5	1
T2M3I7	RuvB-like helicase OS=Hydra vulgaris	3.5	1
T2M3N8	Septin-9 OS=Hydra vulgaris	4.5	2
T2M3U5	Sarcosine dehydrogenase,mitochondrial (Fragment) OS=Hydra vulgaris	1	1
T2M4B6	Vacuolar protein sorting-associated protein 45 OS=Hydra vulgaris	3.8	2
T2M4D5	Leucyl-tRNA synthetase,cytoplasmic (Fragment) OS=Hydra vulgaris	1.6	1
T2M4H6	Succinate-CoA ligase subunit beta (Fragment) OS=Hydra vulgaris	1.9	1
T2M4H7	Costars family protein C6orf115 OS=Hydra vulgaris	15.5	1
T2M4K8	Dentin sialophosphoprotein (Fragment) OS=Hydra vulgaris	1	1
T2M4N6	Guanine nucleotide-binding protein subunit beta-4 (Fragment) OS=Hydra vulgaris	9.7	3
T2M5B3	Phospholipid-transporting ATPase (Fragment) OS=Hydra vulgaris	3.4	2
T2M5D3	Protein transport protein Sec61 subunit alpha isoform 2 OS=Hydra vulgaris	2.3	1
T2M644	Microtubule-associated proteins 1A/1B light chain 3C OS=Hydra vulgaris	32.8	3
T2M694	Prohibitin OS=Hydra vulgaris	7.2	2
T2M6B6	Ethanolamine-phosphate cytidyltransferase OS=Hydra vulgaris	3.5	2
T2M6G7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Hydra vulgaris	1.4	1
T2M6J7	Alanine--glyoxylate aminotransferase 2, mitochondrial OS=Hydra vulgaris	4.1	1
T2M6L6	T-complex protein 1 subunit eta OS=Hydra vulgaris	6	3
T2M7J1	Vacuolar protein sorting-associated protein 35 (Fragment) OS=Hydra vulgaris	2.4	2
T2M7Z5	Ras-related protein Rab-3C OS=Hydra vulgaris	4.7	1
T2M8F7	Actin-related protein 2/3 complex subunit 1A (Fragment) OS=Hydra vulgaris	3.8	1
T2M9I3	Programmed cell death 6-interacting protein (Fragment) OS=Hydra vulgaris	1.1	1
T2MAB0	Staphylococcal nuclease domain-containing protein OS=Hydra vulgaris	2.6	2
T2MAB9	Tubulin alpha-1A chain (Fragment) OS=Hydra vulgaris	22.6	14
T2MAN2	Voltage-dependent calcium channel subunit alpha-2/delta-4 (Fragment) OS=Hydra vulgaris	0.7	1
T2MB89	Pre-mRNA-processing-splicing factor 8 OS=Hydra vulgaris	0.9	2
T2MBN1	Kynurenine--oxoglutarate transaminase 3 OS=Hydra vulgaris	2.9	1
T2MCX1	10-formyltetrahydrofolate dehydrogenase OS=Hydra vulgaris	1.3	1
T2MCX5	Vacuolar protein sorting-associated protein 26B (Fragment) OS=Hydra vulgaris	4	1

T2MD34	Serine/threonine protein phosphatase 2A regulatory subunit OS=Hydra vulgaris	2.8	1
T2MD44	Major vault protein OS=Hydra vulgaris	4.4	4
T2MDB0	Eukaryotic initiation factor 4A-II OS=Hydra vulgaris	3.4	1
T2MDG4	Flotillin-2 OS=Hydra vulgaris	9.1	4
T2MDI5	Septin-6 (Fragment) OS=Hydra vulgaris	3.7	1
T2MDK8	Spliceosome RNA helicase DDX39B OS=Hydra vulgaris	7.6	3
T2MDT0	Cytoplasmic dynein 1 heavy chain 1 OS=Hydra vulgaris	1.9	7
T2ME03	Quinone oxidoreductase OS=Hydra vulgaris	3.7	1
T2ME25	Guanine nucleotide-binding protein G(I) subunit alpha-1 OS=Hydra vulgaris	11.3	4
T2ME66	Ras-related protein Rab-11A OS=Hydra vulgaris	20.2	4
T2ME72	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Hydra vulgaris	3.4	1
T2MEA3	Myosin-1e (Fragment) OS=Hydra vulgaris	1.9	1
T2MEB5	ADP-ribosylation factor 1 OS=Hydra vulgaris	37.6	6
T2MEB6	26S protease regulatory subunit 8 OS=Hydra vulgaris	7.7	2
T2MEH3	Casein kinase II subunit alpha OS=Hydra vulgaris	5.1	2
T2MEI1	AP-2 complex subunit beta (Fragment) OS=Hydra vulgaris	5.7	4
T2MEI3	40S ribosomal protein S21 (Fragment) OS=Hydra vulgaris	17.3	1
T2MEK8	Ras-related protein Rab-1A OS=Hydra vulgaris	37.6	5
T2MEN2	40S ribosomal protein S6 OS=Hydra vulgaris	4.8	1
T2MEN5	Clathrin heavy chain OS=Hydra vulgaris	9.9	13
T2MEP0	26S protease regulatory subunit 10B OS=Hydra vulgaris	5.9	2
T2MEP2	40S ribosomal protein S18 OS=Hydra vulgaris	11.6	2
T2MEQ7	26S protease regulatory subunit 4 OS=Hydra vulgaris	5.7	2
T2MES1	40S ribosomal protein S15a OS=Hydra vulgaris	10.8	1
T2MET6	Ras-related protein Rap-1b OS=Hydra vulgaris	19.7	4
T2MEV0	Ras-related protein Rab-4B (Fragment) OS=Hydra vulgaris	5.8	1
T2MEV1	Tubulin beta chain (Fragment) OS=Hydra vulgaris	40.9	17
T2MEW2	Actin-related protein 3 OS=Hydra vulgaris	7.9	2
T2MEW9	Calcineurin subunit B type 1 OS=Hydra vulgaris	5.9	1
T2MEY1	60S ribosomal protein L11 (Fragment) OS=Hydra vulgaris	7.2	1
T2MF15	Eukaryotic peptide chain release factor subunit 1 OS=Hydra vulgaris	4.7	2
T2MF40	Tyrosine--tRNA ligase OS=Hydra vulgaris	1.4	1
T2MF93	Ras-related protein Rab-14 (Fragment) OS=Hydra vulgaris	28.4	5
T2MFD2	60S ribosomal protein L26 OS=Hydra vulgaris	6.2	1
T2MFH7	Poly(RC)-binding protein 3 (Fragment) OS=Hydra vulgaris	4.1	1
T2MFJ1	Stress-70 protein, mitochondrial (Fragment) OS=Hydra vulgaris	8.2	3
T2MFJ6	AP complex subunit sigma (Fragment) OS=Hydra vulgaris	5.3	1
T2MFJ8	Protein transport protein Sec24C OS=Hydra vulgaris	1.2	1
T2MFK0	Isocitrate dehydrogenase [NADP],mitochondrial (Fragment) OS=Hydra vulgaris	4.5	2
T2MFM1	Transitional endoplasmic reticulum ATPase (Fragment) OS=Hydra vulgaris	14.5	9
T2MFN7	Ras GTPase-activating-like protein IQGAP1 OS=Hydra vulgaris	1.1	2
T2MFQ3	Coatomer subunit beta (Fragment) OS=Hydra vulgaris	1	1
T2MFR8	Ras-related protein Rab-7a OS=Hydra vulgaris	39.3	8

T2MFU6	26S proteasome non-ATPase regulatory subunit 7 OS=Hydra vulgaris	5.2	1
T2MFU8	Rab GDP dissociation inhibitor (Fragment) OS=Hydra vulgaris	6.3	2
T2MFW8	T-complex protein 1 subunit delta OS=Hydra vulgaris	1.5	1
T2MFX1	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Hydra vulgaris	2.9	2
T2MFY6	Hippocalcin-like protein 1 OS=Hydra vulgaris	12.6	3
T2MFZ8	V-type proton ATPase catalytic subunit A OS=Hydra vulgaris	5.1	2
T2MG06	Transaldolase OS=Hydra vulgaris	6.2	2
T2MG36	Myosin-10 OS=Hydra vulgaris	2.6	5
T2MG47	Radixin OS=Hydra vulgaris	4.3	2
T2MG56	Coatomer subunit delta OS=Hydra vulgaris	1.9	1
T2MG68	Proteasome subunit beta OS=Hydra vulgaris	6.2	1
T2MGD8	Eukaryotic initiation factor 4A-III (Fragment) OS=Hydra vulgaris	2.6	1
T2MGF7	Malate dehydrogenase,mitochondrial OS=Hydra vulgaris	13.7	3
T2MGG5	Proteasome subunit alpha type OS=Hydra vulgaris	9.6	2
T2MGG7	ADP-ribosylation factor-like protein 3 OS=Hydra vulgaris	6.1	1
T2MGH4	Proteasome subunit alpha type OS=Hydra vulgaris	3.6	1
T2MGI7	ADP/ATP translocase 3 (Fragment) OS=Hydra vulgaris	9.4	3
T2MGN9	Fructose-1,6-bisphosphatase 1 (Fragment) OS=Hydra vulgaris	3.2	1
T2MGP8	Serine hydroxymethyltransferase,cytosolic OS=Hydra vulgaris	3	1
T2MGR0	60S ribosomal protein L17 OS=Hydra vulgaris	5.5	1
T2MGR5	60S ribosomal protein L7 (Fragment) OS=Hydra vulgaris	5.4	1
T2MGS3	cAMP-dependent protein kinase catalytic subunit alpha OS=Hydra vulgaris	8.3	2
T2MGT2	Transketolase OS=Hydra vulgaris	3.5	2
T2MGX7	60S ribosomal protein L13 (Fragment) OS=Hydra vulgaris	4.7	1
T2MGZ6	ATP synthase subunit alpha OS=Hydra vulgaris	20.2	9
T2MH23	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial (Fragment) OS=Hydra vulgaris	2.5	1
T2MH41	78 kDa glucose-regulated protein OS=Hydra vulgaris	5.9	4
T2MH44	Vacuolar proton pump subunit B (Fragment) OS=Hydra vulgaris	15.4	5
T2MH46	Filamin-A OS=Hydra vulgaris	0.9	3
T2MH95	Vinculin OS=Hydra vulgaris	1	1
T2MHE8	Aspartyl-tRNA synthetase,cytoplasmic OS=Hydra vulgaris	4	2
T2MHH5	Myosin-6 OS=Hydra vulgaris	4	7
T2MHI3	Flotillin-1 (Fragment) OS=Hydra vulgaris	3.4	1
T2MHI5	Alpha-actinin-1 OS=Hydra vulgaris	5.2	5
T2MHJ0	Non-specific serine/threonine protein kinase OS=Hydra vulgaris	5.6	2
T2MHJ7	60 kDa heat shock protein,mitochondrial (Fragment) OS=Hydra vulgaris	2	1
T2MHN7	Citrate synthase OS=Hydra vulgaris	2.6	1
T2MHT5	Heat shock protein HSP 90-alpha OS=Hydra vulgaris	9.8	9
T2MHY4	Argininosuccinate synthase (Fragment) OS=Hydra vulgaris	2.9	1
T2MIB9	AP-2 complex subunit alpha OS=Hydra vulgaris	3.8	3
T2MIJ7	Dysferlin OS=Hydra vulgaris	0.9	2
T2MIQ9	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial (Fragment) OS=Hydra vulgaris	1.8	1
T2MIR7	WD repeat-containing protein 1 OS=Hydra vulgaris	1.6	1

T2MIZ1	Arp2/3 complex 34 kDa subunit OS=Hydra vulgaris	3.7	1
T2MK48	Fucose mutarotase OS=Hydra vulgaris	13.6	1
W8PTQ2	Peroxiredoxin 4 OS=Cyanea capillata	27.9	6

2. In-solution digestion

2.1 Nematocyst extracted by 2% SDS couple with sonication and digested with trypsin enzyme

Table G-4. List of proteins identified (271 proteins) from nematocyst of highly venomous jellyfish by using extraction of SDS coupled with sonication. The proteins were derived from in-solution digestion experiment. Database of taxonomy Cnidaria (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
A0A3M6UR37	Eukaryotic translation initiation factor 3 subunit I OS=Pocillopora damicornis	3.8	1
T2MC16	Transmembrane emp24 domain-containing protein 2 OS=Hydra vulgaris	4.6	1
E5F7D0	Non-muscle actin II OS=Hydractinia echinata	59.3	19
T2MGY6	Sodium/potassium-transporting ATPase subunit alpha OS=Hydra vulgaris	3	2
P38984	40S ribosomal protein SA OS=Hydra viridissima	4.1	1
P41113	Actin-3 OS=Podocoryna carnea	57.7	19
P62184	Calmodulin OS=Renilla reniformis	33.6	3
B1PM92	Calmodulin OS=Acropora muricata	58.4	4
A0A0D3RWT7	Histone H3 (Fragment) OS=Halitholus cirratus	47.1	1
A0A0C2I839	Cytosol aminopeptidase OS=Thelohanellus kitauei	2.4	1
A0A1V0IGH5	Histone H2B OS=Hydra vulgaris	11.2	1
A0A0C2IX04	Actin, cytoplasmic 1 OS=Thelohanellus kitauei	29.3	10
A0A0C2J3J1	60 kDa heat shock protein, mitochondrial OS=Thelohanellus kitauei	2.1	1
A7S4S2	Predicted protein OS=Nematostella vectensis	7	2
A0A0C2MMZ6	Eukaryotic initiation factor 4A-III OS=Thelohanellus kitauei	5.8	2
A0A0C2MNQ3	Myosin-10 OS=Thelohanellus kitauei	2.3	2
A0A0C2MT43	Heat shock protein HSP 90-alpha 1 OS=Thelohanellus kitauei	1.7	1
A0A0C2MZD7	Uncharacterized protein OS=Thelohanellus kitauei	11.6	1
A0A0C2N200	Ras-related protein RABA2a OS=Thelohanellus kitauei	5.3	1
A0A0C2N354	ATP synthase subunit beta OS=Thelohanellus kitauei	9	3
A0A0C2N442	Ras-related protein Rab-11A OS=Thelohanellus kitauei	5.3	1
A0A0C2N4T5	ATP synthase subunit alpha OS=Thelohanellus kitauei	12.1	5
A0A0C2N6K0	Uncharacterized protein OS=Thelohanellus kitauei	10.8	1
A0A0C4VZ14	78 kDa glycose-regulated protein (Fragment) OS=Capnella imbricata	7.1	2
A0A2B4STX3	Heat shock protein 70 B2 OS=Stylophora pistillata	4.4	2
A0A169Q0T5	Glyceraldehyde-3-phosphate dehydrogenase OS=Aurelia sp. SETO	4.5	1
A0A1B3IQX8	Histone H2A OS=Hydractinia echinata	29	2
A0A1L2A726	Superoxide dismutase [Cu-Zn] OS=Cyanea capillata	18.2	2

A0A1U9XQR0	Fructose-bisphosphate aldolase OS=Aurelia sp. 1 GW-2014	6.6	2
A0A3M6TX36	Protein kinase domain-containing protein OS=Pocillopora damicornis	5.2	1
A0A2B4R3V3	Flagellar hook protein FlgE (Fragment) OS=Stylophora pistillata	3.1	1
A0A2B4R8X2	Spliceosome RNA helicase Ddx39b OS=Stylophora pistillata	3	1
A0A2B4R9T9	Chaperone protein DnaK OS=Stylophora pistillata	2.3	1
A7RQD8	Predicted protein OS=Nematostella vectensis	29.7	2
T2MHV0	Aldehyde dehydrogenase,mitochondrial OS=Hydra vulgaris	2.3	1
A0A2B4RDH6	Coiled-coil domain-containing protein 171 OS=Stylophora pistillata	0.8	1
T2MEZ1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial (Fragment) OS=Hydra vulgaris	3.2	1
A0A2B4RGE2	DNA repair protein complementing XP-G cells-like OS=Stylophora pistillata	1.4	1
A0A2B4RHG2	V-type proton ATPase catalytic subunit A OS=Stylophora pistillata	11.5	4
A0A2B4RHH5	Enoyl-CoA hydratase, mitochondrial OS=Stylophora pistillata	6	1
A0A2B4RHZ5	Ras-related C3 botulinum toxin substrate 1 OS=Stylophora pistillata	17.8	2
A7SSV8	Polyadenylate-binding protein OS=Nematostella vectensis	1.9	1
A0A3M6V529	Ribosomal_L23eN domain-containing protein (Fragment) OS=Pocillopora damicornis	7.5	1
A0A2B4RIG6	Glycolipid transfer protein OS=Stylophora pistillata	2.2	1
A0A2B4RJH1	Tubulin beta chain OS=Stylophora pistillata	64.9	21
A0A3M6TIL0	Uncharacterized protein OS=Pocillopora damicornis	6.5	1
A0A2B4RKT5	Actin-related protein 2 OS=Stylophora pistillata	15.2	4
A0A3M6V3V6	Uncharacterized protein OS=Pocillopora damicornis	7.2	1
A7SQS1	Malate dehydrogenase OS=Nematostella vectensis	4.7	1
A0A2B4RQL7	Protein Daple OS=Stylophora pistillata	0.5	1
A0A2B4RQN6	Uncharacterized protein OS=Stylophora pistillata	7.8	1
A0A3M6V4M9	Uncharacterized protein OS=Pocillopora damicornis	4.3	1
A7SRR4	Predicted protein OS=Nematostella vectensis	11.7	1
Q93116	Ub52 OS=Acropora millepora	34.1	4
A0A2B4RSY7	ADP-ribosylation factor 1 OS=Stylophora pistillata	27.8	3
A0A2B4RTB1	Tubulin alpha-1C chain OS=Stylophora pistillata	56.6	9
A0A2B4RU80	Coatomer subunit beta OS=Stylophora pistillata	1.9	1
Q2F6G0	Prohibitin (Fragment) OS=Anthopleura elegantissima	10	1
A0A2B4RX14	Ras-related protein Rab-5B OS=Stylophora pistillata	5.6	1
A7S494	40S ribosomal protein S27 OS=Nematostella vectensis	15.5	1
T2M4N6	Guanine nucleotide-binding protein subunit beta-4 (Fragment) OS=Hydra vulgaris	4	1
A0A2B4S092	Multifunctional fusion protein OS=Stylophora pistillata	0.4	1
A7T660	Glutamate dehydrogenase OS=Nematostella vectensis	5.5	1
A0A2B4S129	Peroxiredoxin-1 OS=Stylophora pistillata	4	1
T2MERO	40S ribosomal protein S14 OS=Hydra vulgaris	9.3	2
Q6YCH0	Ribosomal protein S3 (Fragment) OS=Hydra vulgaris	10.5	2
A7SWV8	Predicted protein OS=Nematostella vectensis	3.9	1
E0YPA3	Heat shock protein 70 OS=Seriatopora hystrix	3.6	2
A0A2B4S319	Non-specific serine/threonine protein kinase OS=Stylophora pistillata	5.4	2
A7SG05	GTP-binding nuclear protein OS=Nematostella vectensis	6	1
A0A3M6UK04	Uncharacterized protein OS=Pocillopora damicornis	0.8	2

T2MEG1	Cell division control protein 42 homolog OS=Hydra vulgaris	9.4	1
A0A3M6TPH2	RuvB-like helicase OS=Pocillopora damicornis	3.7	1
A0A3M6UUZ3	Uncharacterized protein OS=Pocillopora damicornis	6.1	1
A0A2B4S5E4	ADP-ribosylation factor 6 OS=Stylophora pistillata	14.9	2
A0A2B4S5R7	Uncharacterized protein OS=Stylophora pistillata	11.5	1
A0A3M6TNI0	AAA domain-containing protein OS=Pocillopora damicornis	4.6	1
A0A2B4S6M0	Tubulin alpha-1D chain OS=Stylophora pistillata	41.2	14
A7SHC3	Predicted protein (Fragment) OS=Nematostella vectensis	3.3	1
A0A2B4S736	Vacuolar proton pump subunit B OS=Stylophora pistillata	5.8	2
A0A2B4S8M8	Aminopeptidase OS=Stylophora pistillata	1.2	1
A7SIB3	Predicted protein OS=Nematostella vectensis	1.4	1
A7SU78	Predicted protein OS=Nematostella vectensis	3	1
T2MEK8	Ras-related protein Rab-1A OS=Hydra vulgaris	27.2	4
A0A3M6V4Z0	Uncharacterized protein OS=Pocillopora damicornis	0.1	1
T2MEW2	Actin-related protein 3 OS=Hydra vulgaris	5	1
A0A3M6UX22	AMP-binding domain-containing protein OS=Pocillopora damicornis	2.1	1
A0A2B4SCP3	Peptidylprolyl isomerase OS=Stylophora pistillata	9.9	1
Q5IGV0	DEAD box helicase PL10 (Fragment) OS=Nematostella vectensis	3.8	1
A0A2B4SD19	ATP-citrate synthase OS=Stylophora pistillata	1.5	1
A0A2B4SF60	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Stylophora pistillata	3.8	1
A0A3M6U683	AAA domain-containing protein OS=Pocillopora damicornis	6.6	2
A0A2B4SGJ7	Elongation factor 2 OS=Stylophora pistillata	5.2	4
A0A3M6TSM5	Uncharacterized protein OS=Pocillopora damicornis	1.5	1
A0A2B4SJ34	Heat shock protein 75 kDa, mitochondrial OS=Stylophora pistillata	1.6	1
A7SPP0	ATP synthase subunit beta OS=Nematostella vectensis	16.6	5
T2MGG2	Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment) OS=Hydra vulgaris	5.9	1
A0A2B4SM05	Myosin heavy chain, striated muscle OS=Stylophora pistillata	1.6	4
A0A3M6UV35	Citrate synthase OS=Pocillopora damicornis	5.6	1
A7RV73	Vacuolar protein sorting-associated protein 29 OS=Nematostella vectensis	7.1	1
A7SI51	Proteasome subunit alpha type (Fragment) OS=Nematostella vectensis	6.5	1
A7SMW8	Predicted protein OS=Nematostella vectensis	8.1	2
A7SHU3	Predicted protein OS=Nematostella vectensis	14.2	2
A0A2B4SSG8	Actin, cytoplasmic OS=Stylophora pistillata	21	5
A0A3M6V2N5	Adenosylhomocysteinase OS=Pocillopora damicornis	2.8	1
A7RGH4	Predicted protein OS=Nematostella vectensis	6.5	2
A0A2B4SU74	G protein-coupled receptor kinase OS=Stylophora pistillata	4.9	2
A0A2B4SUW9	Isocitrate dehydrogenase [NADP] OS=Stylophora pistillata	5.3	2
A7SQP1	Predicted protein OS=Nematostella vectensis	15.2	2
A7RID7	Predicted protein OS=Nematostella vectensis	5.9	1
A0A3M6T9T2	Coatmer subunit beta OS=Pocillopora damicornis	1.2	1
A0A2B4T1C4	ATP synthase subunit alpha OS=Stylophora pistillata	11.8	5
A0A2Z5WH73	Myosin heavy chain OS=Aurelia sp. 2017-HT	11.5	28
A0A2Z5WH75	Actin-2 OS=Aurelia sp. 2017-HT	64.1	20

