MINISTRY OF EDUCATION AND TRAINING
CAN THO UNIVERSITY

SOCIALIST REPUBLIC OF VIETNAM
Independence - Freedom - Happiness

SUBJECT OUTLINE DETAILS

1. Subject: Proteomics
- **Code:** BT306C
- **Credits: 3**
- **Hours:** 45 theory and exercise hours.

2. Management Unit:
- Department of Molecular Biotechnology
- Biotechnology Research and Development Institute

3. Prerequisites: Biochemistry I & II (BC461C & BC462C)

4. Subject objectives:
The purpose of this subject is to provide students: (1) basic information about proteomics, (2) studying in gene expression, (3) application of genomics in plant breeding.

4.1. Knowledge:
Students will develop knowledge and understanding of:
4.1.1. The organiztion of proteomics;
4.1.2. The principles of proteomics in discovering gene;
4.1.3. The application of proteomics in plant breeding.

4.2. Skills:
4.2.1. Ability to understand proteomics analysis of species.
4.2.2. Apply investigative and problem-solving skills.
4.2.3. Knowing how to analyze proteomics and explain the results after analysis.

4.3. Attitude:
4.3.1. Students are encouraged to develop positive values and informed critical attitudes.
4.3.2. Being hard-working student.
4.3.3. Honesty in presenting analysis results.

5. Brief description of subject content:
Proteomics describes the determination of the amino acid sequence as well as many further analysis used to discover functional and structural protein. The subject focus on protein structure, protein function, gene expression, how to find proteomic database on the web, and some applied of proteomics such as gene expression and micro array.

6. Subject content structure:

	Content	Hours	Objectives
Chapter 1.	**Introduction to Proteomics**	3	4.1.1, 4.2, 4.3.
1.1.	What is Proteomics?		
1.2.	Kinds of Proteomics: Expressional, Structural and		
1.3.	Functional		

1.4.	Bioinformatics and Proteomics Summary		
Chapter 2.	**High Througput Methods in Proteomics**	5	4.1.1,
2.1.	Proteomics in diverse technologies		4.1.2,
2.2.	Proteomics tools (Molecular Biology Tools): SAGE, DNA Microarray (or DNA chips), Yeast two-hybrid analysis, Immuno-precipitation/pull-down, GFP Tagging & Microscopy		4.2, 4.3.
2.3.	Proteomics Tools: Separate and Display Tools, SDS-PAGEs, Isoelectric Focus (IEF), 2D-Gel principles, Protein Array, Protein chips		
2.4.	Protein Identification tools: Microsequencing, Protein ID by MS and 2D-gel		
2.5.	Protein structure tools: X-ray Crystallography, NMR Spectroscopy, Protein expression,		
Chapter 3.	**2D Gel Analysis**	4	4.1.1,
3.1.	What is 2D gel?		4.1.2, 4.2,
3.2.	Steps in 2D GE		4.3.
3.3.	2D Gel Freeware		
3.4.	Competing Technologies		
3.5.	Westing Blotting		
3.6.	Conclusions		
Chapter 4.	**Mass Spectrometry: Methods and Theory**	5	, 4.1.1,
4.1.	MS Principles		4.1.2, 4.1.3
4.2.	MS history		4.2, 4.3.
4.3.	Typical Mass Spectrometer		
4.4.	Mass Spectrometer Schematic: Ion source, Mass Filter, Detector		
4.5.	Proteomics Application		
4.6.	Conclusion		
Chapter 5.	**Mass Spectrometric Peptide Identification Using**	4	4.1.1,
5.1.	**MASCOT** Why is MASCOT? 5.1.1 MASCOT databases		4.1.2,4.1.3 4.2, 4.3.
5.2.	5.1.2 MASCOT Scoring		
5.3.	MOWSE (Molecular Weight Search)		
5.4.	MS-MS Sequencing Conclusions		
Chapter 6.	**Protein and Proteome Annotation**	5	4.1.1,
6.1.	What is Protein annotation?		4.1.2, 4.1.3
6.2.	Protein versus Proteome Annotation		4.2, 4.3.
6.3.	Annotation Methods		
6.4.	Common Softwares		
6.5.	Proteome Analyst		
6.6.	Proteome Statistics		
6.7.	Conclusions		

