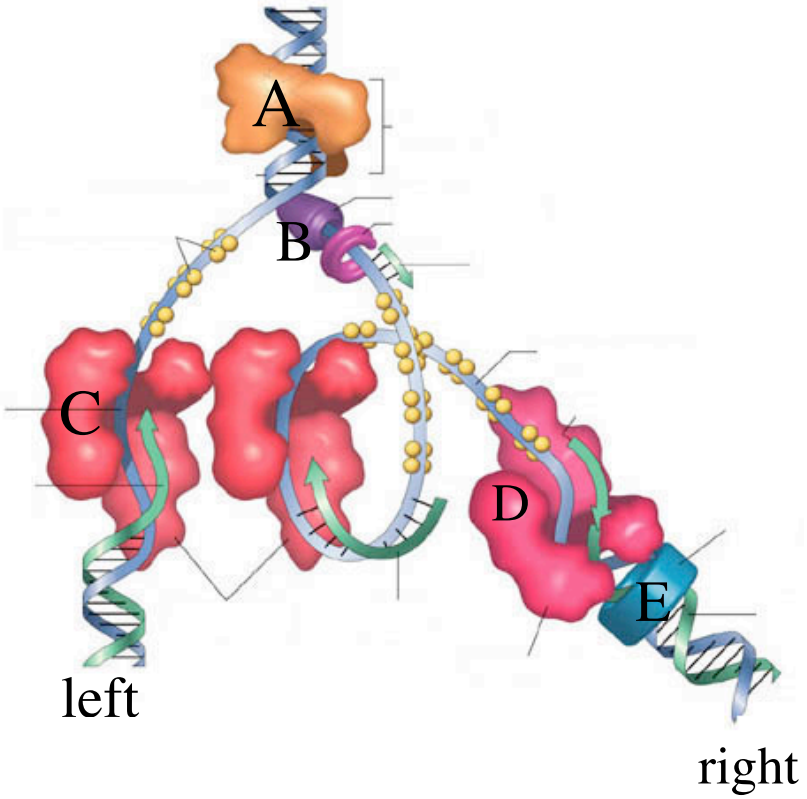

For the following statements about DNA replication & referring to the above picture (if necessary)
Mark A for True and B for False.

1. Left strand, lagging strand synthesis, reading the template 3' to 5'
2. Right strand, leading strand sysnthesis, reading the template 3' to 5'
3. Okazaki fragments on the right
4. The beta clamp is involved in DNA synthesis on both the left and right
5. supercoiling the DNA duplex occurs near E
6. Single strand binding proteins promote duplex (double stranded) DNA

Identify the following 3 to the letters in the above picture of Replication

7. Helicase
8. Gyrase
9. Ligase
10. Polymerase I
11. Polymerase III

Match the following to the next 4 questions
A. Mismatch B. Direct Repair C. Primer Excision D. Base excision E. Nucleotide Excision

12. Repair that involves DNA Polymerase III
13. Repair that involves only the Klenow Fragment's activities
14. Type of repair that fixes pyrimidine dimers using a photolyase
15. Repair that involves all the activities of DNA Polymerase I

 print name:_____

16. Can DNA Polymerase I fragment remove the RNA primer from Okazaki fragments?
    A. Yes, it has the ability to ligate the DNA nicks together
    B. No, because it is not a very processive enzyme
    C. No, because it lacks the 5'-> 3' exonuclease
    D. No, because it lacks the 3'-> 5' exonuclease
    E. The RNA primer does not need to be removed

17. What are the common functions of DNA polymerase III and Klenow fragment?
    A. 3' to 5' polymerase & 3' to 5' exonuclease
    B. 5' to 3' polymerase & 5' to 3' exonuclease
    C. 5' to 3' polymerase & 3' to 5' exonuclease
    D. 5' to 3' polymerase, 3' to 5' exonuclease, & 5' to 3' exonuclease
    E. 5' to 3' polymerase & 3' to 5' endonuclease

18. What is the role TATA or Pribnow box in the initiation of transcription in prokaryotes?
    A. It binds of the sigma subunit which can then recruit RNA polymerase
    B. It forces the sigma subunit from the RNA polymerase holoenzyme to initiate transcription
    C. It marks the place where the mRNA transcript is begun
    D. It is the area where a helicase unwinds the DNA
    E. It is recognized by the sigma subunit of the RNA polymerase holoenzyme