A0A2Z5WH78	Ser-Thr kinase OS=Aurelia sp. 2017-HT	5.2	3
A0A2Z5WH80	Myosin regulatory light chain OS=Aurelia sp. 2017-HT	46.2	6
A0A2Z5WH81	Myosin essential light chain OS=Aurelia sp. 2017-HT	7.3	1
A0A2Z5WH82	Tropomyosin-1 OS=Aurelia sp. 2017-HT	10.7	3
A7RRG4	Actin-related protein 2/3 complex subunit 4 OS=Nematostella vectensis	11.9	1
A0A3M6T5Z6	NifU_N domain-containing protein (Fragment) OS=Pocillopora damicornis	18.5	1
A0A3M6T656	Uncharacterized protein OS=Pocillopora damicornis	0.2	1
A0A3M6TEB1	PPM-type phosphatase domain-containing protein OS=Pocillopora damicornis	1.6	1
A7T856	Predicted protein (Fragment) OS=Nematostella vectensis	19.6	1
A7TAP4	Predicted protein (Fragment) OS=Nematostella vectensis	7.5	1
A0A3M6TIF8	Uncharacterized protein OS=Pocillopora damicornis	5.1	1
A0A3M6TVL9	Uncharacterized protein OS=Pocillopora damicornis	2.1	1
A0A3M6TZ50	Uncharacterized protein OS=Pocillopora damicornis	10.9	3
A7RSB9	Predicted protein OS=Nematostella vectensis	4.5	3
A0A3M6U1Z2	Uncharacterized protein OS=Pocillopora damicornis	2.7	1
A0A3M6U507	Calponin-homology (CH) domain-containing protein OS=Pocillopora damicornis	5.4	1
A0A3M6U5G6	Uncharacterized protein OS=Pocillopora damicornis	16.2	1
A0A3M6UBG5	Clathrin heavy chain OS=Pocillopora damicornis	4.6	5
A0A3M6UBT2	AAA domain-containing protein OS=Pocillopora damicornis	8.8	2
A0A3M6UKG7	Uncharacterized protein OS=Pocillopora damicornis	3.4	1
A0A3M6UKT7	Uncharacterized protein OS=Pocillopora damicornis	5	3
A0A3M6UP81	Uncharacterized protein OS=Pocillopora damicornis	53.2	15
A7S766	Predicted protein OS=Nematostella vectensis	3.8	1
A7RYC0	Glutathione reductase OS=Nematostella vectensis	2.8	1
A0A3M6URD5	Uncharacterized protein OS=Pocillopora damicornis	2.1	1
Q6EIK7	Rab7 OS=Aiptasia pulchella	18	3
A0A3M6UX10	EGF-like domain-containing protein OS=Pocillopora damicornis	0.7	1
A7T6G0	Annexin OS=Nematostella vectensis	8.9	3
A0A3M6UZQ7	Uncharacterized protein OS=Pocillopora damicornis	1.4	1
A4UAH1	Beta-catenin OS=Podocoryna carnea	3.7	2
A9YTR1	Peptidyl-prolyl cis-trans isomerase (Fragment) OS=Exaiaptasia pallida	11	1
A7RGV0	Predicted protein OS=Nematostella vectensis	3.5	1
A7RIF0	T-complex protein 1 subunit eta OS=Nematostella vectensis	2.2	1
A7RKR4	Predicted protein OS=Nematostella vectensis	3.8	2
A7RNE1	Predicted protein OS=Nematostella vectensis	3	1
A7RNH9	Predicted protein OS=Nematostella vectensis	2.4	1
A7RNL3	Predicted protein OS=Nematostella vectensis	0.8	2
A7RPK0	Predicted protein OS=Nematostella vectensis	0.5	1
A7RT97	Predicted protein OS=Nematostella vectensis	3.2	2
A7T120	F-actin-capping protein subunit beta (Fragment) OS=Nematostella vectensis	18.5	1
A7RUF9	Predicted protein (Fragment) OS=Nematostella vectensis	8.9	1
A7RUT1	Tubulin alpha chain OS=Nematostella vectensis	56.4	15
A7RVC0	Clathrin heavy chain OS=Nematostella vectensis	5.1	6

A7RVD9	Tubulin alpha chain OS=Nematostella vectensis	43.3	12
A7RXC8	Predicted protein OS=Nematostella vectensis	2.8	1
A7S0L1	Vacuolar proton pump subunit B OS=Nematostella vectensis	5.1	2
A7S183	Predicted protein OS=Nematostella vectensis	4.2	1
A7S378	Isocitrate dehydrogenase [NADP] OS=Nematostella vectensis	3.2	1
A7S3I0	Predicted protein (Fragment) OS=Nematostella vectensis	4.4	3
A7S5Z0	Predicted protein OS=Nematostella vectensis	7.8	2
A7S6I6	Predicted protein OS=Nematostella vectensis	18.3	2
A7S6F3	Glutamate dehydrogenase OS=Nematostella vectensis	4.6	2
A7T9G3	Predicted protein OS=Nematostella vectensis	16.2	1
A7S7K4	Predicted protein OS=Nematostella vectensis	7.9	2
A7S7S5	Predicted protein OS=Nematostella vectensis	2.6	1
A7S8G2	Predicted protein OS=Nematostella vectensis	6.4	1
A7S8Z2	RuvB-like helicase OS=Nematostella vectensis	4.9	2
T2MF79	Transforming protein RhoA OS=Hydra vulgaris	21.4	2
A7SB00	Protein transport protein SEC23 OS=Nematostella vectensis	1.6	1
A7SDY3	Tubulin alpha chain OS=Nematostella vectensis	53.2	15
A7SF39	Predicted protein OS=Nematostella vectensis	3.3	1
A7T6B7	Casein kinase II subunit beta (Fragment) OS=Nematostella vectensis	26.7	1
A7SG65	Predicted protein OS=Nematostella vectensis	4	2
A7SHH5	Protein disulfide-isomerase (Fragment) OS=Nematostella vectensis	2.5	1
A7SJL4	Predicted protein OS=Nematostella vectensis	2.9	2
A7SMZ7	Dynein light chain roadblock OS=Nematostella vectensis	12.5	1
A7SPQ4	Predicted protein OS=Nematostella vectensis	9	2
A7SRK8	Adenosylhomocysteinase OS=Nematostella vectensis	5.4	2
A7SSK5	Predicted protein OS=Nematostella vectensis	5.1	1
A7SSL5	Predicted protein OS=Nematostella vectensis	3.3	2
A7T5Y2	Predicted protein OS=Nematostella vectensis	5.5	1
A7SZW4	Purple acid phosphatase (Fragment) OS=Nematostella vectensis	1.9	1
A7T1L2	Histone H2B OS=Nematostella vectensis	15.6	1
A7T2R3	Predicted protein (Fragment) OS=Nematostella vectensis	1.8	1
A7T3E5	Predicted protein (Fragment) OS=Nematostella vectensis	6.1	1
A7T4T2	Predicted protein OS=Nematostella vectensis	2.6	1
A7T5A3	Predicted protein OS=Nematostella vectensis	2.7	1
A7TCL7	Histone H2A OS=Nematostella vectensis	23.9	4
B2KTD5	Dickkopf protein 3 OS=Clytia hemisphaerica	7.9	1
B3EZX6	Ribosomal protein S5 (Fragment) OS=Cyanea capillata	14.6	2
C1IS27	Clathrin heavy chain (Fragment) OS=Carukia barnesi	12.8	2
C1IS28	Clathrin heavy chain (Fragment) OS=Carukia barnesi	10.1	2
C7SP37	Glyceraldehyde 3-phosphate dehydrogenase (Fragment) OS=Anemonia sulcata	17.9	2
D1FP01	Elongation factor 1-alpha OS=Malo kingi	13.5	4
D1FX74	HSP70-1 OS=Chironex fleckeri	3.5	2
D7F487	Actin (Fragment) OS=Porites compressa	64.2	5

G3LIV9	Heat shock cognate protein 71 OS=Hydractinia echinata	6.7	4
I2G9E9	Myosin II heavy chain, smooth/non-muscle-type (Fragment) OS=Clytia hemisphaerica	6.2	2
M4JUI0	Elongation factor 2 (Fragment) OS=Chloromyxum fluviatile	9.7	2
K0A063	Beta-actin (Fragment) OS=Chrysaora quinquecirrha	60.4	15
M1E2A8	Calmodulin (Fragment) OS=Rhizostoma octopus	42.6	3
M1G2E5	Ras2 (Fragment) OS=Hydractinia echinata	17.7	2
Q0H8V3	Heat shock protein 70 (Fragment) OS=Cnidaria environmental sample	12.2	2
Q6B4R5	Elongation factor 1-alpha OS=Scleronephthya gracillimum	11.9	5
Q56GW1	60S ribosomal protein L12 (Fragment) OS=Hydractinia echinata	16.5	1
Q56GW5	40S ribosomal protein S4 (Fragment) OS=Hydractinia echinata	14.3	1
Q5EN87	Putative tyrosine-rich heat shock protein (Fragment) OS=Aurelia aurita	4.5	1
Q5EN91	Putative 3-hydroxyacyl-Coenzyme A dehydrogenase (Fragment) OS=Aurelia aurita	26.9	3
Q5XPR4	NaK-ATPase alpha subunit (Fragment) OS=Hydractinia echinata	6.6	1
Q6PTK3	Triosephosphate isomerase (Fragment) OS=Obelia sp. KJP-2004	6.2	1
Q6PTK8	ATP synthase subunit beta (Fragment) OS=Obelia sp. KJP-2004	17.6	4
Q7YZI4	90-kDa heat-shock protein (Fragment) OS=Aurelia aurita	16.7	5
Q7YZK4	Tubulin beta chain (Fragment) OS=Aurelia aurita	70.8	20
Q8MV93	Myosin heavy chain type II (Fragment) OS=Podocoryna carnea	5.7	2
Q9GUZ6	PL10-related protein CnPL10 (Fragment) OS=Sanderia malayensis	24.6	2
Q9NDL6	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Sanderia malayensis	55	2
R9S2M2	Elongation factor 1-alpha OS=Aurelia aurita	12.6	6
T2M2X1	Adenylate kinase isoenzyme 5 OS=Hydra vulgaris	3.3	2
T2M388	Calcium/calmodulin-dependent protein kinase type II subunit alpha OS=Hydra vulgaris	4.8	2
T2M4D5	Leucyl-tRNA synthetase,cytoplasmic (Fragment) OS=Hydra vulgaris	1.6	1
T2M5D3	Protein transport protein Sec61 subunit alpha isoform 2 OS=Hydra vulgaris	2.3	1
T2MBN1	Kynurenine--oxoglutarate transaminase 3 OS=Hydra vulgaris	2.9	1
T2MD09	Splicing factor 3B subunit 3 OS=Hydra vulgaris	1.1	1
T2MD34	Serine/threonine protein phosphatase 2A regulatory subunit OS=Hydra vulgaris	2.8	1
T2MDB0	Eukaryotic initiation factor 4A-II OS=Hydra vulgaris	5.9	2
T2MDG4	Flotillin-2 OS=Hydra vulgaris	6.5	2
T2MDS7	Src substrate cortactin OS=Hydra vulgaris	1.7	1
T2ME03	Quinone oxidoreductase OS=Hydra vulgaris	3.7	1
T2ME39	Dynamin-1 (Fragment) OS=Hydra vulgaris	3.5	1
T2MEB5	ADP-ribosylation factor 1 OS=Hydra vulgaris	27.6	3
T2MEI3	40S ribosomal protein S21 (Fragment) OS=Hydra vulgaris	28.6	2
T2MEN5	Clathrin heavy chain OS=Hydra vulgaris	3.9	4
T2MEY1	60S ribosomal protein L11 (Fragment) OS=Hydra vulgaris	7.2	1
T2MF60	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Hydra vulgaris	4.8	1
T2MF93	Ras-related protein Rab-14 (Fragment) OS=Hydra vulgaris	7.5	2
T2MFH7	Poly(RC)-binding protein 3 (Fragment) OS=Hydra vulgaris	4.1	1
T2MFH8	Seryl-tRNA synthetase,cytoplasmic (Fragment) OS=Hydra vulgaris	2.6	1
T2MFJ1	Stress-70 protein, mitochondrial (Fragment) OS=Hydra vulgaris	7.9	3

T2MFM1	Transitional endoplasmic reticulum ATPase (Fragment) OS=Hydra vulgaris	8.7	5
T2MFW8	T-complex protein 1 subunit delta OS=Hydra vulgaris	3.2	1
T2MFY6	Hippocalcin-like protein 1 OS=Hydra vulgaris	14.1	2
T2MG06	Transaldolase OS=Hydra vulgaris	3.5	1
T2MG36	Myosin-10 OS=Hydra vulgaris	1.6	3
T2MGN9	Fructose-1,6-bisphosphatase 1 (Fragment) OS=Hydra vulgaris	3.2	1
T2MGP8	Serine hydroxymethyltransferase, cytosolic OS=Hydra vulgaris	3	1
T2MGR0	60S ribosomal protein L17 OS=Hydra vulgaris	5.5	1
T2MGR5	60S ribosomal protein L7 (Fragment) OS=Hydra vulgaris	3.8	1
T2MGS3	cAMP-dependent protein kinase catalytic subunit alpha OS=Hydra vulgaris	4.8	1
T2MGX7	60S ribosomal protein L13 (Fragment) OS=Hydra vulgaris	4.7	1
T2MGZ6	ATP synthase subunit alpha OS=Hydra vulgaris	15	6
T2MH23	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial (Fragment) OS=Hydra vulgaris	2.5	1
T2MH41	78 kDa glucose-regulated protein OS=Hydra vulgaris	1.7	1
T2MH44	Vacuolar proton pump subunit B (Fragment) OS=Hydra vulgaris	6	2
T2MH46	Filamin-A OS=Hydra vulgaris	0.6	1
T2MHD2	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Hydra vulgaris	3.4	1
T2MHE8	Aspartyl-tRNA synthetase, cytoplasmic OS=Hydra vulgaris	1.6	1
T2MHH5	Myosin-6 OS=Hydra vulgaris	3.2	6
T2MHI3	Flotillin-1 (Fragment) OS=Hydra vulgaris	3.4	1
T2MHN7	Citrate synthase OS=Hydra vulgaris	2.6	1
T2MHT5	Heat shock protein HSP 90-alpha OS=Hydra vulgaris	5.3	3
T2MHY4	Argininosuccinate synthase (Fragment) OS=Hydra vulgaris	2.9	1
T2MIR7	WD repeat-containing protein 1 OS=Hydra vulgaris	1.6	1
T2MIV7	Endothelial differentiation-related factor 1 OS=Hydra vulgaris	10.1	1
T2MIZ8	Exportin-1 (Fragment) OS=Hydra vulgaris	1.8	1
T2MJ29	Down syndrome critical region protein 3 OS=Hydra vulgaris	5.8	1
T2MJJ5	Myosin regulatory light chain 12B OS=Hydra vulgaris	21.8	3
W8PTQ2	Peroxiredoxin 4 OS=Cyanea capillata	18.2	4

2.2 Nematocyst extracted by PBS buffer couple with ultrasonication and digested with trypsin enzyme

Table G-5. List of proteins identified (295 proteins) from nematocyst of highly venomous jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were derived from in-solution digestion experiment. Database of taxonomy Cnidaria (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
T2MGY6	Sodium/potassium-transporting ATPase subunit alpha OS=Hydra vulgaris	3.8	3
T2MGR0	60S ribosomal protein L17 OS=Hydra vulgaris	11.5	2
P38984	40S ribosomal protein SA OS=Hydra viridissima	4.1	1

P4I113	Actin-3 OS=Podocoryna carnea	47.3	21
L0I7B7	Calmodulin (Fragment) OS=Hydractinia polyclina	15.3	1
A7S9A5	Predicted protein OS=Nematostella vectensis	3.8	1
A0A3M6TM92	Proteasome subunit alpha type OS=Pocillopora damicornis	6.1	1
A7RVW7	Predicted protein (Fragment) OS=Nematostella vectensis	6.2	1
A0A0C2MY51	60S ribosomal protein L27a OS=Thelohanellus kitauei	9	1
A0A0C2N354	ATP synthase subunit beta OS=Thelohanellus kitauei	11.1	4
A0A0C2N442	Ras-related protein Rab-11A OS=Thelohanellus kitauei	5.3	1
A0A0C4VZ14	78 kDa glycose-regulated protein (Fragment) OS=Capnella imbricata	16.1	4
A0A2B4STX3	Heat shock protein 70 B2 OS=Stylophora pistillata	6.1	3
L0I703	Calmodulin (Fragment) OS=Schuchertinia conchicola	18.6	1
A0A169Q0T5	Glyceraldehyde-3-phosphate dehydrogenase OS=Aurelia sp. SETO	7.7	2
A0A1L2A726	Superoxide dismutase [Cu-Zn] OS=Cyanea capillata	24	4
A0A1U9XQR0	Fructose-bisphosphate aldolase OS=Aurelia sp. 1 GW-2014	6.6	2
A7SFQ0	Mitogen-activated protein kinase OS=Nematostella vectensis	8.1	2
A0A288W1V6	Mitogen-activated protein kinase OS=Aurelia aurita	3.9	1
A0A2B4R8X2	Spliceosome RNA helicase Ddx39b OS=Stylophora pistillata	5.4	2
A0A2B4R8Y1	Uncharacterized protein OS=Stylophora pistillata	6.9	1
A0A2B4R9G5	Histone H2B OS=Stylophora pistillata	6.6	1
A0A2B4R9Q9	Histone H4 OS=Stylophora pistillata	39.2	13
A0A2B4R9T9	Chaperone protein DnaK OS=Stylophora pistillata	2.3	1
A0A2B4RAR4	60S ribosomal protein L4 (Fragment) OS=Stylophora pistillata	4.3	1
A7RQD8	Predicted protein OS=Nematostella vectensis	29.7	2
A0A2B4RBR2	REST corepressor 2 OS=Stylophora pistillata	2.6	1
A7SWU4	Predicted protein (Fragment) OS=Nematostella vectensis	8	2
T2MEZ1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial (Fragment) OS=Hydra vulgaris	8.5	3
A0A2B4RFA5	Serine/threonine-protein phosphatase OS=Stylophora pistillata	18.8	2
A7RKR4	Predicted protein OS=Nematostella vectensis	2.5	1
A0A2B4RHG2	V-type proton ATPase catalytic subunit A OS=Stylophora pistillata	12.8	4
A0A2B4RHH5	Enoyl-CoA hydratase, mitochondrial OS=Stylophora pistillata	6	1
A0A2B4RHZ5	Ras-related C3 botulinum toxin substrate 1 OS=Stylophora pistillata	18.9	2
A0A2B4RJH1	Tubulin beta chain OS=Stylophora pistillata	68	29
A0A3M6TIL0	Uncharacterized protein OS=Pocillopora damicornis	6.5	1
A0A3M6U938	Kinesin motor domain-containing protein OS=Pocillopora damicornis	2.3	1
A0A2B4RKT3	26S proteasome non-ATPase regulatory subunit 2 OS=Stylophora pistillata	1.7	1
A0A2B4RKT5	Actin-related protein 2 OS=Stylophora pistillata	10	3
A0A3M6V3V6	Uncharacterized protein OS=Pocillopora damicornis	14.4	2
A0A2B4RNB3	Centrosomal protein of 290 kDa OS=Stylophora pistillata	0.7	1
A0A2B4RPA9	Clathrin heavy chain OS=Stylophora pistillata	3	3
A0A2B4RPD3	Endoplasmic reticulum chaperone OS=Stylophora pistillata	2.7	2
A7S548	Predicted protein (Fragment) OS=Nematostella vectensis	6.9	1
A7SRR4	Predicted protein OS=Nematostella vectensis	17.5	2
A0A2B4RRK2	Tubulin beta chain OS=Stylophora pistillata	31.2	18

