MCQS FILE OF BIF 101

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12.5%

79)Humans have over…… genes.

25000

80)These genes may produce……..different proteins.

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81)We need help of….. to store and recall data.

Computers

82)Computers can …… process this information.

Quickly

83)If you carefully search this online data with a bit of biology it is…..

Gold mine

84)Biology easily has……exciting years problems.

500

85)Life, disease and……. Are better understood.

Evolution

86) ……. can be better developed after understanding molecular basis of life.

Drugs

87) …… and systems biology are other research areas in bioinformatics.

Protein structure, protein-protein interaction

88)Bioinformatics has enabled us to generate….data and its utilization.

Omic

89)Bioinformatics is relatively …… scientific area.

Young

90) Identification of hitherto unknown types as well as ……

Roles of RNA

91)Bioinformatics is full of……and…..

Challenges, opportunities

92)Accurate solution of protein structure is one of the……. Problem.

Toughest

93)Some medicines have……on patients.

Side effects

94)….. is the century of bioinformatics.

21

95)An era of personalized medicines and ….. of several common diseas.

Eradication

96)Genetic information flow from ….to…..

DNA, RNA

97)All living cells …. their DNA when they divide.

Replicate

98)During cell division each daughter cell…. A copy of genome from the aren't cell.

Receive

99)…….. is the process by which two identical copies of DNA are made from an original molecule.

Replication

100)Replication occurs in the cells …… to cell division.

Prior

101)Important is that information does not …. From protein to DNA or RNA.

Flow

102)Flow of information from RNA …… DNA.

Backwards

103)By the end of …. Hypothesis was adopted chromosomal DNA function as a template.

1953

104)RNA molecules are move in ….

Cytoplasm

105)In ….. referred the information of central dogma.

1953

106)Central dogma referred by ……

Francis Crick

107)RNA chains are acts as a template for the synthesis of ……

DNA

108)Central dogma are original proclaimed …. Ears.

50

109)Transformation of information in DNA in those molecules is termed….

Central dogma

110)Central dogma is…

DNA>RNA>Proteins

111)Proteins are used in constructing on ….

Cells

112)DNA and RNA molecules are built up from …. Types of molecules.

Four

113)These four types of molecules are called ….

Nucleotides

114)Nucleotides are….

Adenine, Cytosine, uracil and guanine

115)DNA has ….

A, T ,C, G

116) RNA has …

A, U, G, C

117)DNA is ….. stranded.

Double

118)RNA is …. Stranded.

Single

119)RNA helps to produce….

Proteins

120)….. mRNA nucleotides forms a codon.

Three

121)tRNA has …. Nucleotides.

75-80

122)Conformation of tRNA allows it to bind …

Ribosomes

123)…. Are built up of proteins and carbohydrate.

Cells

124)Molecules are produced after …. Of DNA into proteins.

Transformation

125)Adenosine pairs with …

Thymine

126)Cytidine pairs with …

Guanosine

127)Process of ….. decodes these bases in DNA.

Transcription

128)In RNA Uracil only pairs with …..

Adenosine

129)DNA gives rise to ….

RNA

130)There are …. Types of ribonucleotides.

Four

131)Ribonucleotides are depending on the types of ….. bases.

Nitrogenous

132)There are …. Types of ribonucleic acid.

Three

133)Three ribonucleic acids are….

mRNA, tRNA, rRNA

134)mRNA is the types of RNA that carries information from…. To…

DNA to proteins

135)Process of forming mRNA is called….

Transcription

136)mRNA maybe ….

Monocistronic

137)Length of mRNA is depend on ….

Length of gene

138) …… serve as adapter molecules in the process of protein synthesis.

tRNA

139)They are …. Linked to an amino acid at one end.

Covalently

140)…. Are components of ribosomes.

rRNA

141)rRNA is the …. material.

Predominant

142)rRNA constitutes about …. Of ribosomes.

60%

143)rRNA has number of …..

