Faculty of Computers & Information, Assiut University
4th Level
Final Exam
Duration: 2 hours

1

الإسم الرباعي (بالعربي فقط) *

عائشة محمدصفوت عبدالرحمن محمد

2

رقم الجلوس *

1620175047

3

المستوي *

○ الاول

○ الثاني

○ الثالث

○ رابعة 2013

○ رابعة 2014

○ رابعة 2015

○ رابعة 2016

◉ رابعة 2017

4

البرنامج *

○ عام

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○ هندسة

5

رقم المعمل *

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6

رقم الكمبيوتر *

19

7

الكود (قد تمت مراجعة بيانات الطالب ورقم الجلوس) *

koOY

8

The problem of protein structure prediction is how to determine the location of each atom in the protein structure.
(3 Points)

◉ True

○ False

9

Protein structures can be divided into three groups: globular proteins, fibrous proteins, and
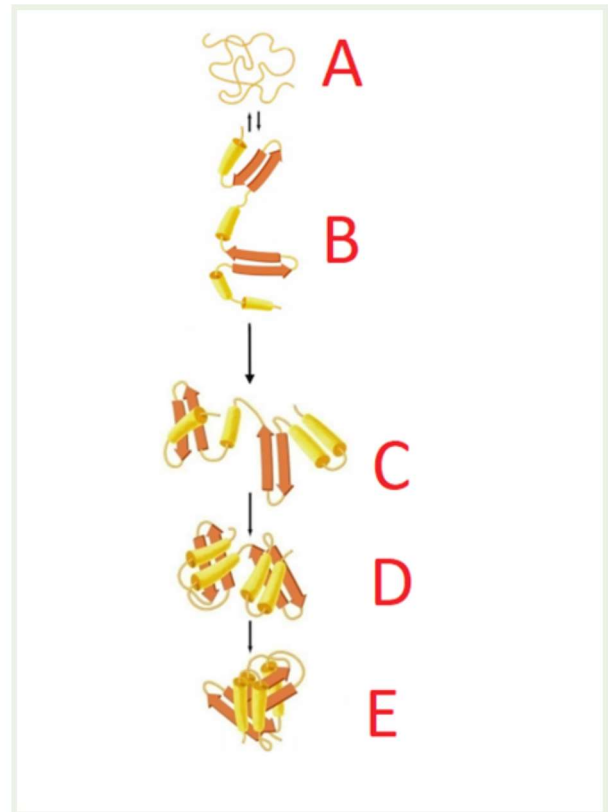integral membrane proteins.
(3 Points)

◉ True

○ False

10

What is C?
(3 Points)

○ Native Structure

◉ Super secondary structure

○ Primary structure

○ Domains and the complete folded chain

○ Secondary structure

11

The protein structure may contain only one domain.
(3 Points)

○ True

◉ False

12

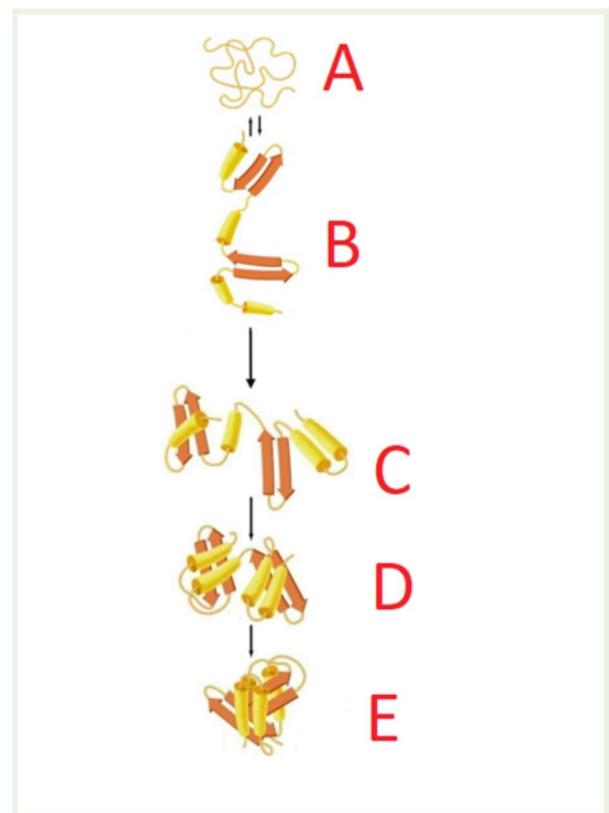All protein amino acids are folded into the 3D structure.
(3 Points)

○ True

◉ False

13

The best protein structure is that can MAXIMIZE the energy function,
(3 Points)

○ True

◉ False

14

What is D?
(3 Points)