Q93116	Ub52 OS=Acropora millepora	19.4	2
A0A2B4RTB1	Tubulin alpha-1C chain OS=Stylophora pistillata	41.8	13
A0A2B4RTH4	Phosphoenolpyruvate carboxykinase, cytosolic [GTP] OS=Stylophora pistillata	2.2	1
A0A2B4RTL7	N-acetyltransferase ESCO1 OS=Stylophora pistillata	2.7	1
A7RXR8	Predicted protein OS=Nematostella vectensis	12.2	1
T2M3D0	Nucleolar protein 58 OS=Hydra vulgaris	2.6	1
A0A3M6UGY3	UBIQUITIN_CONJUGAT_2 domain-containing protein OS=Pocillopora damicornis	21.1	3
A0A2B4RXU3	Peptidyl-prolyl cis-trans isomerase OS=Stylophora pistillata	5.5	1
A7S494	40S ribosomal protein S27 OS=Nematostella vectensis	15.5	1
A7RTW3	Predicted protein OS=Nematostella vectensis	2.6	1
T2M4N6	Guanine nucleotide-binding protein subunit beta-4 (Fragment) OS=Hydra vulgaris	9.4	2
A0A2B4S0G4	T-complex protein 1 subunit zeta OS=Stylophora pistillata	4.9	1
A7T660	Glutamate dehydrogenase OS=Nematostella vectensis	5.5	1
A0A3M6UQ08	Nucleoside diphosphate kinase OS=Pocillopora damicornis	5.9	2
A0A2B4S2V2	Cathepsin B OS=Stylophora pistillata	5.7	1
A7SYN6	Predicted protein OS=Nematostella vectensis	3	1
A0A2B4S3R6	Cytochrome c oxidase subunit 6B1 OS=Stylophora pistillata	7.7	1
A7SFJ3	Predicted protein OS=Nematostella vectensis	12.2	3
A7SG05	GTP-binding nuclear protein OS=Nematostella vectensis	10.1	2
A0A3M6UK04	Uncharacterized protein OS=Pocillopora damicornis	0.4	1
T2MEG1	Cell division control protein 42 homolog OS=Hydra vulgaris	11	2
A0A3M6TNI0	AAA domain-containing protein OS=Pocillopora damicornis	4.6	1
A0A3M6UQS3	UBA_e1_C domain-containing protein OS=Pocillopora damicornis	1.4	1
A0A2B4S6M0	Tubulin alpha-1D chain OS=Stylophora pistillata	39.6	19
A0A2B4S736	Vacuolar proton pump subunit B OS=Stylophora pistillata	20.2	5
A0A2B4S8M8	Aminopeptidase OS=Stylophora pistillata	1.2	1
A0A3M6TK98	Uncharacterized protein OS=Pocillopora damicornis	2.6	1
T2MGT3	Calcium-transporting ATPase OS=Hydra vulgaris	1.8	1
A7SU78	Predicted protein OS=Nematostella vectensis	5.2	2
A0A3M6UDC7	Uncharacterized protein OS=Pocillopora damicornis	10.6	2
A0A2B4SCP3	Peptidylprolyl isomerase OS=Stylophora pistillata	10.6	2
A0A2B4SD19	ATP-citrate synthase OS=Stylophora pistillata	1.5	1
A0A2B4SGD3	Mechanosensory protein 2 OS=Stylophora pistillata	10.3	3
A0A2B4SE68	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Stylophora pistillata	3	1
A0A3M6U2E3	40S ribosomal protein S8 OS=Pocillopora damicornis	7.7	1
A0A2B4SG59	Uncharacterized protein C5orf42-like OS=Stylophora pistillata	0.4	1
A0A2B4SGR4	Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Stylophora pistillata	2.7	1
A0A2B4SGY9	Flotillin-1 OS=Stylophora pistillata	4.9	2
A0A3M6TKN8	Transaldolase OS=Pocillopora damicornis	3.4	1
M1G2E5	Ras2 (Fragment) OS=Hydractinia echinata	12.5	2
A0A3M6TSM5	Uncharacterized protein OS=Pocillopora damicornis	2.3	2
A7SPP0	ATP synthase subunit beta OS=Nematostella vectensis	16.3	5

A0A3M6V078	Rab GDP dissociation inhibitor OS=Pocillopora damicornis	4.5	1
T2MGG2	Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment) OS=Hydra vulgaris	5.9	1
A0A3M6TT74	Uncharacterized protein OS=Pocillopora damicornis	1	1
A7RV73	Vacuolar protein sorting-associated protein 29 OS=Nematostella vectensis	7.1	1
A0A2B4SPX6	Plastin-3 OS=Stylophora pistillata	1	2
A7SI51	Proteasome subunit alpha type (Fragment) OS=Nematostella vectensis	6.5	1
A7SKL5	Predicted protein (Fragment) OS=Nematostella vectensis	3	1
A7SHU3	Predicted protein OS=Nematostella vectensis	33.5	6
A0A3M6TRH7	Uncharacterized protein OS=Pocillopora damicornis	0.2	1
A0A2B4SRN5	Uncharacterized protein OS=Stylophora pistillata	1.1	1
A0A3M6V2N5	Adenosylhomocysteinase OS=Pocillopora damicornis	2.8	1
A7T2Q5	Serine/threonine-protein phosphatase OS=Nematostella vectensis	4.5	1
A0A2B4SV07	Tubulin beta chain OS=Stylophora pistillata	58.9	27
A7SQP1	Predicted protein OS=Nematostella vectensis	8.6	2
A7RID7	Predicted protein OS=Nematostella vectensis	5.9	1
A0A3M6TLP2	Uncharacterized protein OS=Pocillopora damicornis	13.1	2
A0A2B4SZ14	Sorting nexin-19 OS=Stylophora pistillata	1.4	1
A7SXE6	Predicted protein (Fragment) OS=Nematostella vectensis	3.5	1
A7T5T2	Predicted protein (Fragment) OS=Nematostella vectensis	22.2	1
A0A2B4T1C4	ATP synthase subunit alpha OS=Stylophora pistillata	19.9	10
A7S5C8	Predicted protein (Fragment) OS=Nematostella vectensis	2.1	1
B5MFZ9	Beta tubulin (Fragment) OS=Pocillopora verrucosa	58.9	10
A0A2Z5WH73	Myosin heavy chain OS=Aurelia sp. 2017-HT	12.7	29
A0A2Z5WH75	Actin-2 OS=Aurelia sp. 2017-HT	55.9	22
A0A2Z5WH78	Ser-Thr kinase OS=Aurelia sp. 2017-HT	5.2	3
A0A2Z5WH80	Myosin regulatory light chain OS=Aurelia sp. 2017-HT	44.4	7
A0A2Z5WH82	Tropomyosin-1 OS=Aurelia sp. 2017-HT	6.6	2
A7RK57	Predicted protein (Fragment) OS=Nematostella vectensis	2.5	1
A0A3M6T5Z6	NifU_N domain-containing protein (Fragment) OS=Pocillopora damicornis	18.5	1
A0A3M6T5Z9	Uncharacterized protein OS=Pocillopora damicornis	0.7	1
A7S2J5	Predicted protein OS=Nematostella vectensis	24.2	4
A0A3M6T6X2	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	11.4	1
A0A3M6T7E3	Uncharacterized protein OS=Pocillopora damicornis	10.6	2
A0A3M6TAD6	Uncharacterized protein OS=Pocillopora damicornis	3.4	1
A7T856	Predicted protein (Fragment) OS=Nematostella vectensis	19.6	1
A0A3M6TKC4	Uncharacterized protein OS=Pocillopora damicornis	4.9	1
A0A3M6TVL9	Uncharacterized protein OS=Pocillopora damicornis	4.1	3
A0A3M6TVV7	Hcy-binding domain-containing protein OS=Pocillopora damicornis	4.4	1
A0A3M6TYR5	CARMIL_C domain-containing protein OS=Pocillopora damicornis	0.8	1
A0A3M6U454	Histone H2A OS=Pocillopora damicornis	17.4	2
A0A3M6U507	Calponin-homology (CH) domain-containing protein OS=Pocillopora damicornis	5.4	1
A0A3M6UI08	Uncharacterized protein OS=Pocillopora damicornis	1.4	1
A0A3M6UKT7	Uncharacterized protein OS=Pocillopora damicornis	3.8	2

A0A3M6UP81	Uncharacterized protein OS=Pocillopora damicornis	46	17
A7S766	Predicted protein OS=Nematostella vectensis	3.8	1
A0A3M6UPR6	Uncharacterized protein OS=Pocillopora damicornis	2.9	1
A0A3M6UPZ4	Uncharacterized protein OS=Pocillopora damicornis	4.5	3
A0A3M6UUU1	Uncharacterized protein OS=Pocillopora damicornis	3.5	1
A0A3M6UXC6	Uncharacterized protein OS=Pocillopora damicornis	3.3	1
A0A3M6UZ63	Annexin OS=Pocillopora damicornis	6.3	4
A0A3M6V674	Uncharacterized protein OS=Pocillopora damicornis	3.8	1
A7RHS7	Predicted protein OS=Nematostella vectensis	4.6	2
A7RIF0	T-complex protein 1 subunit eta OS=Nematostella vectensis	4.8	2
A7RJZ8	Predicted protein OS=Nematostella vectensis	3.3	1
A7RLY5	Predicted protein OS=Nematostella vectensis	3.9	1
A7RMQ8	Proteasome subunit alpha type OS=Nematostella vectensis	9	1
A7T182	Predicted protein OS=Nematostella vectensis	11.5	4
A7RN57	Predicted protein (Fragment) OS=Nematostella vectensis	40.7	1
A7RNE1	Predicted protein OS=Nematostella vectensis	6.6	2
A7RNH9	Predicted protein OS=Nematostella vectensis	2.4	1
A7RNL3	Predicted protein OS=Nematostella vectensis	0.8	2
A7RQF7	Predicted protein OS=Nematostella vectensis	12.9	2
A7RQR3	10-formyltetrahydrofolate dehydrogenase OS=Nematostella vectensis	1.4	1
T2MFU6	26S proteasome non-ATPase regulatory subunit 7 OS=Hydra vulgaris	7.3	1
A7T836	Predicted protein (Fragment) OS=Nematostella vectensis	3.3	1
A7RTJ5	Predicted protein OS=Nematostella vectensis	6.8	2
A7RUF9	Predicted protein (Fragment) OS=Nematostella vectensis	8.9	2
A7RVD9	Tubulin alpha chain OS=Nematostella vectensis	41.1	16
A7RVM2	Predicted protein OS=Nematostella vectensis	6.9	1
A7S018	Obg-like ATPase 1 OS=Nematostella vectensis	3.8	1
A7S214	Predicted protein OS=Nematostella vectensis	13.8	2
A7S3I0	Predicted protein (Fragment) OS=Nematostella vectensis	5.2	5
A7S5Z0	Predicted protein OS=Nematostella vectensis	8.3	3
A7T9G3	Predicted protein OS=Nematostella vectensis	28.6	3
T2M3I7	RuvB-like helicase OS=Hydra vulgaris	3.1	1
A7S7K4	Predicted protein OS=Nematostella vectensis	7.9	2
A7S7S5	Predicted protein OS=Nematostella vectensis	2.6	1
A7S8G2	Predicted protein OS=Nematostella vectensis	11.4	3
A7SB00	Protein transport protein SEC23 OS=Nematostella vectensis	1.6	1
A7SBU6	Predicted protein OS=Nematostella vectensis	6.1	2
A7SCJ3	Succinate dehydrogenase (quinone) (Fragment) OS=Nematostella vectensis	5.3	2
A7SCK6	Predicted protein OS=Nematostella vectensis	11.3	2
A7SEA7	Predicted protein OS=Nematostella vectensis	38	16
A7SF39	Predicted protein OS=Nematostella vectensis	3.3	1
T2MH90	26S protease regulatory subunit 6A OS=Hydra vulgaris	4	1
A7SHH5	Protein disulfide-isomerase (Fragment) OS=Nematostella vectensis	2.5	1
A7SJ61	Predicted protein OS=Nematostella vectensis	8.6	5

A7SJR5	Predicted protein OS=Nematostella vectensis	1.2	1
A7SK96	40S ribosomal protein S12 OS=Nematostella vectensis	13.5	2
A7SMZ7	Dynein light chain roadblock OS=Nematostella vectensis	16.7	1
A7SQ60	Predicted protein OS=Nematostella vectensis	15.3	4
A7SQV3	Proteasome subunit beta OS=Nematostella vectensis	9.7	2
A7SRJ0	Non-specific serine/threonine protein kinase OS=Nematostella vectensis	3.4	1
A7SRK8	Adenosylhomocysteinase OS=Nematostella vectensis	8.8	3
A7SSL5	Predicted protein OS=Nematostella vectensis	4.9	3
A7SSV8	Polyadenylate-binding protein OS=Nematostella vectensis	2.6	1
A7STZ5	Predicted protein (Fragment) OS=Nematostella vectensis	0.7	1
A7T5Y2	Predicted protein OS=Nematostella vectensis	5.5	1
A7SWV8	Predicted protein OS=Nematostella vectensis	11.5	2
A7SWY0	Predicted protein (Fragment) OS=Nematostella vectensis	15.8	1
A7SXD7	Protein disulfide-isomerase OS=Nematostella vectensis	2.7	1
A7SXN2	Peptidyl-prolyl cis-trans isomerase OS=Nematostella vectensis	29.4	3
A7T0V9	Predicted protein OS=Nematostella vectensis	30.8	2
A7T1L2	Histone H2B OS=Nematostella vectensis	15.6	1
A7T288	T-complex protein 1 subunit delta OS=Nematostella vectensis	2.1	1
A7T4C2	Predicted protein (Fragment) OS=Nematostella vectensis	58.9	8
A7T6F7	Predicted protein (Fragment) OS=Nematostella vectensis	24.1	1
A7T8T4	Tubulin beta chain OS=Nematostella vectensis	27.7	3
A7TCL7	Histone H2A OS=Nematostella vectensis	38.3	12
A8DRV3	Vacuolar ATP synthase subunit B (Fragment) OS=Urticina eques	20.7	2
B3EZK6	Ribosomal protein S5 (Fragment) OS=Cyanea capillata	14	2
B5MG02	Beta tubulin (Fragment) OS=Cirrhopathes sp. TW24	50.7	7
C1IJE5	Smooth muscle myosin heavy chain 11 isoform-like protein (Fragment) OS=Myxobolus cerebrialis	4.4	1
C1IS27	Clathrin heavy chain (Fragment) OS=Carukia barnesi	8.8	1
C1K2L2	Beta-actin (Fragment) OS=Orbicella franksi	25	1
C7SP37	Glyceraldehyde 3-phosphate dehydrogenase (Fragment) OS=Anemonia sulcata	18.4	2
D1FP01	Elongation factor 1-alpha OS=Malo kingi	13.2	4
D1FX74	HSP70-1 OS=Chironex fleckeri	3.5	2
D2JYS2	Beta-catenin OS=Hydractinia echinata	11.4	5
G3LIV9	Heat shock cognate protein 71 OS=Hydractinia echinata	6.9	5
G9ISX7	Cytochrome c oxidase subunit 2 OS=Pelagia noctiluca	8.1	1
I2G9E9	Myosin II heavy chain, smooth/non-muscle-type (Fragment) OS=Clytia hemisphaerica	3.4	1
Q8I822	14-3-3 protein A OS=Hydra vulgaris	7.2	2
K0A063	Beta-actin (Fragment) OS=Chrysaora quinquecirrha	58.9	21
M1E2P9	Calmodulin (Fragment) OS=Rhizostoma octopus	22.8	1
Q0H8V3	Heat shock protein 70 (Fragment) OS=Cnidaria environmental sample	12.2	2
Q56GW1	60S ribosomal protein L12 (Fragment) OS=Hydractinia echinata	16.5	1
Q5EN91	Putative 3-hydroxyacyl-Coenzyme A dehydrogenase (Fragment) OS=Aurelia aurita	25.7	3
Q5WR13	Non-muscle actin (Fragment) OS=Hydra viridissima	50.6	9
Q5XPR4	NaK-ATPase alpha subunit (Fragment) OS=Hydractinia echinata	6.6	1

Q6PTK3	Triosephosphate isomerase (Fragment) OS=Obelia sp. KJP-2004	6.2	1
Q6PTK8	ATP synthase subunit beta (Fragment) OS=Obelia sp. KJP-2004	20.1	6
Q6YCH0	Ribosomal protein S3 (Fragment) OS=Hydra vulgaris	18.5	4
Q7YZI4	90-kDa heat-shock protein (Fragment) OS=Aurelia aurita	17.1	6
Q7YZJ5	Elongation factor 2 (Fragment) OS=Aurelia aurita	9.9	2
Q7YZK4	Tubulin beta chain (Fragment) OS=Aurelia aurita	74.2	27
Q7YZL5	Tubulin alpha chain (Fragment) OS=Aurelia aurita	57.8	19
Q8I8C6	Putative beta-actin (Fragment) OS=Myxobolus insidiosus	21.7	1
Q9GUZ6	PL10-related protein CnPL10 (Fragment) OS=Sanderia malayensis	14.8	1
Q9NDL6	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Sanderia malayensis	76.2	4
R9S2M2	Elongation factor 1-alpha OS=Aurelia aurita	11.2	5
T2M2W2	Talin-2 OS=Hydra vulgaris	1.2	2
T2M2X1	Adenylate kinase isoenzyme 5 OS=Hydra vulgaris	3.3	2
T2M3N8	Septin-9 OS=Hydra vulgaris	5.7	2
T2M489	LIM domain and actin-binding protein 1 OS=Hydra vulgaris	3	1
T2M4D5	Leucyl-tRNA synthetase,cytoplasmic (Fragment) OS=Hydra vulgaris	1.6	1
T2M4H7	Costars family protein C6orf115 OS=Hydra vulgaris	15.5	1
T2M4L8	Glyoxalase domain-containing protein 4 OS=Hydra vulgaris	6.5	1
T2M6J7	Alanine--glyoxylate aminotransferase 2, mitochondrial OS=Hydra vulgaris	4.1	1
T2M6L6	T-complex protein 1 subunit eta OS=Hydra vulgaris	3.8	2
T2MAB9	Tubulin alpha-1A chain (Fragment) OS=Hydra vulgaris	17	11
T2MBN1	Kynurenine--oxoglutarate transaminase 3 OS=Hydra vulgaris	2.9	1
T2MD44	Major vault protein OS=Hydra vulgaris	2.9	2
T2MD57	Calcium-transporting ATPase OS=Hydra vulgaris	4.2	6
T2MDB0	Eukaryotic initiation factor 4A-II OS=Hydra vulgaris	11	3
T2MDE9	Spectrin alpha chain, brain (Fragment) OS=Hydra vulgaris	0.5	1
T2MDG4	Flotillin-2 OS=Hydra vulgaris	5.6	3
T2MDT0	Cytoplasmic dynein 1 heavy chain 1 OS=Hydra vulgaris	0.6	2
T2ME39	Dynamin-1 (Fragment) OS=Hydra vulgaris	3.5	1
T2ME66	Ras-related protein Rab-11A OS=Hydra vulgaris	6	1
T2ME72	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Hydra vulgaris	3.4	1
T2MEB5	ADP-ribosylation factor 1 OS=Hydra vulgaris	13.8	2
T2MEB6	26S protease regulatory subunit 8 OS=Hydra vulgaris	5.1	1
T2MEI1	AP-2 complex subunit beta (Fragment) OS=Hydra vulgaris	5.4	3
T2MEN5	Clathrin heavy chain OS=Hydra vulgaris	4.6	5
T2MEQ7	26S protease regulatory subunit 4 OS=Hydra vulgaris	5.7	2
T2MEV1	Tubulin beta chain (Fragment) OS=Hydra vulgaris	37.1	17
T2MEY1	60S ribosomal protein L11 (Fragment) OS=Hydra vulgaris	7.2	1
T2MF17	Ras-related C3 botulinum toxin substrate 1 OS=Hydra vulgaris	10.9	2
T2MF93	Ras-related protein Rab-14 (Fragment) OS=Hydra vulgaris	29.4	4
T2MFG0	Transmembrane emp24 domain-containing protein 10 (Fragment) OS=Hydra vulgaris	4	1
T2MFH7	Poly(RC)-binding protein 3 (Fragment) OS=Hydra vulgaris	4.1	1
T2MFJ1	Stress-70 protein, mitochondrial (Fragment) OS=Hydra vulgaris	5.7	2

