

学校编码: 10384

分类号 \_\_\_\_\_ 密级 \_\_\_\_\_

学号: 22620070153922

UDC \_\_\_\_\_

廈門大學

博 士 学 位 论 文

南海颗粒有机物和溶解有机物宏蛋白质组  
学研究

Metaproteomics of particulate organic matter and dissolved  
organic matter in the South China Sea

董宏坡

指导教师姓名: 王大志 教授

专 业 名 称: 环境科学

论文提交日期: 2011 年 10 月

论文答辩时间: 2011 年 10 月

学位授予日期:

答辩委员会主席: \_\_\_\_\_

评 阅 人: \_\_\_\_\_

2011 年 10 月

## 厦门大学学位论文原创性声明

本人提交的学位论文是本人在导师指导下,独立完成的研究成果。本人在论文写作中参考其他个人或集体已经发表的研究成果,均在文中以适当方式明确标明,并符合法律规范和《厦门大学研究生学术活动规范(试行)》。

声明人(签名):

年 月 日

## 厦门大学学位论文著作权使用声明

本人同意厦门大学根据《中华人民共和国学位条例暂行实施办法》等规定保留和使用此学位论文，并向主管部门或其指定机构送交学位论文（包括纸质版和电子版），允许学位论文进入厦门大学图书馆及其数据库被查阅、借阅。本人同意厦门大学将学位论文加入全国博士、硕士学位论文共建单位数据库进行检索，将学位论文的标题和摘要汇编出版，采用影印、缩印或者其它方式合理复制学位论文。

本学位论文属于：

1. 经厦门大学保密委员会审查核定的保密学位论文，于 年 月 日解密，解密后适用上述授权。

2. 不保密，适用上述授权。

（请在以上相应括号内打“√”或填上相应内容。保密学位论文应是已经厦门大学保密委员会审定过的学位论文，未经厦门大学保密委员会审定的学位论文均为公开学位论文。此声明栏不填写的，默认为公开学位论文，均适用上述授权。）

作者签名：

日期： 年 月 日

# 目 录

摘 要 .....	vii
<b>第一章 前言 .....</b>	<b>1</b>
1.1 海洋颗粒有机物研究概况 .....	1
1.1.1 海洋颗粒有机物 (POM) 概念 .....	1
1.1.2 海洋颗粒有机物种类、组成和来源 .....	1
1.2 海洋溶解有机物研究概况 .....	9
1.2.1 海洋溶解有机物 (DOM) 概念 .....	9
1.2.2 海洋溶解有机物种类、组成和来源 .....	10
1.2.3 海洋溶解有机物动力学和保护机制 .....	12
1.3 海洋环境蛋白质组学研究概述 .....	15
1.3.1 蛋白质组学研究方法和发展趋势 .....	16
1.3.2 海洋颗粒蛋白研究进展 .....	18
1.3.3 海洋溶解蛋白的研究进展 .....	20
1.4 本文的研究目的和内容 .....	21
<b>第二章 海洋颗粒蛋白鸟枪蛋白质组学研究方法的建立 .....</b>	<b>24</b>
摘要 .....	24
2.1 前言 .....	24
2.2 材料和方法 .....	25
2.2.1 样品采集 .....	25
2.2.2 颗粒蛋白提取和定量 .....	26
2.2.3 颗粒蛋白二维双向凝胶电泳 .....	27
2.2.4 颗粒蛋白一维凝胶电泳分离和胶内酶解 .....	27
2.2.5 质谱分析 .....	27
2.2.6 颗粒蛋白的生物信息学分析 .....	28
2.3 结果 .....	31
2.3.1 颗粒蛋白提取和二维双向电泳分离 .....	31
2.3.2 颗粒蛋白的鉴定和表征 .....	31
2.4 讨论 .....	36
<b>第三章 南海颗粒有机物宏蛋白质组学研究 .....</b>	<b>40</b>
摘要 .....	40
3.1 前言 .....	40