◯ Native Structure

◯ Super secondary structure

◯ Primary structure

⦿ Domains and the complete folded chain

◯ Secondary structure

15

We do NOT need protein structure to predict protein functions from sequences
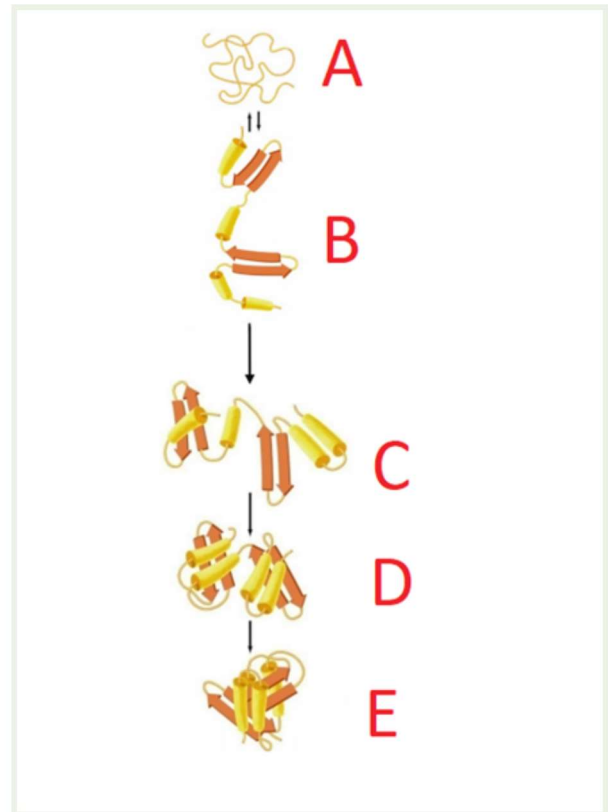(3 Points)

◯ True

⦿ False

16

A* search method is used to search for the native structure in the Rosetta
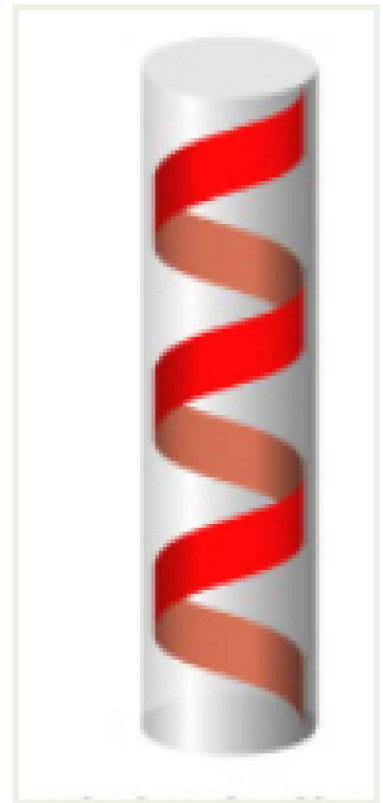package.
(3 Points)

◯ True

⦿ False

17

What is B?
(3 Points)

○ Native Structure

○ Super secondary structure

○ Primary structure

○ Domains and the complete folded chain

◉ Secondary structure

18

The next protein structure is the tertiary structure.
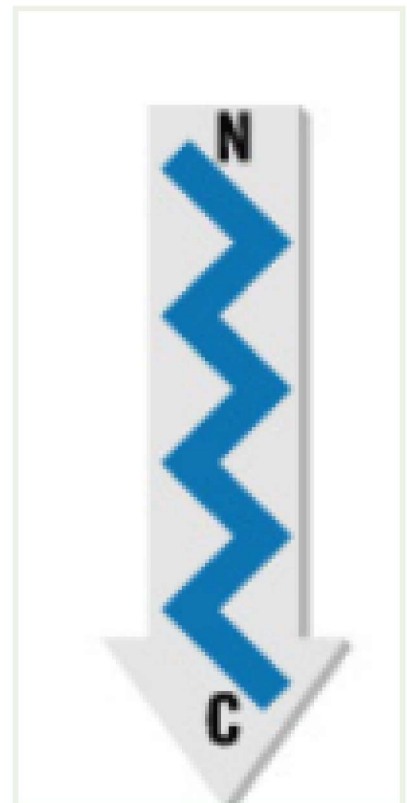(3 Points)

○ True

● False

19

The next protein structure is the tertiary structure.
(3 Points)