T2MFM1	Transitional endoplasmic reticulum ATPase (Fragment) OS=Hydra vulgaris	19	11
T2MFR8	Ras-related protein Rab-7a OS=Hydra vulgaris	32	6
T2MFY6	Hippocalcin-like protein 1 OS=Hydra vulgaris	6.8	1
T2MFZ8	V-type proton ATPase catalytic subunit A OS=Hydra vulgaris	10.9	4
T2MG06	Transaldolase OS=Hydra vulgaris	3.5	1
T2MG46	T-complex protein 1 subunit epsilon OS=Hydra vulgaris	3	1
T2MGF7	Malate dehydrogenase,mitochondrial OS=Hydra vulgaris	5.6	1
T2MGG5	Proteasome subunit alpha type OS=Hydra vulgaris	6.1	1
T2MGP8	Serine hydroxymethyltransferase,cytosolic OS=Hydra vulgaris	3	1
T2MGS3	cAMP-dependent protein kinase catalytic subunit alpha OS=Hydra vulgaris	4.8	1
T2MGZ6	ATP synthase subunit alpha OS=Hydra vulgaris	16.3	8
T2MH18	Adenosylhomocysteinase OS=Hydra vulgaris	2.3	1
T2MH23	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial (Fragment) OS=Hydra vulgaris	2.5	1
T2MH41	78 kDa glucose-regulated protein OS=Hydra vulgaris	3.3	2
T2MH46	Filamin-A OS=Hydra vulgaris	0.6	1
T2MH95	Vinculin OS=Hydra vulgaris	1	1
T2MHH5	Myosin-6 OS=Hydra vulgaris	3.2	5
T2MHI5	Alpha-actinin-1 OS=Hydra vulgaris	4.6	5
T2MHJ0	Non-specific serine/threonine protein kinase OS=Hydra vulgaris	6.8	2
T2MHJ7	60 kDa heat shock protein,mitochondrial (Fragment) OS=Hydra vulgaris	2	1
T2MHN7	Citrate synthase OS=Hydra vulgaris	2.6	1
T2MHT5	Heat shock protein HSP 90-alpha OS=Hydra vulgaris	6.9	5
T2MHZ2	Dynamin-like 120 kDa protein,mitochondrial OS=Hydra vulgaris	1.2	1
T2MI89	LIM domain-binding protein 3 OS=Hydra vulgaris	2.4	1
T2MI97	Dystrobrevin beta (Fragment) OS=Hydra vulgaris	1.7	1
T2MIF5	Endothelin-converting enzyme 2 OS=Hydra vulgaris	3.1	1
T2MIR7	WD repeat-containing protein 1 OS=Hydra vulgaris	1.6	1
T2MIT5	Protein diaphanous homolog 2 OS=Hydra vulgaris	1.1	1
T2MIV7	Endothelial differentiation-related factor 1 OS=Hydra vulgaris	10.1	1
T2MIX5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial OS=Hydra vulgaris	11.2	2
T2MJ29	Down syndrome critical region protein 3 OS=Hydra vulgaris	5.8	1
U3PBW0	Beta actin (Fragment) OS=Aurelia aurita	41.7	11
W8PTQ2	Peroxisredoxin 4 OS=Cyanea capillata	30.4	8
W8Q1J8	Glyceraldehyde-3-phosphate dehydrogenase OS=Cyanea capillata	12.8	3

2.3 Nematocyst extracted by PBS buffer couple with ultrasonication and digested with PNGase and trypsin enzyme

Table G-6. List of proteins identified (383 proteins) from nematocyst of highly venomous jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were derived from in-solution digestion experiment. Database of taxonomy Cnidaria (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
T2MGY6	Sodium/potassium-transporting ATPase subunit alpha OS=Hydra vulgaris	4	3
P37380	60S ribosomal protein L17 OS=Podocoryna carnea	13.7	2
P38984	40S ribosomal protein SA OS=Hydra viridissima	4.1	1
P41113	Actin-3 OS=Podocoryna carnea	52.9	15
M1G4Y4	Ras1 (Fragment) OS=Hydractinia echinata	13.4	1
B1PM92	Calmodulin OS=Acropora muricata	22.8	2
A7S9A5	Predicted protein OS=Nematostella vectensis	3.8	1
A0A069DM56	Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Clytia hemisphaerica	4	1
A0A0C2ICD9	Uncharacterized protein OS=Thelohanellus kitauei	4.3	1
A0A1V0IGH5	Histone H2B OS=Hydra vulgaris	11.2	1
T2MF79	Transforming protein RhoA OS=Hydra vulgaris	16.7	3
A0A0C2M952	T-complex protein 1 subunit alpha OS=Thelohanellus kitauei	1.8	1
A0A0C2MAD5	GMP reductase 1 OS=Thelohanellus kitauei	8.6	1
A0A0C2MNH0	Stress-70 protein, mitochondrial OS=Thelohanellus kitauei	4.1	2
A0A0C2MT43	Heat shock protein HSP 90-alpha 1 OS=Thelohanellus kitauei	1.7	1
A7RVW7	Predicted protein (Fragment) OS=Nematostella vectensis	6.2	1
A0A0C2N1N8	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Thelohanellus kitauei	4.8	1
A0A0C2N354	ATP synthase subunit beta OS=Thelohanellus kitauei	9	3
A0A0C4VZ14	78 kDa glycose-regulated protein (Fragment) OS=Capnella imbricata	16.1	4
A0A2B4STX3	Heat shock protein 70 B2 OS=Stylophora pistillata	6.1	3
L0F703	Calmodulin (Fragment) OS=Schuchertinia conchicola	18.6	1
A0A169Q0T5	Glyceraldehyde-3-phosphate dehydrogenase OS=Aurelia sp. SETO	4.5	1
A0A181ZMR8	Beta-actin (Fragment) OS=Sinularia cf. cruciata GS-2016	26.6	6
A0A1L2A726	Superoxide dismutase [Cu-Zn] OS=Cyanea capillata	18.2	3
A0A1U9XQR0	Fructose-bisphosphate aldolase OS=Aurelia sp. 1 GW-2014	3.9	1
A0A288W1V0	Mitogen-activated protein kinase OS=Aurelia aurita	20.1	3
A0A288W1V6	Mitogen-activated protein kinase OS=Aurelia aurita	8.5	2
A7SB00	Protein transport protein SEC23 OS=Nematostella vectensis	2.1	1
A0A2B4R7X4	Uncharacterized protein OS=Stylophora pistillata	3.9	1
A0A2B4R8X2	Spliceosome RNA helicase Ddx39b OS=Stylophora pistillata	3	1
A0A2B4R9G5	Histone H2B OS=Stylophora pistillata	7.3	2
A0A2B4R9T9	Chaperone protein DnaK OS=Stylophora pistillata	2.3	1
A0A2B4RAR4	60S ribosomal protein L4 (Fragment) OS=Stylophora pistillata	4.3	1
A7RQD8	Predicted protein OS=Nematostella vectensis	29.7	2
T2MEZ1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial (Fragment) OS=Hydra vulgaris	3.6	2
A0A2B4RFA5	Serine/threonine-protein phosphatase OS=Stylophora pistillata	25.3	3
T2M2P0	Coatomer subunit gamma (Fragment) OS=Hydra vulgaris	1.4	1
A0A2B4RHG2	V-type proton ATPase catalytic subunit A OS=Stylophora pistillata	20.7	8
A0A2B4RHH5	Enoyl-CoA hydratase, mitochondrial OS=Stylophora pistillata	6	1
A0A2B4RHZ5	Ras-related C3 botulinum toxin substrate 1 OS=Stylophora pistillata	17.8	2
A0A3M6TI71	Glutamate dehydrogenase OS=Pocillopora damicornis	7.2	2
A0A3M6V529	Ribosomal_L23eN domain-containing protein (Fragment) OS=Pocillopora	7.5	1

	damicornis		
A0A2B4RJH1	Tubulin beta chain OS=Stylophora pistillata	61.5	22
A0A3M6TIL0	Uncharacterized protein OS=Pocillopora damicornis	6.5	1
A0A2B4RK77	Asparagine--tRNA ligase, cytoplasmic OS=Stylophora pistillata	4.6	1
A0A3M6U938	Kinesin motor domain-containing protein OS=Pocillopora damicornis	2.3	1
A0A2B4RKT3	26S proteasome non-ATPase regulatory subunit 2 OS=Stylophora pistillata	3.3	2
A0A2B4RKT5	Actin-related protein 2 OS=Stylophora pistillata	10	3
A0A3M6T5M4	Glucose-6-phosphate 1-dehydrogenase OS=Pocillopora damicornis	1.9	1
A0A2B4RPA9	Clathrin heavy chain OS=Stylophora pistillata	3.8	4
A0A3M6TSZ4	Uncharacterized protein OS=Pocillopora damicornis	2.9	1
A7SQS1	Malate dehydrogenase OS=Nematostella vectensis	4.7	1
A0A2B4RRK2	Tubulin beta chain OS=Stylophora pistillata	26.6	13
Q93116	Ub52 OS=Acropora millepora	19.4	2
A0A2B4RTB1	Tubulin alpha-1C chain OS=Stylophora pistillata	61	16
A0A2B4RTD9	Catenin alpha-2 OS=Stylophora pistillata	1.1	1
A0A2B4RTH4	Phosphoenolpyruvate carboxykinase, cytosolic [GTP] OS=Stylophora pistillata	2.2	1
A0A2B4RTL7	N-acetyltransferase ESCO1 OS=Stylophora pistillata	2.7	1
A7RXR8	Predicted protein OS=Nematostella vectensis	12.2	1
Q2F6G0	Prohibitin (Fragment) OS=Anthopleura elegantissima	10	1
T2M3D0	Nucleolar protein 58 OS=Hydra vulgaris	2.6	1
A0A3M6UCM8	MPN domain-containing protein OS=Pocillopora damicornis	1	1
A0A3M6UGY3	UBIQUITIN_CONJUGAT_2 domain-containing protein OS=Pocillopora damicornis	16.4	2
T2MB56	Hydroxysteroid dehydrogenase-like protein 2 OS=Hydra vulgaris	3.4	1
A0A2B4RXI4	Ras-related protein Rab-5B OS=Stylophora pistillata	5.6	1
A7S494	40S ribosomal protein S27 OS=Nematostella vectensis	15.5	1
A0A2B4RYR5	60S ribosomal protein L5 (Fragment) OS=Stylophora pistillata	7.7	1
A0A2B4RZG2	Guanine nucleotide-binding protein subunit beta OS=Stylophora pistillata	18.7	4
A0A3M6TNT3	Coatomer subunit delta OS=Pocillopora damicornis	2.4	1
A0A2B4S0G4	T-complex protein 1 subunit zeta OS=Stylophora pistillata	4.9	1
Q9Y207	G protein a subunit 3 (Fragment) OS=Hydra vulgaris	5.2	1
A7T660	Glutamate dehydrogenase OS=Nematostella vectensis	5.5	1
A0A2B4S129	Peroxiredoxin-1 OS=Stylophora pistillata	4	1
Q6YCH0	Ribosomal protein S3 (Fragment) OS=Hydra vulgaris	14.7	3
A7RUL8	Predicted protein (Fragment) OS=Nematostella vectensis	3.1	1
A0A2B4S2V2	Cathepsin B OS=Stylophora pistillata	5.7	1
A0A2B4S3I9	Non-specific serine/threonine protein kinase OS=Stylophora pistillata	2.8	1
A7SYN6	Predicted protein OS=Nematostella vectensis	5	3
A0A3M6UH90	Oxysterol-binding protein OS=Pocillopora damicornis	1.7	1
A7SG05	GTP-binding nuclear protein OS=Nematostella vectensis	15.2	3
A0A3M6UK04	Uncharacterized protein OS=Pocillopora damicornis	0.4	1
T2MEG1	Cell division control protein 42 homolog OS=Hydra vulgaris	17.8	3
A0A3M6TBN4	S-AdoMet_synt_C domain-containing protein (Fragment) OS=Pocillopora damicornis	22.7	1
A0A2B4S5E4	ADP-ribosylation factor 6 OS=Stylophora pistillata	8.6	1

A7SJ61	Predicted protein OS=Nematostella vectensis	8.3	5
A0A3M6TNI0	AAA domain-containing protein OS=Pocillopora damicornis	4.6	1
A0A2B4S6M0	Tubulin alpha-1D chain OS=Stylophora pistillata	44.4	21
A0A3M6TI13	10-formyltetrahydrofolate dehydrogenase OS=Pocillopora damicornis	0.6	1
A0A2B4S736	Vacuolar proton pump subunit B OS=Stylophora pistillata	17.7	4
A0A2B4S8M8	Aminopeptidase OS=Stylophora pistillata	1.2	1
A0A3M6TK98	Uncharacterized protein OS=Pocillopora damicornis	2.6	1
T2MGT3	Calcium-transporting ATPase OS=Hydra vulgaris	1.8	1
A7RIX7	Proteasome subunit alpha type OS=Nematostella vectensis	4.1	1
T2MEK8	Ras-related protein Rab-1A OS=Hydra vulgaris	13.9	2
A0A2B4SC25	Sacsin (Fragment) OS=Stylophora pistillata	0.2	1
A0A2B4SC49	Actin-related protein 3 OS=Stylophora pistillata	15.1	3
A0A3M6UX22	AMP-binding domain-containing protein OS=Pocillopora damicornis	2.1	1
A0A2B4SCP3	Peptidylprolyl isomerase OS=Stylophora pistillata	10.6	2
J3T9N7	PL10 OS=Euphyllia ancora	2.6	1
A0A3M6U2E3	40S ribosomal protein S8 OS=Pocillopora damicornis	7.7	1
A0A2B4SG59	Uncharacterized protein C5orf42-like OS=Stylophora pistillata	0.4	1
T2M8Q9	Probable aminopeptidase NPEPL1 OS=Hydra vulgaris	2.6	1
A7RRK9	Predicted protein (Fragment) OS=Nematostella vectensis	3.7	1
A0A2B4SGY9	Flotillin-1 OS=Stylophora pistillata	2.6	1
A0A2B4SH13	Mechanosensory protein 2 OS=Stylophora pistillata	13.7	3
A0A2B4SH39	Methylmalonyl-CoA mutase, mitochondrial OS=Stylophora pistillata	2.1	1
A7SAS1	Predicted protein OS=Nematostella vectensis	23.1	3
A0A3M6TSM5	Uncharacterized protein OS=Pocillopora damicornis	1.5	1
A7SPP0	ATP synthase subunit beta OS=Nematostella vectensis	13.5	4
T2MGG2	Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment) OS=Hydra vulgaris	5.9	1
A0A3M6TT74	Uncharacterized protein OS=Pocillopora damicornis	1	1
T2MGE3	Proteasome subunit alpha type OS=Hydra vulgaris	5	1
Q58I86	Leonardo protein (Fragment) OS=Hydractinia echinata	26.3	2
A7RV73	Vacuolar protein sorting-associated protein 29 OS=Nematostella vectensis	7.1	1
A0A2B4SPX6	Plastin-3 OS=Stylophora pistillata	1	2
A7SI51	Proteasome subunit alpha type (Fragment) OS=Nematostella vectensis	6.5	1
A7SMW8	Predicted protein OS=Nematostella vectensis	5.4	1
A7SHU3	Predicted protein OS=Nematostella vectensis	33.5	6
A0A2B4SR60	AP-2 complex subunit alpha OS=Stylophora pistillata	3	1
A0A2B4SRE9	AP complex subunit beta OS=Stylophora pistillata	3.7	3
A0A3M6V2N5	Adenosylhomocysteinase OS=Pocillopora damicornis	2.8	1
A0A3M6V0Z0	Uncharacterized protein OS=Pocillopora damicornis	0.7	1
Q8IAC3	Actin OS=Galaxea fascicularis	38	11
A0A3M6UZZ8	Uncharacterized protein OS=Pocillopora damicornis	0.8	1
A0A2B4SUQ0	S-phase kinase-associated protein 1 OS=Stylophora pistillata	19.2	2
Q4JG19	Proteasome subunit beta OS=Swiftia exserta	4.9	1
A0A2B4SV07	Tubulin beta chain OS=Stylophora pistillata	54.5	21

A7SQP1	Predicted protein OS=Nematostella vectensis	15.2	3
A7RID7	Predicted protein OS=Nematostella vectensis	5.9	1
A0A3M6TM92	Proteasome subunit alpha type OS=Pocillopora damicornis	16	2
A0A3M6TLP2	Uncharacterized protein OS=Pocillopora damicornis	13.1	2
A7SXE6	Predicted protein (Fragment) OS=Nematostella vectensis	3.5	1
A7T5T2	Predicted protein (Fragment) OS=Nematostella vectensis	22.2	1
A0A2B4T1C4	ATP synthase subunit alpha OS=Stylophora pistillata	16.7	7
A0A2B4T1J8	Dystrophin OS=Stylophora pistillata	0.8	2
A7SBR9	Predicted protein OS=Nematostella vectensis	6.4	2
B5MFZ9	Beta tubulin (Fragment) OS=Pocillopora verrucosa	56.8	8
A0A2Z5WH73	Myosin heavy chain OS=Aurelia sp. 2017-HT	11.5	24
A0A2Z5WH75	Actin-2 OS=Aurelia sp. 2017-HT	61.4	18
A0A2Z5WH78	Ser-Thr kinase OS=Aurelia sp. 2017-HT	5.2	3
A0A2Z5WH80	Myosin regulatory light chain OS=Aurelia sp. 2017-HT	46.2	7
A0A2Z5WH82	Tropomyosin-1 OS=Aurelia sp. 2017-HT	6.6	2
A7RK57	Predicted protein (Fragment) OS=Nematostella vectensis	2.5	1
A0A3M6T5Z6	NifU_N domain-containing protein (Fragment) OS=Pocillopora damicornis	18.5	1
A7S2J5	Predicted protein OS=Nematostella vectensis	22.9	3
A0A3M6TAB1	Cation_ATPase_N domain-containing protein OS=Pocillopora damicornis	4.7	5
A7T856	Predicted protein (Fragment) OS=Nematostella vectensis	19.6	1
A7SXV0	Predicted protein OS=Nematostella vectensis	3	1
A0A3M6TUJ7	Uncharacterized protein OS=Pocillopora damicornis	5.8	3
A7RSB9	Predicted protein OS=Nematostella vectensis	5.2	4
A0A3M6U1Z2	Uncharacterized protein OS=Pocillopora damicornis	2.7	1
A0A3M6U269	Uncharacterized protein OS=Pocillopora damicornis	3.6	1
A0A3M6U507	Calponin-homology (CH) domain-containing protein OS=Pocillopora damicornis	5.4	1
A0A3M6U5Z6	Uncharacterized protein OS=Pocillopora damicornis	7.7	1
A0A3M6UBT2	AAA domain-containing protein OS=Pocillopora damicornis	19.4	5
A0A3M6UGM1	V-type proton ATPase subunit a OS=Pocillopora damicornis	4.4	1
A0A3M6UKT7	Uncharacterized protein OS=Pocillopora damicornis	5.3	3
A0A3M6UMV8	Aconitate hydratase, mitochondrial OS=Pocillopora damicornis	5.2	2
A7S766	Predicted protein OS=Nematostella vectensis	3.8	1
A0A3M6UPR6	Uncharacterized protein OS=Pocillopora damicornis	2.9	1
A0A3M6UPZ4	Uncharacterized protein OS=Pocillopora damicornis	4.3	2
A0A3M6UUU1	Uncharacterized protein OS=Pocillopora damicornis	3.5	1
A0A3M6UWV6	Uncharacterized protein OS=Pocillopora damicornis	1.1	1
A0A3M6UX10	EGF-like domain-containing protein OS=Pocillopora damicornis	0.7	1
A0A3M6UXC6	Uncharacterized protein OS=Pocillopora damicornis	3.3	1
A0A3M6UYC1	cGMP-dependent protein kinase OS=Pocillopora damicornis	1.7	1
A0A3M6UZ63	Annexin OS=Pocillopora damicornis	5.4	2
Q5FB17	Heat shock protein 70 OS=Pocillopora damicornis	7.7	3
A0A3M6V674	Uncharacterized protein OS=Pocillopora damicornis	3.8	1
A3F9E8	Histone H2B (Fragment) OS=Anacropora matthai	9.4	1

A7REY1	Inosine-5-monophosphate dehydrogenase OS=Nematostella vectensis	5.2	1
A7RIF0	T-complex protein 1 subunit eta OS=Nematostella vectensis	4.8	2
A7RJZ8	Predicted protein OS=Nematostella vectensis	3.2	2
A7RLF6	Predicted protein (Fragment) OS=Nematostella vectensis	7.5	1
A7RLY5	Predicted protein OS=Nematostella vectensis	3.9	1
A7RMQ8	Proteasome subunit alpha type OS=Nematostella vectensis	9	2
A7RMZ4	Predicted protein OS=Nematostella vectensis	5.4	1
A7T182	Predicted protein OS=Nematostella vectensis	11.5	4
A7RN57	Predicted protein (Fragment) OS=Nematostella vectensis	40.7	2
A7RNE1	Predicted protein OS=Nematostella vectensis	6.6	2
A7RNH9	Predicted protein OS=Nematostella vectensis	2.4	1
A7RNL3	Predicted protein OS=Nematostella vectensis	0.8	2
A7RNT1	Succinyl-CoA:3-ketoacid-coenzyme A transferase OS=Nematostella vectensis	2.3	1
A7RQF7	Predicted protein OS=Nematostella vectensis	12.9	2
A7RQR3	10-formyltetrahydrofolate dehydrogenase OS=Nematostella vectensis	1.4	1
A7RT23	Methionine aminopeptidase 2 OS=Nematostella vectensis	2.4	1
A7RT97	Predicted protein OS=Nematostella vectensis	3.2	2
A7RTJ5	Predicted protein OS=Nematostella vectensis	6.8	2
A7RTS0	Predicted protein OS=Nematostella vectensis	14.6	1
A7RTW3	Predicted protein OS=Nematostella vectensis	13.2	3
A7T120	F-actin-capping protein subunit beta (Fragment) OS=Nematostella vectensis	25.2	2
A7RUF9	Predicted protein (Fragment) OS=Nematostella vectensis	8.9	1
A7RUT1	Tubulin alpha chain OS=Nematostella vectensis	69.9	25
A7RVC0	Clathrin heavy chain OS=Nematostella vectensis	4.8	6
A7RVD9	Tubulin alpha chain OS=Nematostella vectensis	50.2	20
T2M856	Dynein light chain OS=Hydra vulgaris	20.2	2
A7RVM2	Predicted protein OS=Nematostella vectensis	6.9	1
A7RW02	Predicted protein OS=Nematostella vectensis	4.4	1
A7RXC8	Predicted protein OS=Nematostella vectensis	2.8	1
A7S018	Obg-like ATPase 1 OS=Nematostella vectensis	7.1	2
A7S214	Predicted protein OS=Nematostella vectensis	13.8	2
A7S3I0	Predicted protein (Fragment) OS=Nematostella vectensis	5.2	5
A7S428	Predicted protein OS=Nematostella vectensis	2.7	1
A7S469	Predicted protein OS=Nematostella vectensis	6.9	1
A7S5Z0	Predicted protein OS=Nematostella vectensis	8.3	3
T2M3I7	RuvB-like helicase OS=Hydra vulgaris	5.5	2
A7S7K4	Predicted protein OS=Nematostella vectensis	7.9	2
A7S8G2	Predicted protein OS=Nematostella vectensis	6.4	1
A7S9Y6	Predicted protein OS=Nematostella vectensis	3.7	1
A7SCJ3	Succinate dehydrogenase (quinone) (Fragment) OS=Nematostella vectensis	13.2	4
A7SCK6	Predicted protein OS=Nematostella vectensis	11.3	2
A7SEA7	Predicted protein OS=Nematostella vectensis	51.3	13
A7SEB1	Predicted protein OS=Nematostella vectensis	54.9	14