3.2 材料和方法 .....	41
3.2.1 样品采集.....	41
3.2.2 采样站位理化参数调查.....	42
3.2.3 颗粒蛋白提取和定量.....	42
3.2.4 颗粒蛋白鸟枪蛋白质组分析.....	43
3.2.5 生物信息学分析.....	43
3.3 结果 .....	44
3.3.1 TS1 站位颗粒蛋白和理化参数的垂直变化.....	44
3.3.2 颗粒蛋白的分离和鉴定.....	44
3.3.3 颗粒蛋白的生源性来源.....	47
3.3.4 颗粒蛋白的亚细胞定位.....	49
3.3.5 颗粒蛋白的生物学功能.....	50
3.4 讨论 .....	54
3.4.1 颗粒蛋白的生源性来源.....	54
3.4.2 颗粒蛋白抗降解和保护机制.....	56
3.4.3 颗粒有机物中特有蛋白.....	58
<b>第四章 南海溶解有机物宏蛋白质组学研究.....</b>	<b>61</b>
摘要 .....	61
4.1 前言 .....	61
4.2 材料和方法 .....	63
4.2.1 溶解有机物样品采集和预浓缩.....	63
4.2.2 小分子溶解有机物 (SDOM) 中溶解蛋白制备.....	64
4.2.3 大分子溶解有机物 (LDOM) 中溶解蛋白制备.....	65
4.2.4 溶解蛋白一维电泳分离和酶解.....	65
4.2.5 质谱分析.....	65
4.2.6 蛋白鉴定.....	66
4.2.7 生物信息学分析.....	67
4.3 结果 .....	69
4.3.1 溶解蛋白的分离和鉴定.....	69
4.3.2 溶解蛋白的生源性来源.....	70
4.3.3 溶解蛋白的亚细胞定位.....	71

4.3.4 溶解蛋白的 COG 功能类群分类 .....	72
4.4 讨论 .....	74
4.4.1 溶解蛋白的来源 .....	75
4.4.2 不同水层溶解蛋白特征 .....	77
4.4.3 溶解蛋白的保护机制 .....	78
<b>第五章 南海不同站位表层小分子溶解有机物 (SDOM) 宏蛋白质组 比较研究 .....</b>	<b>81</b>
摘要 .....	81
5.1 前言 .....	81
5.2 材料和方法 .....	83
5.2.1 溶解有机物样品采集和预浓缩 .....	83
5.2.2 小分子溶解有机物 (SDOM) 中溶解蛋白制备 .....	84
5.2.3 溶解性蛋白一维电泳分离和酶解 .....	85
5.2.4 质谱分析 .....	85
5.2.5 蛋白鉴定 .....	85
5.2.6 生物信息学分析 .....	86
5.3 结果 .....	86
5.3.1 表层 SDOM 溶解性蛋白分离和鉴定 .....	86
5.3.2 表层 SDOM 溶解性蛋白生源性来源 .....	87
5.3.3 表层 SDOM 溶解性蛋白 GO 功能分类 .....	89
5.3.4 病毒蛋白 .....	94
5.4 讨论 .....	94
5.4.1 表层 SDOM 中溶解性蛋白生源性来源 .....	95
5.4.2 表层 SDOM 中溶解性蛋白 GO 分类特征 .....	97
5.4.3 表层 SDOM 中的病毒蛋白 .....	100
<b>第六章 总结、创新和展望 .....</b>	<b>103</b>
6.1 总结 .....	103
6.2 论文特色和创新点 .....	104
6.3 论文不足及展望 .....	105
<b>参考文献 .....</b>	<b>107</b>
<b>缩写词列表 .....</b>	<b>126</b>
<b>附录 .....</b>	<b>128</b>

附录 I 双向电泳流程和详细步骤 .....	128
附录 II 胶体考玛斯亮蓝染色方法和蛋白酶切方法 .....	130
附录 III Pelicon 2 切向超滤系统操作步骤和膜包截留性能评价方法 .....	131
附录 IV PlusOne™ 2-D Quant Kit 和 Millipore 搅拌式超滤杯操作步骤 .....	133
附录 V 南海 41-, 200-, 500-, 1000 m 水层颗粒蛋白列表(见光盘)	
附录 VI 南海 41-, 75-, 3000 m 水层溶解蛋白列表 (见光盘)	
附录 VII 南海表层小分子溶解有机物中溶解蛋白列表 (见光盘)	