19. Which of the following is a false statement about initiation of prokaryotic transciption:
    A. The first DNA base that is transcribed is usually a purine on the template strand
    B. Formation of the open promoter complex involves the sigma subunit and tighter binding of the complex to DNA
    C. It ends when the sigma subunit is released after about 8 nucleotides are added
    D. The first RNA base added is usually an adenosine triphosphate or guanosine triphosphate, which retains its triposphate
    E. Initiation does not require a primer.

20. Which of the following is a false statement about elongation in prokaryotic transciption:
    A. The core RNA polymerase synthesizes the mRNA transcript by pairing complementary NTPs to the DNA template strand
    B. Polymerization of RNA is similar to polymerization of DNA. Both involve the addition of a nucleoside triphosphate to a free 3' hydroxyl
    C. Unwinding of the DNA occurs in front of the transcription bubble and rewinding of the DNA occurs after it.
    D. RNA & DNA polyemerases both contain a 3'->5' proofreading exonuclease
    E. The error rate of RNA polymerase during transcription is greater than DNA polymerase

21. Termination of prokaryotic transcription …
    A. occurs through either a stem loop pausing or a helicase separating strands.
    B. occurs once the RNA polymerase reaches a nonsense codon.
    C. Involves the binding of snRNPs to guide the removal of the RNA:DNA hybrid
    D. involves interactions with concurrent translational machinery.
    E. Occurs after the last intron has been transcribed

 print name:_____

22. Which of the following is true about post-transcriptional RNA modifications in prokaryotes
    A. The 5' end of the transcript is capped and the 3' end is polyadenylated.
    B. Introns are spliced out of the transcript to form the mature mRNA.
    C. They do not occur, since translation and trascription are coupled
    D. Splicing of the transcript can be ATP dependent or independent
    E. The operon is usually cut into separate different transcripts to allow concurrent translation

23. Leucine zipper, zinc fingers, and helix turn helix are
    A. protein dimerization motifs to work as protein activators and repressors
    B. motifs that bind DNA through hydrogen bonding only in the major groove.
    C. DNA binding motifs hydrogen bond with the sugar backbone using Mg^{2+}
    D. motifs that bind DNA through hydrogen bonding only in the minor groove.
    E. chaperones for RNA folding into the ribosome.

24. What are the forces that stabilize the DNA double helix.
    A. None of the below
    B. All of the below
    C. Base pairing
    D. Hydrophobic interactions
    E. Ionic interactions

25. What are the main reasons for the high fidelity of DNA Polymerase III?
    A. 3'-5' exonuclease, β-clamp, and helicase
    B. 5'-3' exonuclease, topoisomerase, and base-pairing
    C. balanced dNTP's, base-pairing (hydrogen bonding/shape), and 3'-5' exonuclease
    D. balanced NTP's, base-pairing (ionic interactions), and 3'-5' exonuclease
    E. SSB, Pol I, and ligase

26. Charging of tRNA with an amino acid
    A. in both Type I and II amino-acyl synthetases places the amino acid at the 3' hydroxyl
    B. involves the hydrolysis of ATP to ADP + Pi
    C. initially attaches the amino acid to AMP through the 5' phosphate
    D. always involves the recognition of the tRNA anti-codon to specificy the correct amino acid
    E. takes into account the wobble found at the first residue in the anti-codon

27. Amino acids which are most susceptible to wobble: point mutations at the 3rd position of the codon.
    A. M & W
    B. G, P, & A
    C. W, Y, & F
    D. Hydrophobics
    E. G & C

28. Amino acids which are least susceptible to wobble: point mutations at the 3rd position of the codon.
    A. G, P, & A
    B. W, Y, & F
    C. R, L, & S
    D. charged amino acids

 print name:_____

E. A & T

29. Which of the following is true about the initial of prokaryotic translation.
    A. The large as well as the small subunit or the ribosome are involved throughout the initiation process
    B. IF-3 is responsible for delivering the initiator tRNA to the P site
    C. IF-1 blocks the A site from binding any other tRNA's
    D. ATP is required to place the initial tRNA as well as kick off the initiation factors from the ribosome
    E. Does not require a special formylated methionine as the initiator residue