A7SF39	Predicted protein OS=Nematostella vectensis	6.4	2
A7T6B7	Casein kinase II subunit beta (Fragment) OS=Nematostella vectensis	26.7	1
A7SGG1	Predicted protein OS=Nematostella vectensis	0.7	1
A7SHD8	DNA-directed RNA polymerase subunit beta OS=Nematostella vectensis	2.1	1
A7SHH5	Protein disulfide-isomerase (Fragment) OS=Nematostella vectensis	2.5	1
A7SJL4	Predicted protein OS=Nematostella vectensis	2.9	2
A7SJR5	Predicted protein OS=Nematostella vectensis	1.2	1
A7SP62	V-type proton ATPase subunit G OS=Nematostella vectensis	14.5	1
A7SPQ4	Predicted protein OS=Nematostella vectensis	15.8	2
A7SQ60	Predicted protein OS=Nematostella vectensis	9.5	3
A7SQT8	V-type proton ATPase subunit OS=Nematostella vectensis	3.4	1
A7SRK8	Adenosylhomocysteinase OS=Nematostella vectensis	5.8	2
A7SRR4	Predicted protein OS=Nematostella vectensis	31.8	2
A7SSL5	Predicted protein OS=Nematostella vectensis	7.5	5
A7SSV8	Polyadenylate-binding protein OS=Nematostella vectensis	2.6	1
A7STZ5	Predicted protein (Fragment) OS=Nematostella vectensis	0.7	1
A7SU49	Predicted protein (Fragment) OS=Nematostella vectensis	3.5	1
A7T5Y2	Predicted protein OS=Nematostella vectensis	5.5	1
A7SWV8	Predicted protein OS=Nematostella vectensis	11.5	2
A7SWY0	Predicted protein (Fragment) OS=Nematostella vectensis	15.8	1
A7SXD7	Protein disulfide-isomerase OS=Nematostella vectensis	2.7	1
A7SXN2	Peptidyl-prolyl cis-trans isomerase OS=Nematostella vectensis	25.2	2
A7SYK1	Predicted protein OS=Nematostella vectensis	4.2	1
A7T0V9	Predicted protein OS=Nematostella vectensis	20.3	1
A7T288	T-complex protein 1 subunit delta OS=Nematostella vectensis	2.1	1
A7T4C2	Predicted protein (Fragment) OS=Nematostella vectensis	58.9	5
A7T6F7	Predicted protein (Fragment) OS=Nematostella vectensis	24.1	1
A7TCL7	Histone H2A OS=Nematostella vectensis	38.9	10
A8DRV3	Vacuolar ATP synthase subunit B (Fragment) OS=Urticina eques	20.7	2
B3EZK6	Ribosomal protein S5 (Fragment) OS=Cyanea capillata	16.4	2
B5MG02	Beta tubulin (Fragment) OS=Cirripathes sp. TW24	48.6	6
C1IS27	Clathrin heavy chain (Fragment) OS=Carukia barnesi	8.8	1
C7SP37	Glyceraldehyde 3-phosphate dehydrogenase (Fragment) OS=Anemonia sulcata	18.4	3
D1FP01	Elongation factor 1-alpha OS=Malo kingi	9.4	2
D1FX74	HSP70-1 OS=Chironex fleckeri	3.5	2
D2JYS2	Beta-catenin OS=Hydractinia echinata	10.2	4
E9AI11	Ribosomal protein S6 kinase OS=Hydra vulgaris	3	1
G3LIV9	Heat shock cognate protein 71 OS=Hydractinia echinata	6.7	4
G8DM04	Cytochrome c oxidase subunit 2 OS=Chrysaora quinquecirrha	6.9	1
G9ISY6	NADH-ubiquinone oxidoreductase chain 1 OS=Pelagia noctiluca	6.2	1
G9ISX7	Cytochrome c oxidase subunit 2 OS=Pelagia noctiluca	8.1	1
I2G9E9	Myosin II heavy chain, smooth/non-muscle-type (Fragment) OS=Clytia hemisphaerica	6.2	2
I6ZY10	Elongation factor 2 (Fragment) OS=Myxidium coryphaenoideum	13.8	2

K0A063	Beta-actin (Fragment) OS=Chrysaora quinquecirrha	64.7	17
M1E2P9	Calmodulin (Fragment) OS=Rhizostoma octopus	22.8	1
M1G2E5	Ras2 (Fragment) OS=Hydractinia echinata	17.7	3
Q0H8V3	Heat shock protein 70 (Fragment) OS=Cnidaria environmental sample	12.2	2
Q6B4R5	Elongation factor 1-alpha OS=Scleronephthya gracillimum	7.8	3
Q2XWU1	Rab11 protein OS=Aiptasia pulchella	12.8	2
Q56GW1	60S ribosomal protein L12 (Fragment) OS=Hydractinia echinata	16.5	1
Q56GW5	40S ribosomal protein S4 (Fragment) OS=Hydractinia echinata	14.3	1
Q5EN88	Actin-related protein 2/3 complex subunit 5 OS=Aurelia aurita	7.3	1
Q5EN91	Putative 3-hydroxyacyl-Coenzyme A dehydrogenase (Fragment) OS=Aurelia aurita	32.6	4
Q5WR13	Non-muscle actin (Fragment) OS=Hydra viridissima	47.1	8
Q6PTK3	Triosephosphate isomerase (Fragment) OS=Obelia sp. KJP-2004	11.8	2
Q6PTK8	ATP synthase subunit beta (Fragment) OS=Obelia sp. KJP-2004	14.3	4
Q7YZI4	90-kDa heat-shock protein (Fragment) OS=Aurelia aurita	16.7	5
Q7YZJ5	Elongation factor 2 (Fragment) OS=Aurelia aurita	16.3	4
Q7YZK4	Tubulin beta chain (Fragment) OS=Aurelia aurita	66.7	20
Q8I8B9	Putative beta-actin (Fragment) OS=Kudoa ovivora	70	2
Q8MV93	Myosin heavy chain type II (Fragment) OS=Podocoryna carnea	5.2	1
Q967E1	Heat shock protein 90 OS=Dendronephthya klunzingeri	5.2	3
Q9GUZ6	PL10-related protein CnPL10 (Fragment) OS=Sandaria malayensis	23.8	2
Q9NDL6	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Sandaria malayensis	55	2
Q9Y206	G protein a subunit 4 (Fragment) OS=Hydra vulgaris	4	1
R9S2M2	Elongation factor 1-alpha OS=Aurelia aurita	12.8	5
T2M2S4	V-type proton ATPase subunit D (Fragment) OS=Hydra vulgaris	4	1
T2M2W2	Talin-2 OS=Hydra vulgaris	1.2	2
T2M2X1	Adenylate kinase isoenzyme 5 OS=Hydra vulgaris	1.4	1
T2M338	Stomatin-like protein 2 OS=Hydra vulgaris	3.3	1
T2M3I0	Microtubule-associated protein RP/EB family member 3 (Fragment) OS=Hydra vulgaris	3.2	1
T2M438	Non-specific serine/threonine protein kinase OS=Hydra vulgaris	4.8	1
T2M486	Vacuolar protein sorting-associated protein 29 OS=Hydra vulgaris	7.1	1
T2M489	LIM domain and actin-binding protein 1 OS=Hydra vulgaris	3	1
T2M4D5	Leucyl-tRNA synthetase,cytoplasmic (Fragment) OS=Hydra vulgaris	1.6	1
T2M4H7	Costars family protein C6orf115 OS=Hydra vulgaris	15.5	1
T2M520	Alpha-parvin OS=Hydra vulgaris	3.4	1
T2M6J7	Alanine--glyoxylate aminotransferase 2, mitochondrial OS=Hydra vulgaris	4.1	1
T2M6Z7	26S proteasome non-ATPase regulatory subunit 1 (Fragment) OS=Hydra vulgaris	1.5	1
T2M779	Aconitate hydratase, mitochondrial OS=Hydra vulgaris	4.6	2
T2M870	AP-2 complex subunit mu (Fragment) OS=Hydra vulgaris	7.8	3
T2M8F7	Actin-related protein 2/3 complex subunit 1A (Fragment) OS=Hydra vulgaris	3.8	1
T2MAB0	Staphylococcal nuclease domain-containing protein OS=Hydra vulgaris	1.1	1
T2MAB9	Tubulin alpha-1A chain (Fragment) OS=Hydra vulgaris	23.8	16
T2MB05	RNA-binding motif,single-stranded-interacting protein 3 (Fragment) OS=Hydra vulgaris	2.4	1

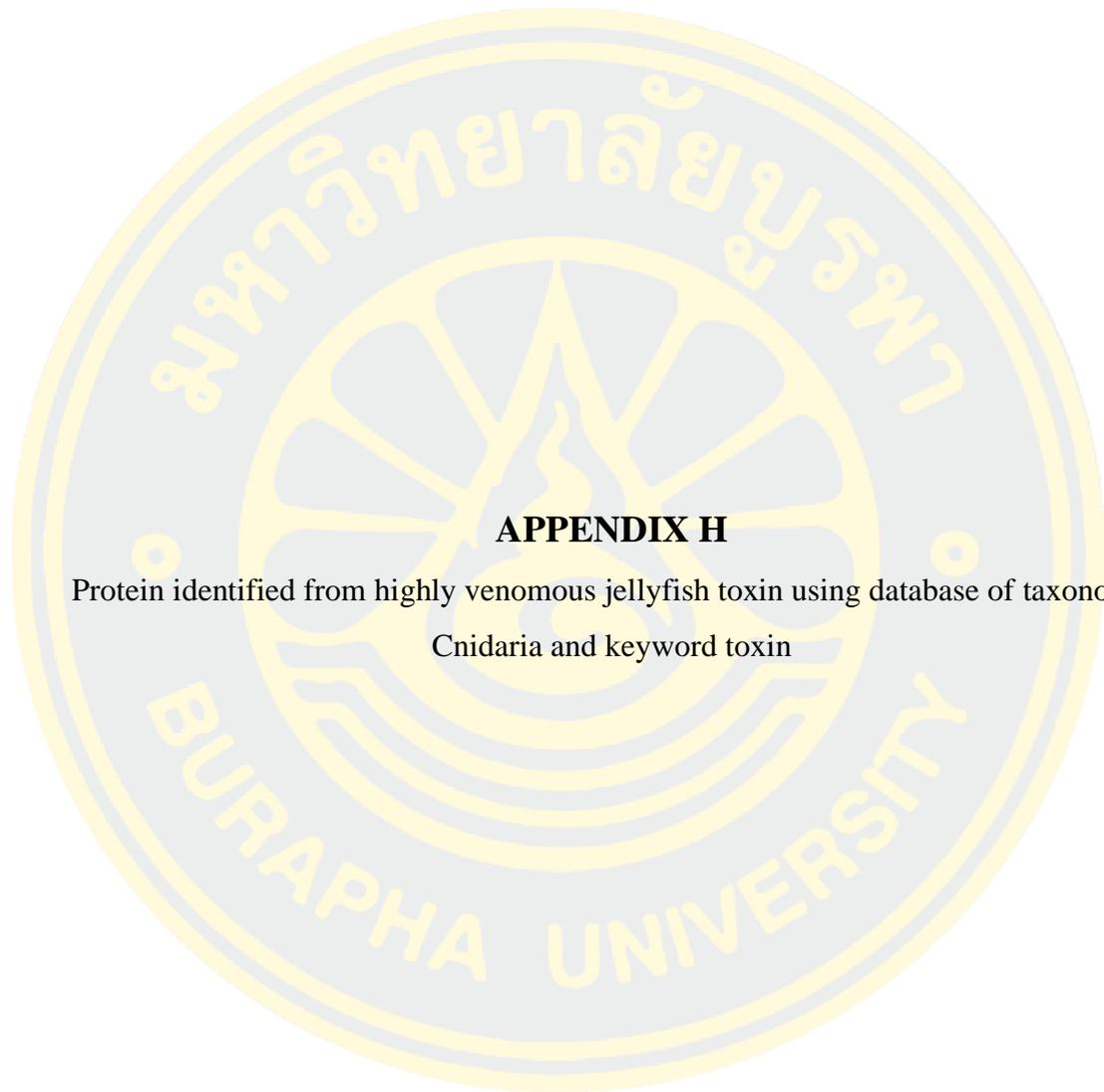
T2MBN1	Kynurenine--oxoglutarate transaminase 3 OS=Hydra vulgaris	2.9	1
T2MCX1	10-formyltetrahydrofolate dehydrogenase OS=Hydra vulgaris	1.3	1
T2MD44	Major vault protein OS=Hydra vulgaris	4.4	3
T2MD57	Calcium-transporting ATPase OS=Hydra vulgaris	4.2	5
T2MDB0	Eukaryotic initiation factor 4A-II OS=Hydra vulgaris	11	3
T2MDB3	NEDD8 OS=Hydra vulgaris	18.4	1
T2MDE9	Spectrin alpha chain, brain (Fragment) OS=Hydra vulgaris	0.5	1
T2MDG4	Flotillin-2 OS=Hydra vulgaris	3.5	2
T2MDT0	Cytoplasmic dynein 1 heavy chain 1 OS=Hydra vulgaris	1.6	4
T2ME03	Quinone oxidoreductase OS=Hydra vulgaris	3.7	1
T2ME39	Dynamin-1 (Fragment) OS=Hydra vulgaris	3.5	1
T2ME59	Serine/threonine-protein phosphatase (Fragment) OS=Hydra vulgaris	15.2	3
T2ME63	2-oxoglutarate dehydrogenase,mitochondrial OS=Hydra vulgaris	1.4	1
T2ME66	Ras-related protein Rab-11A OS=Hydra vulgaris	11.9	2
T2ME72	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Hydra vulgaris	3.4	1
T2MEA3	Myosin-Ie (Fragment) OS=Hydra vulgaris	1.9	2
T2MEB5	ADP-ribosylation factor 1 OS=Hydra vulgaris	13.8	2
T2MEB6	26S protease regulatory subunit 8 OS=Hydra vulgaris	9.6	2
T2MEH3	Casein kinase II subunit alpha OS=Hydra vulgaris	5.1	1
T2MEH6	Dynein light chain Tctex-type 1 OS=Hydra vulgaris	15.9	1
T2MEI1	AP-2 complex subunit beta (Fragment) OS=Hydra vulgaris	4.1	3
T2MEN5	Clathrin heavy chain OS=Hydra vulgaris	5.9	7
T2MEP0	26S protease regulatory subunit 10B OS=Hydra vulgaris	8.9	3
T2MEQ7	26S protease regulatory subunit 4 OS=Hydra vulgaris	11.8	4
T2MES1	40S ribosomal protein S15a OS=Hydra vulgaris	10.8	1
T2MET6	Ras-related protein Rap-1b OS=Hydra vulgaris	8	1
T2MEV1	Tubulin beta chain (Fragment) OS=Hydra vulgaris	40.2	15
T2MEY1	60S ribosomal protein L11 (Fragment) OS=Hydra vulgaris	7.2	1
T2MF60	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Hydra vulgaris	4.8	1
T2MF93	Ras-related protein Rab-14 (Fragment) OS=Hydra vulgaris	36.3	6
T2MFG0	Transmembrane emp24 domain-containing protein 10 (Fragment) OS=Hydra vulgaris	4	1
T2MFH7	Poly(RC)-binding protein 3 (Fragment) OS=Hydra vulgaris	4.1	1
T2MFH8	Seryl-tRNA synthetase,cytoplasmic (Fragment) OS=Hydra vulgaris	8	3
T2MFJ1	Stress-70 protein, mitochondrial (Fragment) OS=Hydra vulgaris	6.7	2
T2MFM1	Transitional endoplasmic reticulum ATPase (Fragment) OS=Hydra vulgaris	15.8	9
T2MFQ3	Coatomer subunit beta (Fragment) OS=Hydra vulgaris	3.3	2
T2MFR0	26S protease regulatory subunit 6B OS=Hydra vulgaris	16.1	3
T2MFR8	Ras-related protein Rab-7a OS=Hydra vulgaris	29.1	5
T2MFU6	26S proteasome non-ATPase regulatory subunit 7 OS=Hydra vulgaris	5.2	1
T2MFU8	Rab GDP dissociation inhibitor (Fragment) OS=Hydra vulgaris	6.3	2
T2MFY6	Hippocalcin-like protein 1 OS=Hydra vulgaris	19.9	3
T2MFZ8	V-type proton ATPase catalytic subunit A OS=Hydra vulgaris	13.8	5
T2MG06	Transaldolase OS=Hydra vulgaris	3.5	1

T2MG86	Vesicle-fusing ATPase OS=Hydra vulgaris	1.3	1
T2MGF7	Malate dehydrogenase,mitochondrial OS=Hydra vulgaris	9.1	2
T2MGG5	Proteasome subunit alpha type OS=Hydra vulgaris	6.1	1
T2MGI7	ADP/ATP translocase 3 (Fragment) OS=Hydra vulgaris	4.3	2
T2MGJ8	Tubulin gamma chain OS=Hydra vulgaris	5.9	1
T2MGL9	40S ribosomal protein S17-like OS=Hydra vulgaris	7.5	1
T2MGP8	Serine hydroxymethyltransferase,cytosolic OS=Hydra vulgaris	3	1
T2MGR5	60S ribosomal protein L7 (Fragment) OS=Hydra vulgaris	5.4	1
T2MGS3	cAMP-dependent protein kinase catalytic subunit alpha OS=Hydra vulgaris	10.3	2
T2MGT2	Transketolase OS=Hydra vulgaris	1.6	1
T2MGZ6	ATP synthase subunit alpha OS=Hydra vulgaris	20	8
T2MH23	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial (Fragment) OS=Hydra vulgaris	2.5	1
T2MH41	78 kDa glucose-regulated protein OS=Hydra vulgaris	4.7	3
T2MH44	Vacuolar proton pump subunit B (Fragment) OS=Hydra vulgaris	17.3	4
T2MH46	Filamin-A OS=Hydra vulgaris	0.6	1
T2MH90	26S protease regulatory subunit 6A OS=Hydra vulgaris	6.1	1
T2MH95	Vinculin OS=Hydra vulgaris	1	1
T2MHA4	Fumarylacetoacetase (Fragment) OS=Hydra vulgaris	2.7	1
T2MHC8	Epsin-2 OS=Hydra vulgaris	3.5	1
T2MHD2	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Hydra vulgaris	3.4	1
T2MHE8	Aspartyl-tRNA synthetase,cytoplasmic OS=Hydra vulgaris	2.3	1
T2MHH5	Myosin-6 OS=Hydra vulgaris	2.8	5
T2MHI3	Flotillin-1 (Fragment) OS=Hydra vulgaris	3.6	2
T2MHI5	Alpha-actinin-1 OS=Hydra vulgaris	4.4	4
T2MHJ0	Non-specific serine/threonine protein kinase OS=Hydra vulgaris	6.8	2
T2MHJ7	60 kDa heat shock protein,mitochondrial (Fragment) OS=Hydra vulgaris	2	1
T2MHN7	Citrate synthase OS=Hydra vulgaris	2.6	1
T2MHT5	Heat shock protein HSP 90-alpha OS=Hydra vulgaris	6.9	5
T2MHT8	60S acidic ribosomal protein P0 OS=Hydra vulgaris	4.1	1
T2MHY0	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2 OS=Hydra vulgaris	2.9	1
T2MHZ2	Dynamin-like 120 kDa protein,mitochondrial OS=Hydra vulgaris	1.2	1
T2MI97	Dystrobrevin beta (Fragment) OS=Hydra vulgaris	1.7	1
T2MIF5	Endothelin-converting enzyme 2 OS=Hydra vulgaris	3.1	1
T2MIQ2	Protein arginine N-methyltransferase (Fragment) OS=Hydra vulgaris	4.3	1
T2MIR7	WD repeat-containing protein 1 OS=Hydra vulgaris	1.6	1
T2MIT5	Protein diaphanous homolog 2 OS=Hydra vulgaris	1.1	1
T2MIX5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial OS=Hydra vulgaris	10.7	1
T2MIZ8	Exportin-1 (Fragment) OS=Hydra vulgaris	1.8	1
T2MJ22	Calumenin OS=Hydra vulgaris	5.4	1
T2MJ29	Down syndrome critical region protein 3 OS=Hydra vulgaris	5.8	1
T2MJJ5	Myosin regulatory light chain 12B OS=Hydra vulgaris	27.1	3
W8PTQ2	Peroxioredoxin 4 OS=Cyanea capillata	18.6	4