## 博士在读期间文章及参加会议情况

## 致谢

厦门大学博硕士论文摘要库

## Content

Chinese Abstract.....	vii
English Abstract.....	x
<b>Chapter 1 Introduction .....</b>	<b>1</b>
<b>1.1 Advances in marine particulate organic matter (POM) .....</b>	<b>1</b>
1.1.1 Definition of marine POM.....	1
1.1.2 Types, composition and origin of marine POM.....	1
<b>1.2 Advances in marine dissolved organic matter (DOM).....</b>	<b>9</b>
1.2.1 Definition of marine DOM .....	9
1.2.2 Types, composition and origin of marine DOM.....	10
1.2.3 Dynamics and protective mechanism of marine DOM.....	12
<b>1.3 Advances in marine environmental proteomics.....</b>	<b>15</b>
1.3.1 Methodology and trends in proteomics.....	16
1.3.2 Advances in marine particulate proteins.....	18
1.3.3 Advances in marine dissolved proteins.....	20
<b>1.4 Objectives and contents of the dissertation.....</b>	<b>21</b>
<b>Chapter 2 Methodology development of metaproteomics of marine OM.....</b>	<b>24</b>
<b>Abstract .....</b>	<b>24</b>
<b>2.1 Introduction .....</b>	<b>24</b>
<b>2.2 Materials and methods.....</b>	<b>25</b>
2.2.1 Sample collection.....	25
2.2.2 Particulate protein extraction and quantification .....	26
2.2.3 Two-dimensional gel electrophoresis of particulate proteins .....	27
2.2.4 One-dimensional SDS-PAGE and in-gel digestion of particulate proteins ..	27
2.2.5 Mass spectrometry analysis .....	27
2.2.6 Bioinformatics analysis of particulate proteins.....	28
<b>2.3 Results.....</b>	<b>31</b>
2.3.1 Particulate protein extraction and two-dimensional gel electrophoresis .....	31
2.3.2 Identification and characterization of particulate proteins using shotgun proteomics.....	31
<b>2.4 Discussion .....</b>	<b>36</b>
<b>Chapter 3 Metaproteomics of marine POM in the South China Sea ..</b>	<b>40</b>
<b>Abstract .....</b>	<b>40</b>



<b>3.1 Introduction</b> .....	40
<b>3.2 Materials and methods</b> .....	41
3.2.1 Sample collection .....	41
3.2.2 Biological and chemical parameters at sampling station .....	42
3.2.3 Particulate protein extraction and determination .....	42
3.2.4 Shotgun proteomic analysis of POM proteins .....	43
3.2.5 Bioinformatics analysis .....	43
<b>3.3 Results</b> .....	44
3.3.1 Vertical variations of particulate protein concentration and other parameters at Station TS1 .....	44
3.3.2 Separation and identification of particulate proteins .....	44
3.3.3 Biological origin of particulate proteins .....	47
3.3.4 Subcellular location of particulate proteins .....	49
3.3.5 Biological process of particulate proteins .....	50
<b>3.4 Discussion</b> .....	54
3.4.1 Source of proteins in POM .....	54
3.4.2 Degradation and preservation of particulate proteins .....	56
3.4.3 Specific proteins in POM .....	58
<b>Chapter 4 Metaproteomics of marine DOM in the South China Sea</b> ·	61
<b>Abstract</b> .....	61
<b>4.1 Introduction</b> .....	61
<b>4.2 Materials and methods</b> .....	63
4.2.1 Sampling and preconcentration of dissolved proteins .....	63
4.2.2 Preparation of the dissolved proteins of SDOM .....	64
4.2.3 Preparation of the dissolved proteins of LDOM .....	65
4.2.4 One SDS-PAGE and enzymatic digestion of dissolved proteins .....	65
4.2.5 Shotgun proteomic analysis of dissolved proteins .....	65
4.2.6 Protein identification .....	66
4.2.7 Bioinformatics analysis .....	67
<b>4.3 Results</b> .....	69
4.3.1 Separation and identification of dissolved proteins .....	69
4.3.2 Biological origin of dissolved proteins .....	70
4.3.3 Subcellular location of dissolved proteins .....	71
4.3.4 COG functional classification of dissolved proteins .....	72