Chapter 7.	**Protein Expression, Structural Proteomics & Bioinformatics**	5	4.1, 4.2, 4.3.
7.1.	Expression questions		
7.2.	Host Cell system?		
7.3.	Codon Bias		
7.4.	Expression/Cloning which protocols?		
7.5.	Single Domain or Multi-Domain?		
7.6.	Domain Prediction		
7.7.	Structural Proteomics and Solubility Prediction		
7.8.	How to purify & how to identify?		
Chapter 8.	**Protein Subcellular Localization**	4	4.1.1, 4.1.2, 4.1.3, 4.2, 4.3.
8.1.	Why is Localization Important?		
8.2.	Prokaryotic versus Eukaryotic cells		
8.3.	Level of annotation		
8.4.	Localization signaling		
8.5.	Subcellular Fractionation		
8.6.	Computational methods for predicting localization		
8.7.	The PSORT Family		
8.8.	Conclusions		
Chapter 9.	**Protein Interactions**	5	4.1.1, 4.1.2, 4.1.3,4.2, 4.3.
9.1.	Protein interactions		
9.1.1.	Discovery		
9.1.2.	Storage		
9.1.3.	Data Mining		
9.2.	Protein Interactions Lab		
9.2.1.	Predicting Protein Interactions		
9.2.2.	Data Mining		
9.3.	Genetic Interactions		
9.4.	Conclusions		
Chapter 10.	**Protein Pathways and Pathway Databases**	5	4.1.1, 4.1.2, 4.1.3,4.2, 4.3.
	Interactions → Networks → Pathways		
10.1.	Pathways and Biological pathways		
10.2.	What the pathway represents?		
10.3.	Co-expression within pathways		
10.4.	BioCyc: Pathway Tools		
10.5.	Completeness of Pathways		
10.6.	Issues with predicting pathways		
10.7.	Conclusions		
10.8.			

7. Teaching method:

- Teaching theories in class
- Group and individual home assignments
- Discussion in class
- Tests/ quizzes
- Final examination

8. Duties of student:

Students have to do the following duties:
- Attending at least 80 % hours of the course
- Participating in group and individual assignments
- Taking the midterm examination
- Proactively implementing self-study
- Taking the final examination

9. Assessment of student learning outcomes:

9.1. Assessment

No.	Point components	Rules and Requirement	Weights	Objectives
1	Overall attendance	- Attend at least 80 % hours of the total hours in the classes	Requirement	4.3.2, 4.3.3
2	Midterm exam	Taking the tests	40%	4.1
3	Final examination	- Taking the final examination	60%	4.1

9.2. Grading

- Grading components and final test scores will be marked on a scale of 10 (0 to 10), rounded to one decimal place.
- Subject score is the sum of all the components of the evaluation multiplied by the corresponding weight. The subject score is marked on a scale of 10 and rounded to one decimal place then is converted to A-B-C-D-F score and score on a scale of 4 under the academic provisions of Cantho University.

10. Materials:

Materials information	Code number
[1]. Proteomics Handout	File-BiRDI website
[2]. Zhu, H. *et al.* Proteomics. Annual Review of Biochemistry 72: 783-812.	Library of BiRDI
[3]. Griffiths *et al.* Modern Genetic Analysis. Online:	http://ncbi.nih.gov
[4]. Suhai, S., 2002. Genomics and Proteomics Functional and Computational Aspects. KLUWER ACADEMIC PUBLISHERS New York, Boston, Dordrecht, London, Moscow	http://www.kluweronline.com
[5]. Hubert Rehm. 2006. Protein Biochemistry and Proteomics. Elsevier Inc.	Library of biochemistry lab, Personal Bookshelf

11. Self-study Guide:

Week	Content	Theory (hours)	Practice (hours)	Students' duties
1	**Chapter 1. Introduction to Proteomics** 1.1 What is Proteomics? 1.2 Kinds of Proteomics: Expressional, Structural and Functional 1.3 Bioinformatics and	3	0	- Previous research and reference: +References/materials: Chapter 1, [1], [2], [5] - Review the contents of the modules studied in class