3. Top-down proteomics

Table G-7. List of protein identified (1 protein) from nematocyst of highly venomous jellyfish by using extraction of 2% SDS coupled with sonication. Proteins without digestion were analyzed by top-down proteomics experiment. Taxonomy Cnidaria database (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	% Coverage	# Peptides
A0A3M6U9V1	Uncharacterized protein OS=Pocillopora damicornis	100	1



APPENDIX H

Protein identified from highly venomous jellyfish toxin using database of taxonomy

Cnidaria and keyword toxin

1. In-gel digestion

1.1 Identification of protein from crude of tentacle

Table H-1. List of proteins identified (11 proteins) from crude tentacles of highly venomous jellyfish. These proteins identified were derived from in-gel digestion experiment. Database of taxonomy Cnidaria and keyword toxin (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
A0A2B4RIA4	ShKT domain-containing protein OS=Stylophora pistillata	Toxin	0.7	1
A0A2B4RMY9	Tenascin-R OS=Stylophora pistillata	Metalloprotease, Toxin	0.9	1
A0A2B4SFF2	Guanine nucleotide exchange factor VAV3 OS=Stylophora pistillata	Metalloprotease, Guanine-nucleotide releasing factor, Hydrolase, Protease, Serine protease, Toxin	2.1	2
A0A2B4SKQ5	Chymotrypsin-like elastase family member 3B OS=Stylophora pistillata	Hydrolase, Protease, Serine protease, Toxin	3.7	1
A0A2B4SWG8	Retinol dehydrogenase 12 OS=Stylophora pistillata	Toxin	2.9	1
A0A3M6TK48	Uncharacterized protein OS=Pocillopora damicornis	Hydrolase, Protease, Serine protease, Toxin	1	1
A0A3M6TTZ7	Metalloendopeptidase (Fragment) OS=Pocillopora damicornis	Metalloprotease, Hydrolase, Protease, Toxin	2.3	2
A0A3M6U0T3	ShKT domain-containing protein OS=Pocillopora damicornis	Toxin	7.8	3
A0A3M6UD47	Metalloendopeptidase (Fragment) OS=Pocillopora damicornis	Hydrolase, Metalloprotease, Protease, Toxin	2.3	1
A0A3M6UY54	Uncharacterized protein OS=Pocillopora damicornis	Toxin	1.2	4
A0A3M6V044	Metalloendopeptidase OS=Pocillopora damicornis	Metalloprotease, Hydrolase, Protease, Toxin	6.3	2

1.2 Identification of protein from nematocyst

Table H-2. List of proteins identified (11 proteins) from nematocyst of highly venomous jellyfish by using extraction of SDS coupled with sonication. The proteins were derived from in-gel digestion experiment. Database of taxonomy Cnidaria and keyword toxin (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
C5NSL2	DELTA-actitoxin-Aas1a OS=Anthopleura asiatica	Pore-forming protein, Hemolysis, Toxin	5.2	1
A0A2B4RHQ6	Cysteine-rich secretory protein LCCL domain-containing 2 OS=Stylophora pistillata	Toxin	2.5	2
A0A2B4RNA2	C-type mannose receptor 2 OS=Stylophora pistillata	Receptor, Toxin	0.5	2
A0A2B4RU94	Cartilage matrix protein OS=Stylophora pistillata	Toxin	5.1	2
A0A2B4RWA8	F-box/LRR-repeat protein 7 OS=Stylophora pistillata	Toxin	1.8	2
A0A2B4S961	Metalloendopeptidase OS=Stylophora pistillata	Metalloprotease, Hydrolase, Protease, Toxin	0.9	1
A0A2B4SFF2	Guanine nucleotide exchange factor VAV3 OS=Stylophora pistillata	Metalloprotease, Guanine-nucleotide releasing factor, Hydrolase, Protease,	0.8	1

		Serine protease, Toxin		
A0A2B4SH47	Collagen alpha-3(VI) chain OS=Stylophora pistillata	Toxin	1.7	2
A0A2B4SWG8	Retinol dehydrogenase 12 OS=Stylophora pistillata	Toxin	2.9	1
A0A3M6UD47	Metalloendopeptidase (Fragment) OS=Pocillopora damicornis	Metalloprotease, Hydrolase, Protease, Toxin	2.3	1
A0A3M6UY54	Uncharacterized protein OS=Pocillopora damicornis	Toxin	0.8	4

Table H-3. List of proteins identified (8 proteins) from nematocyst of highly venomous jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were derived from in-gel digestion experiment. Database of taxonomy Cnidaria and keyword toxin (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P0DN02	U-actitoxin-Avd9c OS=Anemonia viridis	Ion channel impairing toxin, Neurotoxin, Potassium channel impairing toxin, Toxin, Voltage-gated potassium channel impairing toxin	12.5	1
A0A2B4RMY9	Tenascin-R OS=Stylophora pistillata	Metalloprotease, Toxin	2.9	2
A0A2B4RU94	Cartilage matrix protein OS=Stylophora pistillata	Toxin	4.5	2
A0A2B4RX12	Hemicentin-1 OS=Stylophora pistillata	Toxin	0.8	3
A0A2B4SFF2	Guanine nucleotide exchange factor VAV3 OS=Stylophora pistillata	Metalloprotease, Guanine-nucleotide releasing factor, Hydrolase, Protease, Serine protease, Toxin	0.8	1
A0A2B4SKQ5	Chymotrypsin-like elastase family member 3B OS=Stylophora pistillata	Hydrolase, Protease, Serine protease, Toxin	3.7	1
A0A2B4SWG8	Retinol dehydrogenase 12 OS=Stylophora pistillata	Toxin	2.9	1
A0A3M6UY54	Uncharacterized protein OS=Pocillopora damicornis	Toxin	0.7	3

2. In-solution digestion

2.1 Nematocyst extracted by 2% SDS couple with sonication and digested with trypsin enzyme

Table H-4. List of proteins identified (12 proteins) from nematocyst of highly venomous jellyfish by using extraction of 2% SDS coupled with sonication. The proteins were derived from in-solution digestion experiment. Database of taxonomy Cnidaria and keyword toxin (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P0DMZ6	U-actitoxin-Avd8d OS=Anemonia viridis	Toxin	10.8	1

P86459	Delta-actitoxin-Bcg1d OS=Bunodosoma cangicum	Ion channel impairing toxin, Neurotoxin, Toxin, Voltage-gated sodium channel impairing toxin	70.2	1
A0A0S1M193	Type III potassium channel toxin protein OS=Anemonia sulcata	Ion channel, Ion channel impairing toxin, Neurotoxin, Toxin	18.7	1
A0A3M6TN85	Uncharacterized protein OS=Pocillopora damicornis	Toxin	3	1
A0A2B4S879	Chymotrypsin-like protease CTRL-1 OS=Stylophora pistillata	Hydrolase, Protease, Serine protease, Toxin	11.1	2
A0A2B4SFF2	Guanine nucleotide exchange factor VAV3 OS=Stylophora pistillata	Metalloprotease, Guanine-nucleotide releasing factor, Hydrolase, Protease, Serine protease, Toxin	0.8	1
A0A2B4SIN1	Pathogenesis-related leaf protein 4 OS=Stylophora pistillata	Toxin	2.3	1
A0A2B4ST02	Cationic trypsin-3 OS=Stylophora pistillata	Hydrolase, Protease, Serine protease, Toxin	1.8	1
A0A3M6T6K5	ShKT domain-containing protein OS=Pocillopora damicornis	Toxin	22	1
A0A3M6TQD4	Uncharacterized protein OS=Pocillopora damicornis	Toxin	2.3	2
A0A3M6UY54	Uncharacterized protein OS=Pocillopora damicornis	Toxin	1.3	2
A7SKD2	Predicted protein OS=Nematostella vectensis	Toxin	8.5	1

2.2 Nematocyst extracted by PBS buffer couple with ultrasonication and digested with trypsin enzyme

Table H-5. List of proteins identified (18 proteins) from nematocyst of highly venomous jellyfish by using extraction of PBS buffer couple with ultrasonication. The proteins were derived from in-solution digestion experiment. Database of taxonomy Cnidaria and keyword toxin (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P0DMZ6	U-actitoxin-Avd8d OS=Anemonia viridis	Toxin	10.8	1
A0A0S1M161	Sodium channel toxin protein (Fragment) OS=Anemonia sulcata	Ion channel, Neurotoxin, Toxin	37.8	1
A0A2B4RMY9	Tenascin-R OS=Stylophora pistillata	Metalloprotease, Toxin	1	1
A0A2B4RP62	Metalloendopeptidase OS=Stylophora pistillata	Metalloprotease, Hydrolase, Protease, Toxin	1.1	1
A0A2B4RSY5	Peptidase inhibitor R3HDML OS=Stylophora pistillata	Toxin	2.7	1
A0A2B4S6I8	Collagen alpha-1(XII) chain OS=Stylophora pistillata	Toxin	5.2	2
A0A2B4SA86	Thrombospondin-1 OS=Stylophora pistillata	Toxin	2.3	2
A0A2B4SCZ4	Metalloendopeptidase OS=Stylophora pistillata	Metalloprotease, Hydrolase, Protease, Toxin	4.1	1
A0A2B4SWG8	Retinol dehydrogenase 12 OS=Stylophora pistillata	Toxin	4.4	2
A0A2Z2GQG6	Ap_trypsin-like protein (Fragment) OS=Exaiptasia pallida	Hydrolase, Protease, Serine protease, Toxin	2.5	2
A0A3M6TGS0	Metalloendopeptidase OS=Pocillopora damicornis	Metalloprotease, Hydrolase, Protease, Toxin	6.3	1
A0A3M6TM68	ShKT domain-containing protein OS=Pocillopora damicornis	Toxin	7.8	1

A0A3M6TMX2	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	Toxin	11.5	1
A0A3M6TPW8	Uncharacterized protein OS=Pocillopora damicornis	Hydrolase, Protease, Serine protease, Toxin	4.5	2
A0A3M6TQ50	Uncharacterized protein OS=Pocillopora damicornis	Hydrolase, Protease, Serine protease, Toxin	3.5	2
A0A3M6U863	Uncharacterized protein OS=Pocillopora damicornis	Toxin	4.5	1
A0A3M6USV2	Uncharacterized protein OS=Pocillopora damicornis	Toxin	3	2
A7RMF1	Metalloendopeptidase OS=Nematostella vectensis	Metalloprotease, Hydrolase, Protease, Toxin	5.9	3

2.3 Nematocyst extracted by PBS buffer couple with ultrasonication and digested with PNGase and trypsin enzyme

Table H-6. List of proteins identified (15 proteins) from nematocyst of highly venomous jellyfish by using extraction of PBS buffer couple with ultrasonication. The proteins were derived from in-solution digestion experiment. Database of taxonomy Cnidaria and keyword toxin (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P0DMZ6	U-actitoxin-Avd8d OS=Anemonia viridis	Toxin	10.8	1
P0DN02	U-actitoxin-Avd9c OS=Anemonia viridis	Ion channel impairing toxin, Neurotoxin, Potassium channel impairing toxin, Toxin, Voltage-gated potassium channel impairing toxin	12.5	1
Q86FQ0	DELTA-sagatoxin-Srs1a OS=Sagartia rosea	Pore-forming protein, Cytolysis, Hemolysis	3.2	1
Q9Y1U9	DELTA-actitoxin-Aeq1c OS=Actinia equina	Pore-forming protein, Hemolysis	5.1	1
A0A2B4RCC1	Uncharacterized protein OS=Stylophora pistillata	Toxin	11.2	1
A0A2B4RII3	Metalloendopeptidase OS=Stylophora pistillata	Metalloprotease, Hydrolase, Protease, Toxin	3.2	2
A0A2B4RYY7	Lipopolysaccharide cholinephosphotransferase LicD OS=Stylophora pistillata	Toxin, Transferase	1	1
A0A2B4SJQ4	Collagen alpha-3(VI) chain OS=Stylophora pistillata	Toxin	0.5	1
A0A2B4SWG8	Retinol dehydrogenase 12 OS=Stylophora pistillata	Toxin	2.9	1
A0A3M6T4D3	Uncharacterized protein OS=Pocillopora damicornis	Toxin	6.1	1
A0A3M6T4G5	Uncharacterized protein (Fragment) OS=Pocillopora damicornis	Toxin	4	1
A0A3M6T4I6	ShKT domain-containing protein OS=Pocillopora damicornis	Toxin	1.9	1
A0A3M6UDC3	ShKT domain-containing protein (Fragment) OS=Pocillopora damicornis	Toxin	2.3	2
A0A3M6UZV0	Metalloendopeptidase OS=Pocillopora damicornis	Metalloprotease, Hydrolase, Protease, Toxin	2.9	1
A7RMF1	Metalloendopeptidase OS=Nematostella vectensis	Metalloprotease, Hydrolase, Protease, Toxin	2.2	1

3. Top-down proteomics

Table H-7. List of protein identified (1 protein) from nematocyst of highly venomous jellyfish by using extraction of SDS coupled with sonication. Proteins without digestion were analyzed by top-down proteomics experiment. Taxonomy Cnidaria and keyword toxin database (downloaded on 13th August 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P84851	Nephrotoxin PsTX-115 (Fragments) OS=Phyllodiscus semoni	Toxin	100	1



APPENDIX I

Protein identified from highly venomous jellyfish toxin using database of keyword
toxin

1. In-gel digestion

1.1 Identification of protein from crude of tentacle

Table I-1. List of proteins identified (8 proteins) from crude tentacles of highly venomous jellyfish. These proteins identified were derived from in-gel digestion experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
U6C2F8	Conomorphin_Mr1_precursor_1 OS=Conus marmoreus	N/A	12.9	1
A0A0B1YU72	Ribonuclease VapC OS=Burkholderia sp. A9	Hydrolase, Nuclease, Toxin	15.4	1
A0A2N2RJY4	Ribonuclease VapC OS=Betaproteobacteria bacterium HGW-Betaproteobacteria-3	Hydrolase, Nuclease, Toxin	20.4	1
A0A2N3PSC9	Ribonuclease VapC OS=Telmatospirillum siberiense	Hydrolase, Nuclease, Toxin	9.3	1
A0A2V9KM50	Ribonuclease VapC OS=Acidobacteria bacterium	Hydrolase, Nuclease, Toxin	9.1	1
A0A2W6CYK8	Ribonuclease VapC OS=Pseudonocardiales bacterium	Hydrolase, Nuclease, Toxin	15.6	1
A0A501WID1	Ribonuclease VapC OS=Amaricoccus sp. HB172011	Hydrolase, Nuclease, Toxin	9.7	1
M8BRV4	rRNA N-glycosidase OS=Aegilops tauschii	Hydrolase, Protein synthesis inhibitor, Toxin	2.1	1

1.2 Identification of protein from nematocyst

Table I-2. List of proteins identified (11 proteins) from nematocyst of highly venomous jellyfish by using extraction of SDS coupled with sonication. The proteins were derived from in-gel digestion experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
U6C2F8	Conomorphin_Mr1_precursor_1 OS=Conus marmoreus	N/A	12.9	1
A0A0E0KHL4	rRNA N-glycosidase OS=Oryza punctata	Hydrolase, Protein synthesis inhibitor, Toxin	12.6	1
A0A0Q9JMJ9	Ribonuclease VapC OS=Agromyces sp. Soil535	Hydrolase, Nuclease, Toxin	8.5	1
A0A1F6AHL7	Ribonuclease VapC OS=Candidatus Gottesmanbacteria bacterium RIFCSPLOWO2_01_FULL_43_11b	Hydrolase, Nuclease, Toxin	12.8	1
A0A1H9KMH9	Ribonuclease VapC OS=Sphingobium sp. YR768	Hydrolase, Nuclease, Toxin	14.1	1
A0A2B5VDM1	Uncharacterized protein (Fragment) OS=Bacillus toyonensis	Toxin	1.8	1
A0A2N2RJY4	Ribonuclease VapC OS=Betaproteobacteria bacterium HGW-Betaproteobacteria-3	Hydrolase, Nuclease, Toxin	20.4	1
A0A2W7APJ0	Ribonuclease VapC OS=Leptolyngbya sp.	Hydrolase, Nuclease, Toxin	19.4	1
Q1GVA4	Ribonuclease VapC OS=Sphingopyxis alaskensis (strain DSM 13593 / LMG 18877 / RB2256)	Hydrolase, Nuclease, Toxin	5.8	1
A0A537QKL3	Ribonuclease VapC OS=Alphaproteobacteria bacterium	Hydrolase, Nuclease, Toxin	7.9	1
Q9PYD8	Non-structural glycoprotein 4 OS=Lapine	Enterotoxin, Ion channel,	7.4	1

	rotavirus strain R-2	Toxin, Viral ion channel		
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Table I-3. List of proteins identified (15 proteins) from nematocyst of highly venomous jellyfish by using extraction of PBS buffer coupled with ultrasonication. The proteins were derived from in-gel digestion experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
B2DCR8	SE-cephalotoxin OS=Sepia esculenta	Toxin	1.6	2
U6C2F8	Conomorphin_Mr1_precursor_1 OS=Conus marmoreus	N/A	12.9	1
A0A0B1YU72	Ribonuclease VapC OS=Burkholderia sp. A9	Hydrolase, Nuclease, Toxin	15.4	1
A0A0N1LHD3	Ribonuclease VapC OS=alpha proteobacterium AAP81b	Hydrolase, Nuclease, Toxin	5.6	1
A0A1D5UMH8	rRNA N-glycosidase OS=Triticum aestivum	Hydrolase, Protein synthesis inhibitor, Toxin	1.8	1
A0A4U7EHZ3	Ribonuclease VapC OS=Halorubrum sp. SP9	Hydrolase, Nuclease, Toxin	14.7	1
A0A1Q3PYA2	Ribonuclease VapC OS=Actinobacteria bacterium 69-20	Hydrolase, Nuclease, Toxin	7.6	1
W9FP44	Ribonuclease VapC OS=Streptomyces filamentosus NRRL 11379	Hydrolase, Nuclease, Toxin	14.1	1
A0A1V6KFF1	Ribonuclease VapC OS=Deltaproteobacteria bacterium ADurb.Bin002	Endonuclease, Hydrolase, Nuclease, Toxin	10.4	1
A0A371WXY2	Ribonuclease VapC OS=Fulvmarina endophytica	Hydrolase, Nuclease, Toxin	26.9	1
A0A395TZ49	Ribonuclease VapC OS=Vibrio cholerae	Hydrolase, Nuclease, Toxin	8.3	1
A0A501WID1	Ribonuclease VapC OS=Amaricoccus sp. HB172011	Hydrolase, Nuclease, Toxin	9.7	1
A0A537QKL3	Ribonuclease VapC OS=Alphaproteobacteria bacterium	Hydrolase, Nuclease, Toxin	7.9	1
Q6N490	Ribonuclease VapC OS=Rhodospseudomonas palustris (strain ATCC BAA-98 / CGA009)	Hydrolase, Nuclease, Toxin	8.6	1
Q9PYD8	Non-structural glycoprotein 4 OS=Lapine rotavirus strain R-2	Enterotoxin, Ion channel, Toxin, Viral ion channel	7.4	1

2. In-solution digestion

2.1 Nematocyst extracted by 2% SDS couple with sonication and digested with trypsin enzyme

Table I-4. List of proteins identified (30 proteins) from nematocyst of highly venomous jellyfish by using extraction of SDS coupled with sonication. The proteins were derived from in-solution digestion experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P0DJ31	Potassium channel toxin alpha-KTx 23.1 OS=Vaejovis mexicanus smithi	Ion channel impairing toxin, Neurotoxin, Potassium channel impairing toxin, Toxin	19.4	1
P81236	Basic phospholipase A2 acanthin-1 OS=Acanthophis antarcticus	Hemostasis impairing toxin, Hydrolase, Platelet	14.3	1

		aggregation inhibiting toxin, Toxin		
Q3YL96	Toxin CdiA OS=Escherichia coli	Toxin	1.4	1
Q8VUZ6	Phospholipase C OS=Paenoclostridium sordellii	Hydrolase, Toxin, Hemolysis	2	1
V9ZAY0	Venom metalloproteinase antarease-like TtrivMP_A OS=Tityus trivittatus	Hydrolase, Metalloprotease, Protease, Toxin	2	1
A0A077MFD6	Ribonuclease VapC OS=Tetrasphaera jenkinsii Ben 74	Hydrolase, Nuclease, Toxin	20.5	1
A0A242ZLL5	Uncharacterized protein (Fragment) OS=Bacillus thuringiensis serovar londrina	Toxin	3.7	1
A0A0E0KHL4	rRNA N-glycosidase OS=Oryza punctata	Hydrolase, Protein synthesis inhibitor, Toxin	12.6	1
A0A1I6HX39	Ribonuclease VapC OS=Microbacterium sp. cl127	Hydrolase, Nuclease, Toxin	20.8	1
A0A177XRA7	Thiol-activated cytolysin OS=Brevibacillus sp. SKDU10	Cytolysis, Toxin	4.9	1
A0A1F9A484	Ribonuclease VapC OS=Deltaproteobacteria bacterium GWD2_55_8	Hydrolase, Nuclease, Toxin	5.5	1
A0A4U7EHZ3	Ribonuclease VapC OS=Halorubrum sp. SP9	Hydrolase, Nuclease, Toxin	14.7	1
A0A1Q3TGU2	Ribonuclease VapC OS=Microbacterium sp. 67-17	Hydrolase, Nuclease, Toxin	30.5	1
A0A2V9BRS1	Ribonuclease VapC OS=Acidobacteria bacterium	Hydrolase, Nuclease, Toxin	4.5	1
A0A2A6RQ97	Ribonuclease VapC OS=Candidatus Viridilinea mediisalina	Hydrolase, Nuclease, Toxin	19.4	1
A0A2A7F033	Uncharacterized protein (Fragment) OS=Bacillus cereus	Toxin	2.8	1
Q1GVA4	Ribonuclease VapC OS=Sphingopyxis alaskensis (strain DSM 13593 / LMG 18877 / RB2256)	Hydrolase, Nuclease, Toxin	5.8	1
A0A317PHH2	Ribonuclease VapC OS=Hoeftlea marina	Hydrolase, Nuclease, Toxin	12.5	1
A0A328D5U6	rRNA N-glycosidase OS=Cuscuta australis	Hydrolase, Protein synthesis inhibitor, Toxin	5.3	1
A0A3M9XND6	Ribonuclease VapC OS=Methylocystis hirsuta	Hydrolase, Nuclease, Toxin	4.8	1
A0A4Y5YL05	Ribonuclease VapC OS=Microbacterium foliorum	Hydrolase, Nuclease, Toxin	34.1	1
A0A501WID1	Ribonuclease VapC OS=Amaricoccus sp. HB172011	Hydrolase, Nuclease, Toxin	9.7	1
A0A537QKL3	Ribonuclease VapC OS=Alphaproteobacteria bacterium	Hydrolase, Nuclease, Toxin	7.9	1
A0A545Z191	Ribonuclease VapC OS=Rhizobium sp. rho-1.1	Hydrolase, Nuclease, Toxin	6.7	1
B7R495	Ribonuclease VapC OS=Thermococcus sp. AM4	Hydrolase, Nuclease, Toxin	5.9	1
F8U689	Non-structural glycoprotein 4 OS=Rotavirus A	Enterotoxin, Ion channel, Toxin, Viral ion channel	5.1	1
H0SVJ0	Ribonuclease VapC OS=Bradyrhizobium sp. STM 3809	Hydrolase, Nuclease, Toxin	6.3	1
U5KRQ6	Pesticidal protein OS=Bacillus thuringiensis	Toxin	2.2	1
N1LR39	Uncharacterized protein OS=Bacillus sp. GeD10	Toxin	1	1
V9P8G8	Insecticidal protein Cry73Aa OS=Bacillus thuringiensis serovar mogi	Toxin	3.9	1

2.2 Nematocyst extracted by PBS buffer couple with ultrasonication and digested with trypsin enzyme

Table I-5. List of proteins identified (21 proteins) from nematocyst of highly venomous jellyfish by using extraction of PBS buffer coupled with ultrasonication.