<b>4.4 Discussion</b> .....	74
4.4.1 Source of dissolved proteins .....	75
4.4.2 Features of dissolved proteins from different water layers.....	77
4.4.3 Preservation of the dissolved proteins .....	78
<b>Chapter 5 Comparative metaproteomic analysis of marine SDOM in the surface waters in the South China Sea</b> .....	<b>81</b>
<b>Abstract</b> .....	81
<b>5.1 Introduction</b> .....	81
<b>5.2 Materials and methods</b> .....	83
5.2.1 Sampling and preconcentration of dissolved proteins .....	83
5.2.2 Preparation of the dissolved proteins of SDOM .....	84
5.2.3 One-dimensional SDS-PAGE and enzymatic digestion of dissolved proteins.....	85
5.2.4 Shotgun proteomic analysis .....	85
5.2.5 Protein identification.....	85
5.2.6 Bioinformatics analysis.....	86
<b>5.3 Results</b> .....	86
5.3.1 Separation and identification of dissolved proteins of SDOM .....	86
5.3.2 Biological origin of dissolved proteins of SDOM .....	87
5.3.3 GO functional classification of dissolved proteins of SDOM .....	89
5.3.4 Viral proteins.....	94
<b>5.4 Discussion</b> .....	94
5.4.1 Source of dissolved proteins of SDOM .....	95
5.4.2 Features of GO classification of dissolved proteins of SDOM.....	97
5.4.3 Viral proteins in SDOM .....	100
<b>Chapter 6 Summary, creativity and prospect</b> .....	<b>103</b>
<b>6.1 Summary</b> .....	103
<b>6.2 Creativity</b> .....	104
<b>6.3 Problems and prospect</b> .....	104
<b>References</b> .....	<b>105</b>
<b>Table of abbreviations</b> .....	<b>126</b>
<b>Appendix</b> .....	<b>128</b>
<b>Appendix I Protocols of 2-DE</b> .....	126
<b>Appendix II Protocols of colloidal Coomassie Brilliant Blue and enzymatic digestion</b> .....	128
<b>Appendix III Protocols of Pelicon 2 cross-flow ultrafiltration system and evaluation</b>	

of ultrafiltration membrane .....	129
<b>Appendix IV Protocols of PlusOne™ 2-D Quant Kit and stirred ultrafiltration cell .....</b>	<b>131</b>
<b>Appendix V List of all proteins in POM from the 41-, 200-, 500-, 1000 m water layers in the South China Sea</b>	
<b>Appendix VI List of all proteins in DOM from the 41-, 75-, 3000 m water layers in the South China Sea</b>	
<b>Appendix VII List of all proteins in surface SDOM in the South China Sea</b>	
<b>Papers and conferences and awards</b>	
<b>Acknowledgements</b>	

厦门大学博硕士学位论文摘要库

## 摘 要

海洋有机物（包括颗粒和溶解有机物）是全球最大的碳库之一，在全球碳循环中发挥着非常重要的作用。海洋有机物的来源、组成和降解及保护机制研究对深入了解海洋碳的生物地球化学过程和全球气候调节具有重要意义。

本论文将鸟枪蛋白质组学方法应用于海洋有机物研究领域，建立了海洋有机物宏蛋白质组学研究方法，并结合生物信息学分析，比较研究了南海不同站位和不同水层颗粒和溶解有机物的蛋白组成特征，筛选、确认了与海区、水层生物组成特征相关的蛋白质生物标志物，揭示了海区颗粒和溶解性蛋白的生源性来源、分子功能、生物学过程以及蛋白的再矿化和抗降解机制。主要研究结果如下：

（1）优化了海洋颗粒有机物蛋白提取方法，并运用鸟枪蛋白组学技术对颗粒蛋白进行了鉴定，从南海海盆区 41 m 水层颗粒有机物中鉴定到 737 个蛋白，其中 184 个为两个或两个以上肽段匹配的高可信度蛋白，如光合作用蛋白，转运蛋白，分子伴侣和孔蛋白（porins）等。除一些未知功能蛋白外，尚有相当数量的新蛋白也被检测到，这部分蛋白大约占总鉴定蛋白的 30%。海洋颗粒有机物中大量、高可信度蛋白的成功鉴定证明鸟枪蛋白组学方法可应用于海洋颗粒蛋白的研究，为海洋有机物宏蛋白质组学研究提供了理论依据和技术支撑。

（2）运用鸟枪蛋白质组学技术比较研究了南海上层（41 m 和 200 m）和中层（500 m 和 1000 m）颗粒有机物宏蛋白质组。从四个水层颗粒有机物中，一共鉴定到 3035 个一个或一个以上肽段匹配的蛋白，其中 505 个是两个或两个以上肽段匹配的高可信蛋白。蓝细菌是整个水柱颗粒蛋白的最大贡献者，而甲壳类动物和甲藻是 200 m 水层颗粒蛋白的两个主要贡献者。41 m 和 200 m 水层颗粒蛋白的亚细胞定位和生物学过程显著不同：41 m 水层含有丰富的光合作用相关蛋白，而微管蛋白和肌动蛋白则在中层积累，特别是在 200 m 水层。孔蛋白（Porin）、ATP 合成酶、营养盐转运蛋白、分子伴侣和胞外酶在颗粒有机物中被频繁检测到，但它们在整個水柱内呈现出不同的分布模式，揭示在不同水层颗粒有机物中或者在颗粒有机物下沉过程中，发生了复杂的生物地球化学过程。上层和中层颗粒蛋白的来源不同，参与细胞代谢、能量产生和转运功能的蛋白的数量和丰度随水深