Functions

144)mRNA is … stranded when it is formed from DNA.

Single

145)Conformation is mainly achieved by …….. interactions.

Base stacking

146)Protein coding region of mRNA is composed of non-overlapping string of codon called….

ORF

147)Translation starts at 5’ and ends at …..

3’

148)First and last codon of an ORF are called….

Start and stop codon

149)In bacteria start codon is usually ……. Are also used.

5’- AUG-3’, but 5’-GUG3’ and sometimes even 5’-UUG-3’

150)Eukaryotic cells always use … as start codon.

5’-AUG-3’

151)Start codon has … functions.

Two

152)Eukaryotic mRNA almost always contain a …. ORF.

Single

153)Prokaryotic cells have mRNA always contain a …….ORF.

Two or more

154) mRNAs containing multiple ORFs are known as ……RNAs.

Polycistronic

155) Those encoding a single ORF are known as …….RNAs.

Monocistronic

156) To facilitate binding by a ribosome, many prokaryotic ORFs contain a short sequence upstream (on the 5’ side) of the start codon called …..

RBS

157)The RBS typically located …. Bp.

3-9

158) This phenomenon of linked translation between overlapping ORFs is known as ……

Coupling translation

159)Heart of protein synthesis is…

Translation

160)tRNA molecules are between … and … nucleotides.

75,95

161)Dihydrouridine derived from …

Uridine

162)Hypoxanthine plays a role in the process of ….

Codon

163) tRNA molecules to which an amino acid is attached are said to be ……..

Charged

164) tRNAs that lack an amino acid are said to be …..

Un-charged

165)Acyl linkage is …… bond.

High energy

166)Hydrolysis results in a …. change in free energy.

Large

167)Hydrolysis results in a large … in free energy.

Change

168)All aminoacyl-tRNA synthetases attach an amino acid to a tRNA in ….. steps.

Two

169)Two enzymatic steps are …..

Adenylation , tRNA charging

170)Each of the … amino acids is attached to the appropriate tRNA.

20

171)Most amino acid are specified by ……. Codon.

More than one

172)…. Is the macromolecular machine that directs the synthesis of proteins.

Ribosomes

173)Ribosome is larger and more …. Than the minimal machinery.

Complex

174)Polymerizing amino acid is composed of at-least ….

Three

175)And more than ….. different proteins.

50

176)Translation takes place at a rate of …….. amino acid per second.

Only two to 20

177)In prokaryotes transcription and translational machinery are located in …. Compartment.

Same

178)Ribosomes catalyzes a …. Chemical reaction.

Single

179)Ribosomes is composed of …. Subassemblies.

Two

180)Subassemblies of RNA are known as …….

Large and small units

181)Large subunit contain …..

Peptide transferase center

182)Peptidyl responsible for the …. Of peptide bonds.

Formation

183)Small units contain …

Decoding center

184)Both small and large units are buried with in the intact…..

Ribosomes

185)A-site is the binding site for ……

Aminoacylated-tRNA

186)P-site is the binding site for …..

peptidyl tRNA

187)Stop codons are recognized by proteins called..

Release factors

189)…… involves coding of proteins by RNA at ribosomes.

Translation

190)Sequence of amino acid are linked by ….

Peptide bond

191)Proteins are polymers of….

Amino- acids

192)Proteins are range in size from small to …..

Large

193)Twenty different proteins are called ….. proteins.

Standard

194)Each type of protein has a … amino acid sequence.

Unique

195) Linus Pauling and Robert Corey carefully analyzed the….

Peptide bond

196)Six atoms of peptide group are ….

Planar

197) In principle, ϕ and ψ can have any value between….

+180, -180

198)Secondary structure of protein refers to ….

Local conformation

199)Backbone of polypeptide chain extend into …. Structure.

Zig- zag

200)Three dimensional arrangements of atoms of proteins are ….

Tertiary structures

201) A multi-subunit protein is also referred to as a….