30. Which of the following is not true about elongation in prokaryotic translation.
    A. EF-TU places the new incoming charged tRNA in the A site, requiring GTP hydrolysis
    B. The N-terminus remains covalently attached to tRNA
    C. The growing peptide in the P site is transferred onto the open N-terminus of new amino acid in the A site
    D. Movement of the growing peptide attached to the tRNA from the A site to P site rquires EF-G and GTP.
    E. The uncharged tRNA moves from the P site into the E site

31. During termination of translation in prokaryotes
    A. a helicase unwinds the mRNA from the growing peptide
    B. release factors recognize sense codons
    C. the ribosomes peptidyl transferase activity converts to hydrolyze the peptide from the tRNA in the P site
    D. GTP is required for the tRNA to move from the P to E sites
    E. recogniation of the stop codon causes a pause in translation which allows for small and large subunits of the ribosome to disassociate.

32. The primary energy source in prokaryotic translation is
    A. ATP
    B. dATP
    C. GTP
    D. dGTP
    E. requires no energy

33. If Pol I's 5'->3' exonuclease were deleted, the following would be effected:
    A. mismatch repair
    B. base excision repair
    C. both B & D
    D. lagging strand synthesis
    E. A, B, and D

34. Reverse transcriptase has the following activities used in the following order.
    A. RNA directed DNA polymerase, RNAse H, DNA directed DNA polymerase
    B. Primase, RNA directed DNA polymerase, RNAse H, DNA directed DNA polymerase,
    C. RNA directed RNA polymerase, RNAse H, RNA directed DNA polymerase,

 print name:_____

D. RNA directed DNA polymerase, RNAse H, DNA directed DNA polymerase, Ligase
E. 5'->3' exonuclease and 5'->3' DNA polymerase

35. Which of the following statement(s) about topoisomerase I is/are true?
A. Uses ATP
B. Changes linking number by 1
C. Changes linking number by 2
D. Both A & C
E. Splices introns

36. Which of the following statement(s) about topoisomerase II is/are true?
A. Uses ATP
B. Changes linking number by 1
C. Changes linking number by 2
D. Both A & C
E. Splices introns

37. Topoisomerases change the linking number by …
A. physically breaking the covalent DNA backbone
B. increasing the writhe by 3 and decreasing the twist by 3
C. adding a nucleotide to the chain
D. modifying the base
E. None of the above

38. Initiation of transcription in prokaryotes (E. coli specifically) is defined by
A. sigma's involvement in the holoenzyme
B. the amount of single stranded DNA in the transcription bubble
C. the topoisomerase preceding the RNA polymerase
D. the helicase rewinding the DNA
E. the length of the operon

39. Base modifications in rRNA, tRNA, and mRNA mainly involve
A. transesterification
B. methylation
C. amidation
D. base hydrolysis
E. glycosylation

40. Besides the many proteins, what best describes the reagents (substrates, energy sources, building blocks, & co-factors) needed for complete DNA replication.
A. magnesium, NTP's, ddNTP's, single stranded DNA
B. NTP's, dNTP's, magnesium
C. zinc, NTP's, dNTP's, double stranded DNA
D. NTP's, dNTP's, double stranded DNA, magnesium
E. NTP's and magnesium

41. In comparison to DNA polymerase, RNA polymerase differs in the following ways.
A. Has a 3' to 5' exonuclease
B. Uses dNTP's instead of NTP's

 print name:_____

C. Is more accurate
D. Is slower
E. None of the above

42. How many possible DNA sequences can code for the polypeptide GAW (just the coding region)?
A. 24
B. 288
C. 9
D. 200
E. 1

43. If you had only one tRNA synthetase per amino acid, would a cell be viable? And why?
A. Yes - each amino acid is represented
B. No - the code is degenerate
C. Yes - synthetases are not important to translational fidelity
D. No - the nonsense codons would prematurely truncate proteins
E. No - the concentration of tRNA would not be high enough

 print name:_____