迅速减少。浮游动物“粪便打包”和膜的“包裹”作用可能在颗粒蛋白的保护中起着重要作用。

(3) 运用鸟枪蛋白质组学技术比较研究了来自南海表层(10 m 和 75 m)和深海(3000 m)溶解性有机物宏蛋白质组。三个溶解性有机物中,一共鉴定到 182 个蛋白,它们被 286 个专一肽段所匹配。大分子溶解有机物(LDOM, 0.2  $\mu\text{m}$ -0.7  $\mu\text{m}$ ) 组份中的蛋白数量要显著高于小分子溶解有机物组份(SDOM, 5 kD-0.2  $\mu\text{m}$ )。表层和深海 SDOM 的蛋白数量之间没有明显的差异。表层 DOM 中溶解性蛋白的来源多样,包括各种类型的细菌、浮游植物和卵菌类,而古生菌、变形菌和某些浮游植物类群是深海 DOM 的主要贡献者。参与细胞骨架组织、能量产生和转化、蛋白翻译后修饰、蛋白更新和再折叠的蛋白在表层 LDOM 丰度相当高,而参与蛋白合成相关蛋白在深海 LDOM 中更加丰富。参与物质转运和代谢、细胞壁或细胞膜或被膜的生物发生以及光合作用相关蛋白在 75 m LDOM 中相当丰富。参与氨基酸转运和代谢的 ABC 转运蛋白是 10 m SDOM 中最丰富的蛋白,而参与能量生产和转化的 methylenetetrahydromethanopterin 还原酶是 75 m 和 3000 m SDOM 中丰度最高的蛋白。在海洋垂直剖面上,溶解性蛋白的来源多样化并呈现动态的变化,每个水层都具有自己独特的蛋白,仅有非常少量、来自表层的溶解性蛋白能够被保护并输送到深海。

(4) 运用鸟枪蛋白质组技术结合全球采样组合蛋白数据库比较研究了南海陆架和海盆表层小分子溶解性有机物(5 kD-0.2  $\mu\text{m}$ )宏蛋白质组。从四个表层溶解性有机物中鉴定到 806 个蛋白,它们被 1477 个专一肽段(unique peptides)和 3291 幅谱图所匹配。表层小分子溶解性有机物中大部分蛋白源于细菌和病毒,仅有非常少的蛋白来自浮游植物。尽管不同细菌类群在不同采样站位表现出一定的丰度差异,但细菌类群变化不大,表明一些特定的细菌类群调节着该海区表层小分子溶解有机物的蛋白组成。一些已经在颗粒有机物和大分子溶解有机物中鉴定到的转运蛋白,如尿素 ABC 转运蛋白、氨转运蛋白、谷氨酸盐 ABC 转运蛋白、TonB-依赖受体和 porin 孔蛋白也在本研究中鉴定到。一些新型的转运蛋白,如细菌铁蛋白、变形菌视紫红质、TRAP 二羧酸转运蛋白、亚精胺周质空间结合蛋白和糖 ABC 转运蛋白则首次在溶解有机物中鉴定到。四个站位之间溶解性蛋白功能类群和种类分布非常相似,提示着蛋白功能类群和种类丰度上的差异可能主要由每个站位微生物群落结构调控。鉴定的病毒蛋白主要来自三个科:肌尾噬菌

体科、短尾噬菌体科和长尾噬菌体科。肌尾噬菌体科病毒蛋白丰度要明显高于其它两个科，暗示肌尾噬菌体科病毒可能有更强的生存能力，能够在病毒群落中迅速地发展成为优势种群。大部分病毒蛋白为病毒外部的蛋白衣壳，说明病毒粒子不同组份存在不同的更新时间。

**关键词：**南海；颗粒有机物；溶解有机物；鸟枪蛋白组学；宏蛋白质组学；亚细胞定位；蛋白分子功能；生物学过程

厦门大学博硕士论文摘要库

## Abstract

Marine organic matter, including particulate and dissolved organic matter, is one of the largest carbon pools in the world and plays a very important role in global carbon cycle. The study of sources, composition and mechanism of degradation and protection of marine organic matters will provide in-depth understanding of marine carbon biogeochemistry and global climate regulation.