◯ True

⦿ False

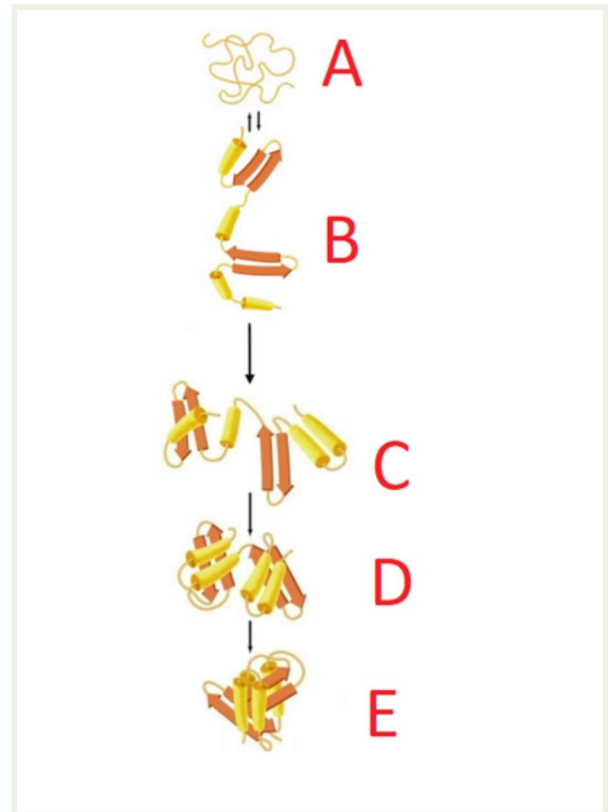20

The next protein structure is called beta-strands.
(3 Points)

⦿ True

◯ False

21

What is E?
(3 Points)

A

B

C

D

E

⦿ Native Structure

◯ Super secondary structure

◯ Primary structure

◯ Domains and the complete folded chain

◯ Secondary structure

22

SCOP database contains the class architecture topology homologous superfamily.
(2 Points)

◯ True

⦿ False

23

The super-secondary structure: arrangement of elements of same secondary structure into motifs.
(3 Points)

○ True

○ False

24

The Φ angle is the angle between C_alpha and C atoms
(3 Points)

○ True

○ False

25

The energy function for protein structure is divided into two parts: bonded and non-bonded interactions.
(3 Points)

○ True

○ False

26

The Ψ angle is the angle between C_alpha and N atoms.
(3 Points)

○ True

◉ False

27

All needed information for protein folding is encoded into protein sequence.
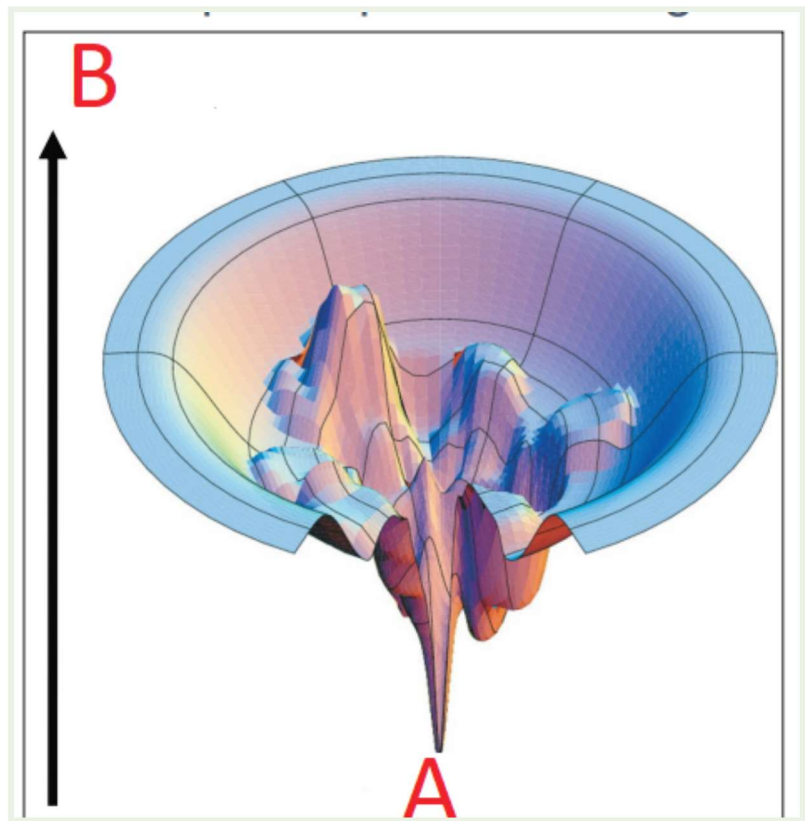(3 Points)

◉ True

○ False

28

We can draw The Ramachandran plot for each amino acid from the PDB
database.
(3 Points)

◉ True

○ False

29

The A in the next figure is the native structure.
(3 Points)

- ◉ True
- ○ False

30

the motif is usually not stable by itself.
(3 Points)

- ◉ True
- ○ False

31

There are about 1,000,000 proteins in nature.
(3 Points)

- ○ True

○ False

32

pyROSETTA is a useful package that deals with protein structure files.
(3 Points)