The proteins were derived from in-solution digestion experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
A0A1E1WVW0	Putative sodium channel toxin OS=Tityus obscurus	Ion channel	25.6	1
P81236	Basic phospholipase A2 acanthin-1 OS=Acanthophis antarcticus	Hemostasis impairing toxin, Hydrolase, Platelet aggregation inhibiting toxin, Toxin	14.3	1
A0A011PV41	Ribonuclease VapC OS=Candidatus Accumulibacter sp. BA-94	Hydrolase, Nuclease, Toxin	16.1	1
J0H8B2	Ribonuclease VapC OS=Rhizobium leguminosarum bv. trifolii WSM597	Hydrolase, Nuclease, Toxin	12.9	1
A0A1C3X147	Ribonuclease VapC OS=Bradyrhizobium yuanmingense	Hydrolase, Nuclease, Toxin	13.7	1
A0A158HYV6	Ribonuclease VapC OS=Caballeronia udeis	Hydrolase, Nuclease, Toxin	13.8	1
A0A1F4CVA5	Ribonuclease VapC OS=Betaproteobacteria bacterium RIFCSPLOWO2_12_FULL_62_13	Hydrolase, Nuclease, Toxin	14.5	1
A0A1F7F8I2	Ribonuclease VapC OS=Candidatus Raymondbacteria bacterium RIFOXYD12_FULL_49_13	Hydrolase, Nuclease, Toxin	18.2	1
A0A1Q9AJU9	Ribonuclease VapC OS=Rhizobium rhizosphaerae	Hydrolase, Nuclease, Toxin	14.3	1
A0A1V2TCS5	Ribonuclease VapC OS=Nocardia donostiensis	Hydrolase, Nuclease, Toxin	8.3	1
A0A2J6MZ21	Ribonuclease VapC OS=Candidatus Bathyarchaeota archaeon	Hydrolase, Nuclease, Toxin	14.7	1
A0A5H2YLW0	Ribonuclease VapC OS=Bradyrhizobium sp. SG09	Hydrolase, Nuclease, Toxin	17.2	1
A0A5J5SWC6	rRNA N-glycosidase OS=Gossypium barbadense	Hydrolase, Protein synthesis inhibitor, Toxin	3.1	1
A0A2V8TG76	Ribonuclease VapC OS=Acidobacteria bacterium	Hydrolase, Nuclease, Toxin	14.8	1
A0A2V9L3N3	Ribonuclease VapC OS=Acidobacteria bacterium	Hydrolase, Nuclease, Toxin	12.4	1
A0A317PHH2	Ribonuclease VapC OS=Hoefflea marina	Hydrolase, Nuclease, Toxin	12.5	1
A0A437GEG9	Ribonuclease VapC OS=Rhizobium meliloti	Hydrolase, Nuclease, Toxin	15	1
A0A4P5VSN4	Ribonuclease VapC OS=Deltaproteobacteria bacterium	Hydrolase, Nuclease, Toxin	8.3	1
A0A4S4DHD6	rRNA N-glycosidase OS=Camellia sinensis var. sinensis	Hydrolase, Protein synthesis inhibitor, Toxin	5.9	1
A0A537HQ33	Ribonuclease VapC OS=Candidatus Bathyarchaeota archaeon	Hydrolase, Nuclease, Toxin	9.4	1
L8TNN1	Ribonuclease VapC OS=Arthrobacter nitrophenolicus	Hydrolase, Nuclease, Toxin	20	1

2.3 Nematocyst extracted by PBS buffer couple with ultrasonication and digested with PNGase and trypsin enzyme

Table I-6. List of proteins identified (27 proteins) from nematocyst of highly venomous jellyfish by using extraction of PBS buffer coupled with ultrasonication.

The proteins were derived from in-solution digestion experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
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A0RZC6	A.superbus venom factor 2 OS=Austrelaps superbus	Complement system impairing toxin, Toxin	0.8	1
Q07833	tRNA nuclease WapA OS=Bacillus subtilis (strain 168)	Endonuclease, Hydrolase, Nuclease, Toxin	0.6	1
P84017	U13-ctenitoxin-Pn1b OS=Phoneutria nigriventer	Neurotoxin, Toxin	77.4	1
A0A011PV41	Ribonuclease VapC OS=Candidatus Accumilibacter sp. BA-94	Hydrolase, Nuclease, Toxin	16.1	1
A0A0E0D4I0	rRNA N-glycosidase OS=Oryza meridionalis	Hydrolase, Protein synthesis inhibitor, Toxin	4.9	1
A0A259DX00	Ribonuclease VapC OS=Novosphingobium sp. 17-62-19	Hydrolase, Nuclease, Toxin	9.2	1
A0A0K2SA00	Conotoxin Superfamily T OS=Conus episcopatus	N/A	21.7	1
A0A126NT20	Ribonuclease VapC OS=Bosea sp. PAMC 26642	Hydrolase, Nuclease, Toxin	9.5	1
A0A142HGL8	Ribonuclease VapC OS=Hymenobacter sp. PAMC 26554	Hydrolase, Nuclease, Toxin	9.2	1
A0A497MDR4	Ribonuclease VapC OS=Candidatus Bathyarchaeota archaeon	Hydrolase, Nuclease, Toxin	9.2	1
A0A165Z1Z1	Ribonuclease VapC OS=Methanobrevibacter curvatus	Endonuclease, Hydrolase, Nuclease, Toxin	9.6	1
A0A2A7GRW2	Ricin B-type lectin domain-containing protein OS=Bacillus thuringiensis	Toxin	1.6	1
A0A2H0YM68	Ribonuclease VapC OS=Candidatus Nealsonbacteria bacterium CG08_land_8_20_14_0_20_38_20	Hydrolase, Nuclease, Toxin	9.2	1
A0A2V6TK09	Ribonuclease VapC OS=Candidatus Rokubacteria bacterium	Hydrolase, Nuclease, Toxin	6.5	1
A0A317PHH2	Ribonuclease VapC OS=Hoeflea marina	Hydrolase, Nuclease, Toxin	12.5	1
A0A346CJI5	Conotoxin superfamily T (Fragment) OS=Conus ermineus	N/A	21.3	1
A0A368TGY4	Ribonuclease VapC OS=Methanophagales archaeon	Hydrolase, Nuclease, Toxin	10.5	1
A0A3M2KWH1	Ribonuclease VapC OS=Nocardia stercoris	Hydrolase, Nuclease, Toxin	9.2	1
A0A453E807	Uncharacterized protein OS=Aegilops tauschii subsp. strangulata	N/A	5.9	1
A0A4R5UJL0	Ribonuclease VapC OS=Rhizobium sp. SPY-1	Hydrolase, Nuclease, Toxin	9.4	1
A0A501WID1	Ribonuclease VapC OS=Amaricoccus sp. HB172011	Hydrolase, Nuclease, Toxin	9.7	1
A0A532CJZ6	Ribonuclease VapC OS=Nitrospira sp.	Hydrolase, Nuclease, Toxin	10.5	1
A0A533HZM6	Ribonuclease VapC OS=Paracoccus denitrificans	Hydrolase, Nuclease, Toxin	9.7	1
A0A5A4WID3	Ribonuclease VapC OS=Mycobacterium avium subsp. hominissuis	Hydrolase, Nuclease, Toxin	17.1	1
A0A5C7WWH8	Ribonuclease VapC OS=Mycobacterium sp.	Hydrolase, Nuclease, Toxin	9.1	1
Q9PYD8	Non-structural glycoprotein 4 OS=Lapine rotavirus strain R-2	Enterotoxin, Ion channel, Toxin, Viral ion channel	7.4	1
V5N8R1	Botulinum neurotoxin OS=Clostridium botulinum	Hydrolase, Metalloprotease, Neurotoxin, Protease, Toxin	1.8	1

3. Top-down proteomics

Table I-7. List of protein identified (3 proteins) from nematocyst of highly venomous jellyfish by using extraction of SDS coupled with sonication. Proteins without digestion were analyzed by top-down proteomics experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
P0CU60	Cycloamanide D OS=Amanita phalloides	Toxin	100	1
P0DJK5	Bradykinin-potentiating peptide 10d OS=Bothrops fonsecai	Hypotensive agent, Metalloenzyme inhibitor, Metalloprotease inhibitor, Protease inhibitor, Toxin	100	1
H9N3S7	Alpha-conotoxin (Fragment) OS=Conus lividus	Acetylcholine receptor inhibiting toxin, Neurotoxin, Postsynaptic neurotoxin, Toxin	100	1

Table I-8. List of protein identified (7 proteins) from nematocyst of highly venomous jellyfish by using extraction of PBS buffer couple with ultrasonication. Proteins without digestion were analyzed by top-down proteomics experiment. Database of keyword toxin (downloaded on 2nd June 2020) was used to protein identify.

Accession	Description	Functions	% Coverage	# Peptides
B3EWW2	Short cationic peptide-4f OS=Cupiennius salei	Toxin	100	1
P0C7S4	Bradykinin-potentiating peptide 9a OS=Bothrops neuwiedi	Hypotensive agent, Metalloenzyme inhibitor, Metalloprotease inhibitor, Protease inhibitor, Toxin	100	1
P0DJJ6	Snake venom metalloproteinase BleucMP (Fragment) OS=Bothrops leucurus	Fibrinogenolytic toxin, Fibrinolytic toxin, Hemostasis impairing toxin, Hydrolase, Metalloprotease, Protease, Toxin	100	1
P0DM98	Conopeptide-pc OS=Conus pictus	Toxin	100	1
P84465	Tetrapandin-1 OS=Pandinus imperator	Calcium channel impairing toxin, Ion channel impairing toxin, Toxin	100	1
P84691	Toxin To61 (Fragment) OS=Tityus obscurus	Toxin	100	1
P86942	Conotoxin pc16a OS=Conus pictus	Neurotoxin, Toxin	100	1



APPENDIX J

Identification of novel protein from toxins of edible and highly venomous jellyfish
using De Novo sequencing

1. Identification of novel proteins from the top-down proteomics by using De Novo sequencing

Table J-1. List of novel peptides identified (112 peptides) from nematocyst of edible jellyfish by using SDS for protein extraction.

Peptides	De Novo Score (%)	Sequence length	Molecular weight
LGEYGFQNALLVR	99	13	1478.7881
LLDGGFE	99	7	749.3596
FVEGGDF	99	7	769.3282
LFEGDL	99	6	692.3381
LTGPEG	99	6	572.2806
LLEM(+15.99)DL	99	6	748.3677
LTSDGL	99	6	604.3068
PTLEM(+15.99)	99	5	605.2731
LTLM(+15.99)DYGDAQ	99	10	1141.4961
LLETLPK	99	7	812.5007
PGGPGGPGP	99	9	691.3289
LLTNP	99	5	556.3221
PGGPGP	99	6	480.2332
PGGPGGGPP	99	9	691.3289
VLGDGGF	99	7	663.3228
TGFGLKV	99	7	720.417
LLPP	99	4	438.2842
LGPPGPP	99	7	633.3486
FLENGM(+15.99)	99	6	725.3054
VLDFGN	99	6	663.3228
LTAGPM(+15.99)P	99	7	701.3418
PGGLP	99	5	439.243
LVVEM(+15.99)	99	5	605.3094
LLEM(+15.99)	99	4	520.2567
VVM(+15.99)P	99	4	460.2356
EEELPPPEA	99	9	1009.4603
LEEVLLKT	99	8	943.559
LLEGL	99	5	543.3268
EFVEM(+15.99)	99	5	669.2679
VGPPPP	99	6	562.3115
LTTEV	99	5	561.301
LGPPGP	99	6	536.2958
VGVGF	99	5	477.2587
LSVDSM(+15.99)	99	6	666.2894
LLEE	99	4	502.2639

LTVDE	99	5	575.2802
LTDTGLGM(+15.99)	99	8	822.3793
VVESTGV	99	7	689.3596
SFGGGTGSG	99	9	725.298
LSPEDL	99	6	672.333
YLEGM(+15.99)	99	5	627.2574
LGPPGGPGP	99	9	747.3915
LLFDD	99	5	621.301
LEPTVVDE	99	8	900.444
TLSNGGV	99	7	646.3286
SGPFGQ	99	6	591.2653
VVEPYN	99	6	719.349
VDASAELGSKL	99	11	1088.5713
LLANN	99	5	543.3016
LAPP	99	4	396.2372
LTGVPGP	99	7	639.3591
LEGTNL	99	6	645.3333
LGGSL	99	5	445.2536
AEVNGM(+15.99)LM(+15.99)PVAKSDSG	99	16	1636.7437
VLGANAPAVEAELKKN	99	16	1622.8992
LLNPP	99	5	552.3271
PGGGPGGPP	99	9	691.3289
LLTNM(+15.99)	99	5	606.3047
TLLQFGKTP	99	9	1003.5702
EAEKPKV	99	7	799.4439
FDLM(+15.99)M(+15.99)	99	5	687.2608
LAVDL	99	5	529.3112
LGALGEAGPGAGPVG	99	15	1221.6353
AGGPGPLPPGGPGP	99	15	1183.5984
LVGKAGM(+15.99)EGEVGRP	99	14	1414.7239
GPTGPLG	99	7	597.3122
LEPLP	99	5	567.3268
EEELPPAEP	99	9	1009.4603
LYGFN	99	5	612.2907
LEEVTKFD	99	8	979.4862
VGPLNN	99	6	612.3231
LLEM(+15.99)L	99	5	633.3408
LVDAGP	99	6	570.3013
LLAPPE	99	6	638.3639
LLTTP	99	5	543.3268
LDVDL	99	5	573.301

LVTSHPLYVPVSHPDE	99	16	1788.9045
FGGGTGSG	99	8	638.266
FVEM(+15.99)	99	4	540.2254
LDPTP	99	5	541.2748
LLTQM(+15.99)	99	5	620.3204
LVGKAGM(+15.99)EGEVGRGP	99	15	1471.7454
LGPSGSAP	99	8	684.3442
EELPPPEA	99	8	880.4178
PLYE	99	4	520.2533
LGAGP	99	5	413.2274
NLGGVKKGPTGP	99	12	1123.635
LLAPP	99	5	509.3213
LM(+15.99)EP	99	4	504.2254
VVYLPEGQGV	99	10	1059.5601
LEVNM(+15.99)	99	5	620.284
LTDPAATT	99	9	885.4443
LGM(+15.99)M(+15.99)P	99	5	579.2397
PGGPGFP	99	7	627.3016
VVAGPLT	99	7	655.3904
FGTV	99	4	422.2165
YLADKPEL	99	8	947.4963
LEYD	99	4	538.2275
LGPPP	99	5	479.2744
LNGTDPEDVLK	99	11	1199.6033
LLSKLPDGGP	99	10	995.5651
LGAAGRPGPLGN	99	12	1078.5884
LLFM(+15.99)	99	4	538.2825
LAGP	99	4	356.2059
LGGAV	99	5	415.2431
FVAGAPEDDV	99	10	1018.4607
LTLGGGE	99	7	645.3333
NFGGGGF	99	7	654.2761
LLNEPT	99	6	685.3646
PGLGM(+15.99)	99	5	489.2257
LDVEM(+15.99)	99	5	621.268
LDEYLADKEP	99	10	1191.5659

Table J-2. List of novel peptides identified (49 peptides) from nematocyst of edible jellyfish by using PBS buffer for protein extraction.

Peptides	De novo Score (%)	Sequence length	Molecular weight
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DEGLRF	99	6	735.3551
LTPELL	99	6	684.4058
VAPEEHPVL	99	9	989.5181
YDESGKNPPP	99	10	1102.4932
FGEF	99	4	498.2114
VLGF	99	4	434.2529
TSVKEPM(+15.99)L	99	8	919.4684
EEELPPPEA	99	9	1009.4603
LVEL	99	4	472.2897
EELPPPEA	99	8	880.4178
FEEERVAL	99	8	991.4974
EEFPKFD	99	7	910.4072
LLDQEL	99	6	729.3909
LVEDF	99	5	621.301
NWDDM(+15.99)	99	5	695.2221
LVEPTDKTVDA	99	11	1186.6082
VGLF	99	4	434.2529
ELEETGRVL	99	9	1044.5452
SDDGVVELF	99	8	880.3814
FLLDE	99	5	635.3166
LTGVDL	99	6	616.3432
DDLDF	99	5	623.2438
EEEAPPPVNP	99	10	1077.4978
LPLL	99	4	454.3155
EEEAPPVPGGP	99	11	1077.4978
DDGVVELF	99	7	793.3494
FTLDE	99	5	623.2802
LGLL	99	4	414.2842
LNDEM(+15.99)KL	99	7	877.4215
EAEKPKVVV	99	9	1011.5964
EALEETGRVLS	99	11	1202.6143
VLDF	99	4	492.2584
LDGDFKV	99	7	792.4017
VEAEVHLE	99	8	924.4553
TFAL	99	4	450.2478
LEDVFS	99	6	708.333
EDDLSRF	99	7	880.3926
TEAPL	99	5	529.2748
LADEVKL	99	7	786.4487
FDDF	99	4	542.2012
LEEDLL	99	6	730.3749

FDDDDL	99	7	835.3235
EETYPPEPA	99	9	1031.4447
SVSVLQEQVM(+15.99)TLNTK	99	15	1691.8765
LPLEDV	99	6	684.3694
VDDTERF	99	7	880.3926
EFTF	99	4	542.2376
LPDEF	99	5	619.2853
VVDLL	99	5	557.3425

Table J-3. List of novel peptides identified (16 peptides) from nematocyst of highly venomous jellyfish by using SDS for protein extraction.

Peptides	De novo Score (%)	Sequence length	Molecular weight
SDLGKEAKDLLNKN	99	14	1543.8206
GPPGP	99	5	423.2118
LDEP	99	4	472.2169
FLGM(+15.99)E	99	5	611.2625
VAPEE	99	5	543.254
VLLDN	99	5	572.317
PGGPP	99	5	423.2118
EDAKPNK	99	7	800.4028
VVVPM(+15.99)	99	5	559.304
YPPP	99	4	472.2321
PVVET	99	5	543.2904
DSLKGKEAKDLLNKN	99	14	1543.8206
FYPGGDTLFGK	99	11	1200.5815
PGPP	99	4	366.1903
APVEE	99	5	543.254
EEVP	99	4	472.2169

Table J-4. List of novel peptides identified (185 peptides) from nematocyst of highly venomous jellyfish by using PBS buffer for protein extraction.