This thesis developed a high resolution and high-throughput method, shotgun proteomics to identify and characterize proteins from marine particulate organic matter (POM) and dissolved organic matter (DOM). Using this approach, protein species, composition and biological origin in POM and DOM from the South China Sea were investigated. Featured proteins which reflected the characteristics of different marine area, water depths and abiotic environment were also identified. Furthermore, according to these protein features, the mechanisms resistant to biodegradation were revealed. The main results were as follows:

(1) Using the shotgun proteomic approach combined with bioinformatic analysis, a total of 737 proteins matching one or more peptides were detected in a POM sample collected from the 41 m water layer in the basin area of the northern South China Sea (SCS). Of these, 184 were identified as high-confidence proteins matching two or more peptides, including photosynthetic proteins, transporters, molecular chaperones and porins. In addition to these proteins with known functions, a significant number of novel proteins (accounting for ~ 30% of the proteins identified) were also identified. The identification of a large number of high-confidence proteins in the POM sample demonstrated that the shotgun proteomic approach is reliable and feasible for the study of particulate proteins, and will provide a powerful tool to comprehensively investigate the nature and dynamics of POM in the ocean.

(2) Using the established shotgun proteomic approach, we characterized particulate organic matter (POM) collected from both the surface (41 m and 200 m) and meso-pelagic layers (500 m and 1000 m) in the western SCS. A total of 3035 proteins matching one or more peptides were detected from four POM samples, 505 of which were identified as high-confidence proteins matching two or more peptides. Cyanobacteria was the largest contributor throughout the water column, while crustaceans and dinophytes were the two major groups contributing to the particulate proteins in the POM collected from 200 m. Subcellular locations and biological

processes of particulate proteins varied significantly between the 41-m and 200-m layers: photosynthesis-associated proteins were highly abundant in the 41-m layer while tubulins and actins accumulated in the midwaters, especially at the 200-m layer. Porins, adenosine triphosphate (ATP) synthases, nutrient transporters, molecular chaperones, and ectoenzymes were frequently detected in the POM samples and presented different distribution patterns within the water column, revealing complex biological processes at the different water layers and/or during the sinking of POM. The sources of surface and midwater particulate proteins are different, and the cellular metabolism, generation of energy and transport processes in POM were attenuated rapidly down ocean water column. Zooplankton fecal pellet packages and membrane encapsulation might play important roles in protecting particulate proteins from degradation.

(3) Metaproteomic of dissolved organic matters (DOM,  $<0.7 \mu\text{m}$  in size) collected from the surface (10-m and 75-m) and bathypelagic (3000-m) layers in the SCS were investigated using the shotgun proteomic approach. A total of 182 proteins matched by 286 unique peptides were identified from three DOM samples. The number of proteins in the large DOM (LDOM,  $0.2\text{-}0.7 \mu\text{m}$  fraction) was significantly greater than that in the small DOM (SDOM,  $5 \text{ kD}\text{-}0.2 \mu\text{m}$  fraction). There was no remarkable difference in the number of proteins between the surface and bathypelagic SDOMs. The sources of dissolved proteins were diverse in surface DOM including various bacterial and phytoplankton groups as well as Oomycetes while the Archaea, Proteobacteria, and some phytoplankton groups were the major contributors to bathypelagic DOM. Proteins involved in cytoskeleton, energy production and conversion, posttranslational modification, protein turnover, and chaperones presented high abundance in surface LDOM while proteins involved in translation, ribosomal structure, and biogenesis were more abundant in bathypelagic LDOM. Proteins involved in transport and metabolism, cell wall or membrane or envelope biogenesis, and photosynthesis were abundant in the 75-m LDOM. A urea ABC transporter assigned to amino acid transport and metabolism was the most abundant protein in the 10-m SDOM while methylenetetrahydromethano- pterin reductase involved in energy production and conversion dominated the protein profiles in the 75- and 3000-m SDOMs. The dissolved proteins in the water column are diverse and dynamic, with each layer characterized by unique proteins, and only a very minor amount of proteins from the surface are protected and transferred to deep sea.



Degree papers are in the "[Xiamen University Electronic Theses and Dissertations Database](#)". Full texts are available in the following ways:

1. If your library is a CALIS member libraries, please log on <http://etd.calis.edu.cn/> and submit requests online, or consult the interlibrary loan department in your library.
2. For users of non-CALIS member libraries, please mail to [etd@xmu.edu.cn](mailto:etd@xmu.edu.cn) for delivery details.

厦门大学博硕士论文摘要库