Multimer

202) A multimer with just a few subunits is called……

Oligomer

203)A single subunit is called…

Protomer

204)Oligomers can have either ….. symmetry.

Rotational, Helical

205) The process of inexact matching while keeping in view the conserved residues is called sequence……

Alignment

206)Pairwise sequence alignment helps to compare …. Sequence.

Two

207)Gaps are … counted.

Not

208)Multiple sequence alignment involves comparison of … or more sequences.

Three

209)Pairwise alignment either local or …

Global

210)MSA can help align …. Sequences.

Multiple

211)Progressive alignment can help perform …

MSA

212) CLUSTAL ia an …

Online tool

213)Pariwise alignment is the alignment of …. Sequences.

Two

214)CLUSTAL is an online tool to perform …

MSA

215)BLAST can be developed in …

1990

216)BLAST is an basic ….

Local alignment tool

217)…. Main types of BLAST .

Two

218)Two main types of BLAST are ….

Proteins, nucleotides

219)Smith waterman can perform …

Local

220)Needleman waterman calculates…

Global

221)FASTA developed in ….

1998

221)First Genebank in ….

1982

222)Genebank is now under

NCBI

223)EMBL developed in …

1980

224)DDBJ eastablised in ….

1984

225)First protein sequenced was collected in…

1951

226) Protein sequence collected by….

Sanger and Tupy method

227)Atlas of protein sequenced by …. In….

Margrett and DAYhoff in 1960

228)Swiss prot is collaboration between ….and …

EBI, SIB

229)GEO is a ….

Public repository

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Health informatics

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80)These genes may produce……..different proteins.

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Modeller is a for.....homology modelling

software

How many steps are included in homology modelling.

Seven

what is the first step of homology modelling

Template recognition and initial alignment

what is the second step of homology modelling

Alignment correction

what is the third step of homology modelling

Backbone generation

what is the fourth step of homology modelling

Loop modeling

what is the fifth step of homology modelling

Side-chain modeling

what is the sixth step of homology modelling

Model optimization

what is the seventh step of homology modelling

Model validation

What are inputs of homology modelling

Python script file,

Sequence alignment & Template (PDB)

How Homology modelling helps predict protein structures?

By using prior structural information

Homology modelling can be done in

programmatic or automated way!

A protein fold is a

secondary structure elements

How protein fold are arranged

relative to each other in space.

What include in common fold?

4-helix bundle and the TIM barrel.

How many stable folds in nature?

5,000

What should kept in mind during fold recognition?

Finding the best fit of a sequence to a set of candidate folds

Fold recognition is also known as

Threading

Fold recognition is a technique

For predicting protein structure

Fold recognition is done when

Homology modelling fail

• In the process of "Threading", we mount an..... sequence on to the backbone of template structures in a folds library

Amino acid

The best match in Threading is computed using a

scoring function

Scoring typically involves using a Z-Score function based on

energy of a molecule

An estimate of accuracy of the predictions in Threading is based on the

confidence score of the modeling

iTASSER helps

predict function of structures output.

threading is useful For the..... with low alignment quality and identity,

"Twilight Zone"

..... cannot be predicted using threading

Novel proteins

3D-1D Bowie Algorithm is proposed by

Bowie et al in 1991

3D-1D Bowie Converts 3D structure into a

1-D string profile

Part of secondary structure including
Alpha helix, and beta-sheet

Pa: j=

prob. of finding amino acid (a) in environment (j)

Pa=

probability of finding (a) anywhere

3D-1D methods convert structure and environment information into

“profiles”

Ab initio methods have **Anfinsen’s thermodynamic hypothesis** at the

center

The ab initio modelling is

Not very accurate

Limitation and defective of ab initio modelling is

• Computationally expensive

• Suitable for protein with less than 100 residues

Energy released during the folding process is
computed for predicting structure

Stabilization is measured by

energy released during the folding process