Peptides	Denovo Score (%)	Sequence length	Molecular weight
EPANVEETAKSE	99	12	1302.594
PANVEETAKSE	99	11	1173.5513
EPATEEPVK	99	9	998.492
PATEEPAKVE	99	10	1069.5291
EPEEEVLVK	99	9	1070.5496
PAVEEPAK	99	8	839.4388
DHELLVK	99	7	852.4705

FAGDDAPR	99	8	847.3824
EPEEEVVTH	99	9	1067.4771
EEEF	99	4	552.2067
EPEEEVVTR	99	9	1086.5193
EPEEELVTR	99	9	1100.5349
PSAPKPEE	99	8	853.4181
PSAPKEPE	99	8	853.4181
PPALDE	99	6	640.3068
APVLSAEK	99	8	813.4596
PEEEVVTR	99	8	957.4767
TSSSLEKSY	99	9	1000.4713
VDGF	99	4	436.1958
LVSTEEQAAEK	99	11	1203.5981
PSAPKEEP	99	8	853.4181
LAGF	99	4	406.2216
EPANVEETAK	99	8	839.4388
LLDTDN	99	6	1086.5193
LGMES	99	5	535.2312
PSAPDDP	99	7	697.2919
VATEETSKVE	99	10	1091.5347
LEEP	99	4	486.2325
EEPANVEETAK	99	11	1215.5618
DDLKKPLT	99	8	928.5229
PAGGDF	99	6	562.2387
PPGPP	99	5	463.243
VVGY	99	4	436.2322
FGGM	99	4	410.1624
VDENEDELTR	99	10	1218.5364
EDESGSLAENR	99	12	1262.5374
PTADVLKEE	99	9	1000.5076
APSAPKPEE	99	9	924.4552
DEESGSLAENR	99	12	1262.5374
ENRPKGF	99	7	846.4348
PPPL	99	4	422.2529
AEEDVTRL	99	8	931.4611
AEERPAEV	99	8	899.4348
VEVVDEDGR	99	9	1016.4774
DPSDGEKVGF	99	10	1049.4666
YDESGPSLVH	99	10	1102.4932
SPAF	99	4	420.2009
PEEEVVTH	99	8	938.4345

EEVVP	99	5	571.2853
VADKMTEEQ	99	9	1049.47
LDEDAPER	99	8	943.4246
REQFSSR	99	7	908.4464
EEPANVEETAKSE	99	13	1431.6365
FTDEQM NAGKN	99	11	1253.5347
DDM(+15.99)GF	99	5	599.1897
DPEDVLR	99	7	842.4134
DEVDDMLR	99	8	991.428
LLEE	99	4	502.2639
TEVNEDRYS	99	9	1111.4783
VEEPAKVE	99	8	899.46
EPATEEPAKVE	99	11	1198.5718
LGGGF	99	5	449.2274
YPTE	99	4	508.2169
EELAP	99	5	557.2697
DESGPSLVHR	99	10	1095.5308
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ALDEDAPER	99	9	1014.4617
PSYP	99	4	462.2114
APTPEM	99	6	644.2839
VVGF	99	4	420.2372
TEEPEEELVTR	99	11	1330.6252
PSAPEP	99	6	596.2806
MPDDAKEPT	99	9	1002.4328
LDDKGNF	99	7	807.3763
TPDGL	99	5	501.2435
GPPGGPGP	99	8	634.3074
EDLDLTESK	99	9	1048.4924
LVSP	99	4	414.2478
EEVTQFDK	99	8	994.4607
PTADVLKE	99	8	871.4651
TEEPEEEVVTR	99	11	1316.6096
EVDDMLR	99	7	876.4011
GPPGGPGPG	99	9	691.3289
EFTDEQM(+15.99)NAGKN	99	12	1398.572
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LDVDDDR	99	7	846.3719
KEVVPKEPE	99	9	1053.5706
TTLGASEEHVQQ	99	12	1298.6104
EDPAAEF	99	7	777.3181

TEDEVDDMLR	99	10	1221.5183
VGDDF	99	5	551.2227
EAAAVGVKQ	99	9	929.4818
PVSY	99	4	464.2271
EASEKEGLR	99	9	1017.509
VLSGGTTM(+15.99)	99	8	780.3688
DDVNDELRL	99	8	974.4305
EPAKVEEPA	99	10	1097.5239
TVVDEVRL	99	7	816.4341
VEEVAKVE	99	8	901.4756
LEEEQNAR	99	8	987.4621
LVDKVTDE	99	8	917.4705
ERQFSSR	99	7	908.4464
TESDELTRP	99	10	1147.5356
EELSGRME	99	8	949.4175
LGTTM(+15.99)	99	5	537.2469
EEVPVKEE	99	8	957.4655
EEEEVSASSR	99	11	1250.5261
EDDTF	99	5	625.2231
DDVKEFS	99	7	838.3708
PFSL	99	4	462.2478
EPAKVDEPAN	99	11	1197.5513
PPENF	99	5	602.27
VLDSGDGVSH	99	10	984.4512
EDEAKNNEEEAPR	99	13	1529.6594
TTAAPSVKQ	99	9	901.4869
EEDPDALAETGR	99	12	1301.5735
QDDESLVR	99	8	960.4512
LQMGTN	99	6	662.3058
EEPEEEVLVK	99	10	1199.592
TTTLQSEEHVQQ	99	12	1399.658
PGPGGPGP	99	8	634.3074
ETEPEEEVVTR	99	11	1316.6096
PEVP	99	4	440.2271
PELP	99	4	454.2427
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EGASDKPKDEAENKTE	99	16	1746.7908
TPGDELEGS	99	9	903.3821
LLAP	99	4	412.2686
LGGGL	99	5	415.2431
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LGAF	99	4	406.2216
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LNEDGKQL	99	8	915.4661
FDETALEK	99	8	951.4549
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DLKEKLN	99	7	858.481
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EEEGW	99	5	648.2391
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ETEPEEEVLVK	99	11	1300.6399
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EEVGKDM(+15.99)	99	7	822.3429
VVVP	99	4	412.2686
LDDGFL	99	6	678.3224
EEPDF	99	5	635.2438
KEVVPKEEP	99	9	1053.5706
LGME	99	4	448.1992
REQSSVSFR	99	9	1094.5469
LDPGNP	99	6	611.2914
VGSEL	99	5	503.2591
LGEM(+15.99)	99	4	464.1941
EDLEQEKAA	99	9	1031.4771
YEEVGVDS	99	8	896.3763
PGGPGPP	99	7	577.2859
EDDTFSSR	99	8	955.3882
DSLEEEQNAR	99	10	1189.521
PAKVEEPA	99	8	839.4388
EEVPVKE	99	7	828.4229
ELPGTM	99	6	646.2996
VLSGGTT	99	7	633.3334
DEELRSPN	99	8	958.4355
EDPEPVR	99	7	840.3977
EPATEEPAK	99	9	970.4607
VEDYVKQN	99	8	993.4767

DDVPEVQK	99	8	928.4501
TTLQSEEHVQQ	99	11	1298.6104
DVM(+15.99)P	99	4	476.1941
NSGGGGGGSSGGRGSGGGSSGGSLNR	99	26	2078.9072
SPVY	99	4	464.2271
EETPAKVEEPATE	99	12	1327.6143
TEPSTETATEAH	99	12	1272.5469
TPYGGP	99	6	590.27
ESGPSLVH	99	8	824.4028
LAGGL	99	5	429.2587
GPPGGGPP	99	8	634.3074
PVEEAEEREAP	99	11	1254.5728
QDSLEEEQNAR	99	11	1317.5796
EEDKAEVSA	99	10	1105.4775





APPENDIX K

Determination of hemolytic activity

1. Determination of hemolytic activity of jellyfish toxins

1.1 Determination of hemolytic activity of toxins from edible jellyfish

Table K-1. Hemolytic activity determination of edible jellyfish toxins at various concentrations.

Edible jellyfish toxins (mg/ml)	Hemolysis (%)				Average \pm SD
	1	2	3	4	
0	0	0	0	0	0
0.046875	3.913	12.183	-	3.913	9.278 \pm 4.651
0.09375	12.035	20.452	-	12.035	21.043 \pm 9.317
0.1875	35.220	46.000	-	35.220	44.917 \pm 9.203
0.375	70.662	68.299	-	80.851	73.270 \pm 6.670
0.75	90.598	99.163	103.150	96.948	97.464 \pm 5.248
1.5	102.559	92.074	109.352	98.572	100.639 \pm 7.239
0.1 % Triton X-100	100	100	100	100	100

1.2 Determination of hemolytic activity of toxins from highly venomous jellyfish

Table K-2. Hemolytic activity determination of highly venomous jellyfish toxins at various concentrations.

highly venomous jellyfish toxins (mg/ml)	Hemolysis (%)			Average \pm SD
	1	2	3	
0	0	0	0	0
0.075	-2.092	-0.679	-0.541	-1.104 \pm 0.858
0.15	-1.793	-0.271	-0.405	-0.823 \pm 0.842
0.3	-1.943	-1.494	-0.947	-1.461 \pm 0.498
0.6	-0.896	-2.309	-0.405	-1.204 \pm 0.988
1.2	-	-2.445	-1.082	-0.378 \pm 2.494
1.4	-	-1.902	-0.811	-1.357 \pm 0.770
0.1 % Triton X-100	100	100	100	100

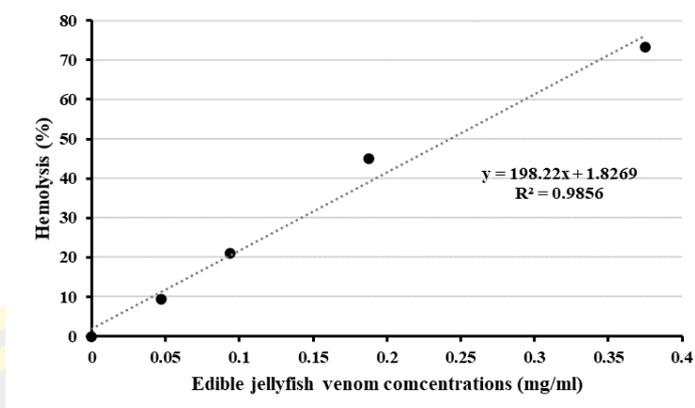


Figure K-1. Standard of hemolytic activity of the toxins from edible at various concentrations.

Calculation of EC50 value of hemolytic activity from edible jellyfish toxins was calculated using equation (1):

$$y = 198.22x + 1.8269 \quad (1)$$

$$y = 50$$

x = concentration of edible jellyfish toxins to generate 50% hemolysis

Table K-3. Three replications of hemolytic activity (EC50 (mg/ml)) from edible jellyfish toxins.

Replication	EC50 (mg/ml)
1	0.270
2	0.253
3	0.208
Average \pm SD	0.243 \pm 0.032



APPENDIX L

Determination of ACE inhibitory activity

1. Determination of ACE inhibitory activity of the jellyfish toxins

1.1 ACE inhibitory activity of edible jellyfish toxins

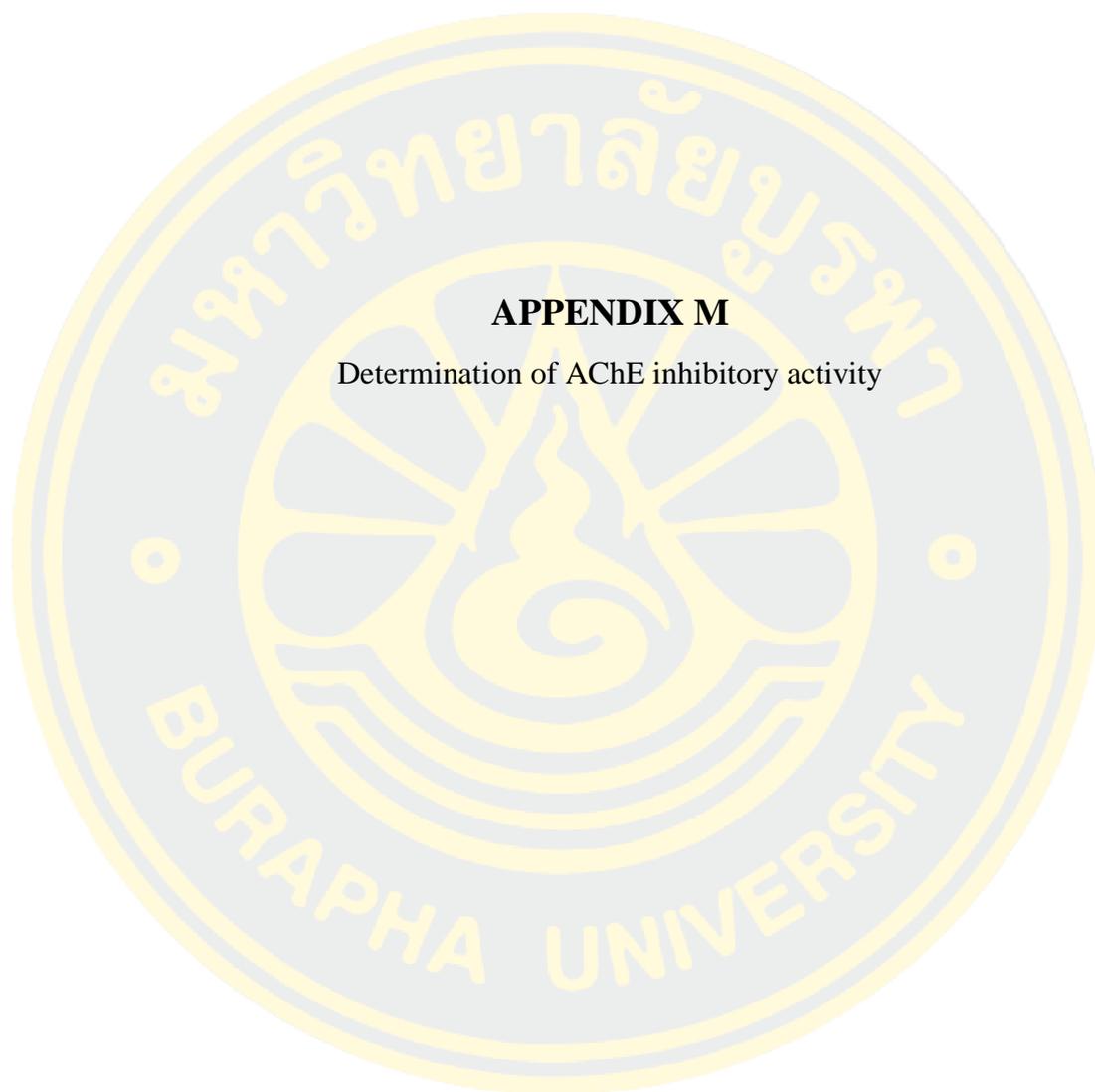
Table L-1. ACE inhibition activity percent of edible jellyfish toxins at several concentrations.

Edible jellyfish toxins (mg/ml)	ACE inhibition (%)				Average \pm SD
	1	2	3	4	
0.125	-62.289	-33.281	-69.754	-	-55.108 \pm 19.267
0.25	-49.866	-40.292	-33.517	-24.183	-36.965 \pm 10.843
0.5	-	-40.169	-44.309	-34.898	-39.792 \pm 4.716
Captopril (1 mg/ml)	126.844	94.050	97.738	81.722	100.089 \pm 19.106

1.2 ACE inhibitory activity of highly venomous jellyfish toxins

Table L-2. ACE inhibition activity percent of highly venomous jellyfish toxins at several concentrations.

highly venomous jellyfish toxins (mg/ml)	ACE inhibition (%)				Average \pm SD
	1	2	3	4	
0.0625	-7.221	-1.854	-6.189	-13.754	-7.255 \pm 4.917445943
0.125	-15.864	-	-14.683	-12.403	-14.317 \pm 1.759
0.25	-	-6.314	0.0185	-7.181	-4.492 \pm 3.930
0.5	-	23.090	3.525	15.118	13.911 \pm 9.838
Captopril (1 mg/ml)	113.113	99.039	100.749	100.831	103.433 \pm 6.505



APPENDIX M

Determination of AChE inhibitory activity

1. Determination of AChE inhibitory activity of the jellyfish toxins

1.1 AChE inhibitory activity of the edible jellyfish toxins

Table M-1. AChE inhibitory percent of toxins from edible jellyfish at different concentrations.

Edible jellyfish toxins (mg/ml)	AChE inhibition (%)					Average \pm SD
	1	2	3	4	5	
0.125	11.299	10.060	10.479	16.809	-	12.162 \pm 3.140
0.25	8.358	5.100	7.676	7.616	12.182	8.187 \pm 2.554
0.5	6.696	6.793	11.072	8.730	12.734	9.205 \pm 2.658
1	10.508	-	-	13.209	19.993	14.570 \pm 4.886
2	-	-	19.429	18.215	26.748	21.464 \pm 4.616
Galantamine (1 mg/ml)	-	73.500	74.147	77.635	77.478	75.690 \pm 2.172

1.2 AChE inhibitory activity of the highly venomous jellyfish toxins

Table M-2. AChE inhibitory percent of toxins from highly venomous jellyfish at different concentrations.

highly venomous jellyfish toxins (mg/ml)	AChE inhibition (%)				Average \pm SD
	1	2	3	4	
0.125	-	-10.510	-1.759	-4.633	-5.634 \pm 4.460
0.25	-3.653	-	-5.670	-8.521	-5.948 \pm 2.445
0.5	-13.748	-10.051	-15.171	-12.956	-12.981 \pm 2.157
1	-19.436	-36.373	-25.588	-27.484	-27.220 \pm 7.002
Galantamine (1 mg/ml)	73.500	74.147	77.635	77.478	75.690 \pm 2.172

BIOGRAPHY

NAME Naphatsawan Panya

DATE OF BIRTH 8 Jun 1995

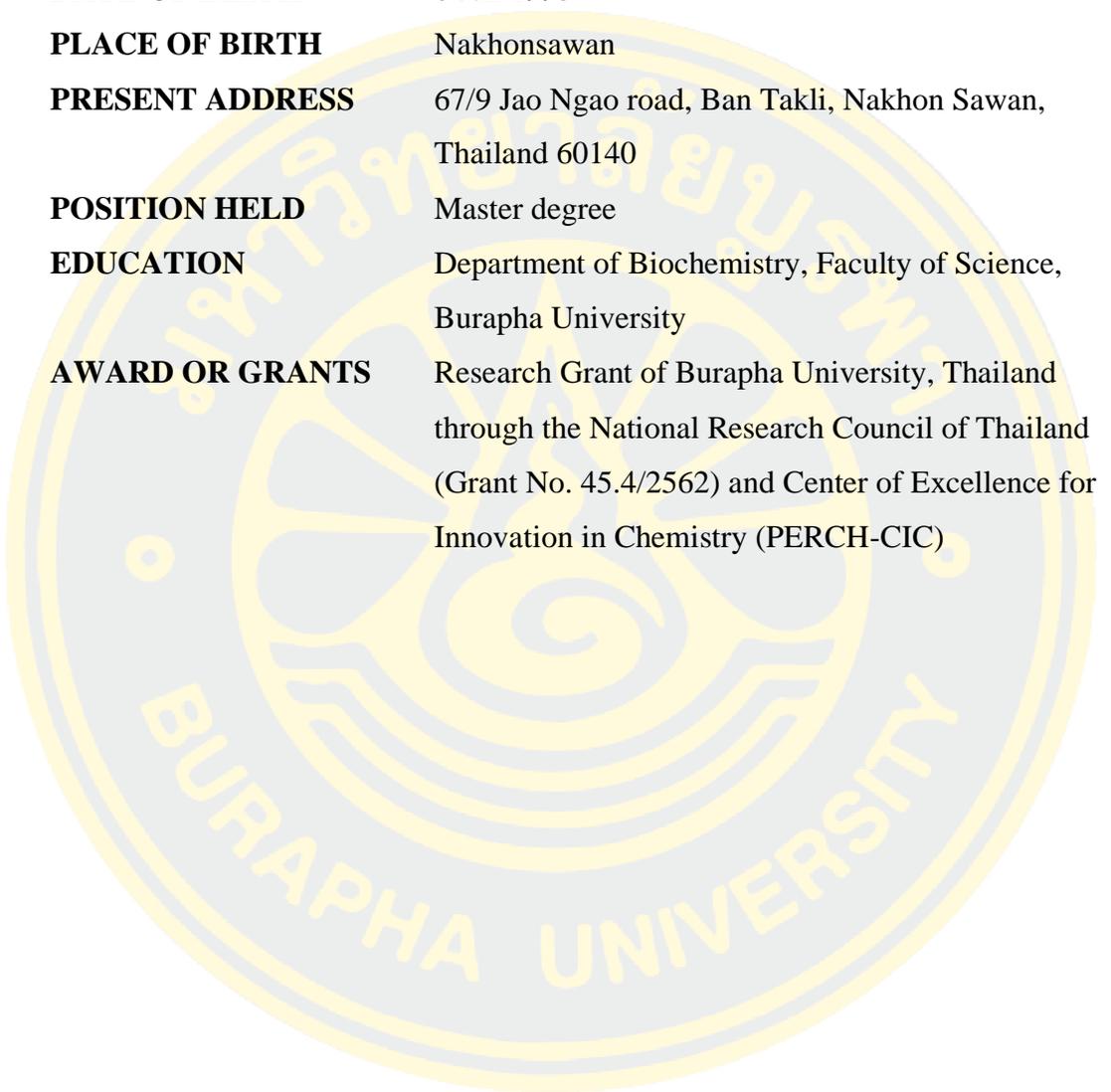
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POSITION HELD Master degree

EDUCATION Department of Biochemistry, Faculty of Science,
Burapha University

AWARD OR GRANTS Research Grant of Burapha University, Thailand
through the National Research Council of Thailand
(Grant No. 45.4/2562) and Center of Excellence for
Innovation in Chemistry (PERCH-CIC)

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REFERENCES



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POSITION HELD Master degree

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AWARDS OR GRANTS