⦿ True

○ False

33

The current protein structure prediction methods use deep learning methods.
(3 Points)

⦿ True

○ False

34

 About 70% of therapeutics are directed towards membrane proteins.
(2 Points)

⦿ True

○ False

35

The domain structure is a stable structure.
(3 Points)

○ True

○ False

36

The protein secondary structure contains two types of beta-strands.
(3 Points)

◉ True

○ False

37

The Levinthal paradox explains the computational difficulty of the protein folding problem.
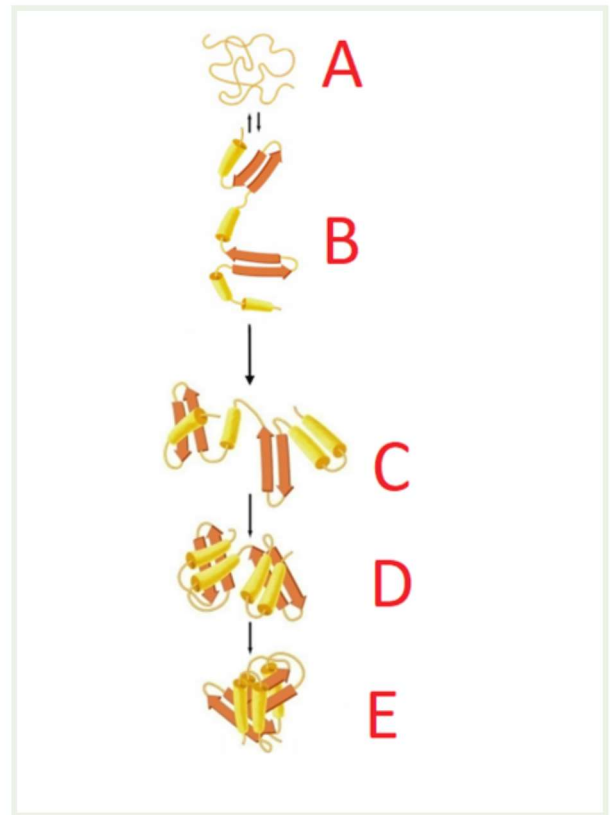(3 Points)

○ True

◉ False

38

pyRosetta has a lot of functions that calculate the energy function for protein structures.
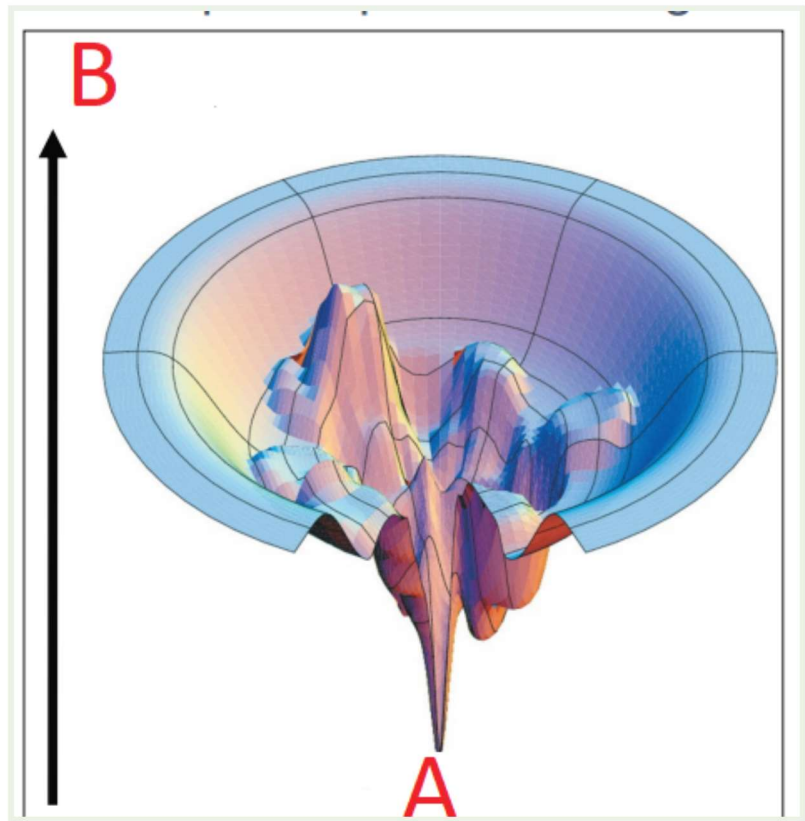(3 Points)

○ True

◉ False

What is A?
(3 Points)

○ Native Structure

○ Super secondary structure

◉ Primary structure

○ Domains and the complete folded chain

○ Secondary structure

The carbon atom in an amino acid is bounded by the oxygen atom.
(3 Points)

○ True

◉ False

The B in the next figure is the time.
(3 Points)

○ True

● False