	Proteomics 1.4 Summary			
2	**Chapter 2. High Througput Methods in Proteomics** 2.1 Proteomics in diverse technologies 2.2 Proteomics tools (Molecular Biology Tools): SAGE, DNA Microarray (or DNA chips), Yeast two-hybrid analysis, Immuno-precipitation/pull-down, GFP Tagging & Microscopy 2.3 Proteomics Tools: Separate and Display Tools, SDS-PAGEs, Isoelectric Focus (IEF), 2D-Gel principles, Protein Array, Protein chips	3	0	Previous research and reference: +References/materials: Chapter 2, [1], [2], [5] - Review the contents of the modules studied in class
3	2.4 Protein Identification tools: Microsequencing, Protein ID by MS and 2D-gel 2.5 Protein structure tools: X-ray Crystallography, NMR Spectroscopy, Protein expression. **Chapter 3. 2D Gel Analysis** 3.1 What is 2D gel? 3.2 Steps in 2D GE	3	0	Previous research and reference: +References/materials: Chapter 2, chapter 3 [1], [2], [5] - Review the contents of the modules studied in class - Make homework assignments
4	3.3 2D Gel Freeware 3.4 Competing Technologies 3.5 Westing Blotting 3.6 Conclusions	3	0	Previous research and reference: +References/materials: Chapter 3, [1], [2], [5] - Review the contents of the modules studied in class
5	**Chapter 4. Mass Spectrometry: Methods and Theory** 4.1 MS Principles 4.2 MS history 4.3 Typical Mass Spectrometer 4.4 Mass Spectrometer Schematic: Ion source, Mass Filter, Detector	3	0	Previous research and reference: +References/materials: Chapter 4, [1], [2], [5], [4] - Review the contents of the modules studied in class - Make homework assignments
6	4.5 Proteomics Application 4.6 Conclusion **Chapter 5. Mass Spectrometric Peptide Identification Using MASCOT**	3	0	Previous research and reference: +References/materials: Chapter 4, chapter 5, [1], [2], [5], [4]

	5.1What is MASCOT? 5.1.1 MASCOT databases			- Review the contents of the modules studied in class
7	5.1.2 MASCOT Scoring 5.2 MOWSE (Molecular Weight Search) 5.3 MS-MS Sequencing 5.4 Conclusions	3	0	Previous research and reference: +References/materials: Chapter 5, [1], [2], [5] - Review the contents of the modules studied in class - Group exercise, discussion
8	**Chapter 6. Protein and Proteome Annotation** 6.1 What is Protein annotation? 6.2 Protein versus Proteome Annotation 6.3 Annotation Methods 6.4 Common Softwares	3	0	Previous research and reference: +References/materials: Chapter 6, [1], [2], [5], [4] - Review the contents of the modules studied in class - Midterm examination
9	6.5 Proteome Analyst 6.6 Proteome Statistics 6.7 Conclusions **Chapter 7. Protein Expression, Structural Proteomics & Bioinformatics** 7.1. Expression questions 7.2. Host Cell system?	3	0	Previous research and reference: +References/materials: Chapter 6, Chapter 7, [1], [2], [5] - Review the contents of the modules studied in class
10	7.3. Codon Bias 7.4. Expression/Cloning which protocols? 7.5. Single Domain or Multi-Domain? 7.6. Domain Prediction	3	0	+References/materials: Chapter 3, Chapter 7, [1], [2], [5] - Review the contents of the modules studied in class - Group exercise, discussion
11	7.7. Structural Proteomics and Solubility Prediction 7.8. How to purify & how to identify? **Chapter 8. Protein Subcellular Localization** 8.1 Why is Localization Important? 8.2 Prokaryotic versus Eukaryotic cells 8.3 Level of annotation 8.4 Localization signaling	3	0	Previous research and reference: +References/materials: Chapter 7, chapter 8, [1], [2], [5] - Review the contents of the modules studied in class - Tests/ quizzes
12	8.5 Subcellular Fractionation 8.6 Computational methods for predicting localization 8.7 The PSORT Family 8.8 Conclusions	3	0	Previous research and reference: +References/materials: Chapter 8, chapter 9, [1], [2], [3], [4], [5]

	Chapter 9. Protein Interactions 9.1 Protein interactions 9.1.1 Discovery 9.1.2 Storage 9.1.3 Data Mining			- Review the contents of the modules studied in class
13	9.2 Protein Interactions Lab 9.2.1 Predicting Protein Interactions 9.2.2 Data Mining 9.3 Genetic Interactions 9.4 Conclusions	3	0	Previous research and reference: +References/materials: Chapter 9, [1], [2], [3], [4], [5] - Review the contents of the modules studied in class - Group exercise, discussion
14	**Chapter 10. Protein Pathways and Pathway Databases** 10.1 Interactions → Networks → Pathways 10.2 Pathways and Biological pathways 10.3 What the pathway represents?	3	0	Previous research and reference: +References/materials: Chapter 10, [1], [2], [3], [4], [5] - Review the contents of the modules studied in class - Tests/ quizzes
15	10.4 Co-expression within pathways 10.5 BioCyc: Pathway Tools 10.6 Completeness of Pathways 10.7 Issues with predicting pathways 10.8 Conclusions	3	0	Previous research and reference: +References/materials: Chapter 10, [1], [2], [3], [4], [4] - Submitted exercise group - Review the entire, final exam preparation

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ON BEHALF OF RECTOR
DEAN/ DIRECTOR

HEAD OF DEPARTMENT