FACULTY OF SCIENCE

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| DEPARTMENT OF BIOCHEMISTRY |  |
| MODULE | BIC3A10 (MOLECULAR BIOLOGY) |
| CAMPUS | APK |
| EXAM | JUNE 2016 |

DATE: 09/06/2016
SESSION: 08h30-11h30

| ASSESSOR(S) | DR MG TLOU |
| :--- | ---: |
|  | DR LA PIATER |

EXTERNAL MODERATOR DR DJ OPPERMAN

DURATION 3 HOURS
MARKS
100

NUMBER OF PAGES: 5 PAGES

INSTRUCTIONS: ANSWER ALL THE QUESTIONS

## QUESTION 1

### 1.1 You are given the information below.

| Alternative Sigma Factors of E. coli |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Sigma Factor | Name |  | Consensus sequences |  |  |
|  |  |  | -35 | Spacing | -10 |
| Housekeeping | $\sigma^{70}$ | RpoD | TTGACA | 16-18 | TATAAT |
| Stationary phase | $\mathbf{\sigma}^{38}$ | RpoS | CCGGCG | 16-18 | CTATACT |
| Nitrogen control | $\sigma^{54}$ | RpoN | TTGGNA | 6 | TTGCA |
| Flagellar motion | $\mathrm{\sigma}^{28}$ | FliA | CTAAA | 15 | GCCGATAA |
| Heat shock | $\sigma^{32}$ | RpoH | CTTGAA | 13-15 | CCCCATNT |
| Extracytoplasmic heatshock | $\mathbf{\sigma}^{24}$ | RpoE | GAACTT | 16 | TCTGAT |

## FEATURES

source

Location/Qualifiers
1..1890
/organism="Escherichia coli str. K12 substr. W3110"
/mol_type="genomic DNA"
/strain="K12"
/isolate="W3110"
/db_xref="taxon:316407"
/map="485 k.bp"
/clone="phage 150"
/clone_lib="Kohara"
protein_bind
14..19
/note="putative NR I (NtrC) consensus binding site"
/bound moiety="NtrC"
repeat_region
protein_bind
promoter

CDS
21..63
/rpt_type=inverted
38..52
/note="putative NRI (NtrC) consensus binding site"
/bound_moiety="NtrC"
105..131
/note="RNA polymerase sigma-N (sigma-54) consensus binding site"
175..513
/gene="glnK"
175..513
/gene="glnK"

ORIGIN
1 aatatttcat cgttggtgca aaaatgtaac gcactgtgca ctgtcatagt gcgttttcat
61 tttcaaactt cttaacttcc tgctctcttt ctcgtttttc atttctggct caccgcttgc
121 aatacctacc atcgtgtagc agaaccatta ccgaattctg accggagggg atctatgaag
181 ctggtgaccg tgataatcaa accattcaag ctggaagacg ttcgtgaagc gttatcttcc
241 attggtattc agggcctgac cgtcaccgaa gtgaaaggtt tcgggcgtca gaaagggcat
301 gccgagctgt accggggggc ggaatacagc gtcaatttcc tgccaaaagt aaaaattgat
361 gtggcgattg ctgatgacca actcgatgaa gtgatcgata tcgtcagtaa ggcggcttac
421 accggaaaaa ttggcgacgg caaaatcttc gtcgctgaat tgcaacgcgt cattcgtatt
481 cgtaccggcg aagccgacga agcggcgctg taatctctgg cacacagcaa caggaacgaa
541 aaatgaagat agcgacgata aaaactgggc ttgcttcact ggcgatgctt ccgggactgg
601 taatggctgc acctgcggtg gccgataaag ccgacaatgc gtttatgatg atttgtactg

### 1.1.1 Discuss the strength of the promoter in detail using the information.

1.1.2 Give the nucleotide numbers of the start and stop codons.
1.2 What is the significance of using the BLAST program and how are the outputs results interpreted?
1.3 Infer the function of ProteinX given your knowledge on the output parameters following alignment.
R.glutinisEPHprotein R.toruloidesEPHprotein R.araucariaeEPH1protein ProteinX
R.glutinisEPHprotein R.toruloidesEPHprotein R.araucariaeEPH1protein ProteinX
R.glutinisEPHprotein R.toruloidesEPHprotein R.araucariaeEPH1protein ProteinX
R.glutinisEPHprotein R.toruloidesEPHprotein R.araucariaeEPH1protein ProteinX

MATHTFASPPTRFTVDIPQSELDELHSRLDKTRWPATEIVPEDG--TDDP 48 MATHTFASPPTRFTVDIPQSELDELHSRLDKTRWPATEIVPEDG--TDDP 48 MATHTFASPPTRFTVDIPQSELDELHSRLDKTRWPATEIVPEDG--TDDP 48 MSEHSFEAPPQPFTVDFAP-HIEDLHRRLDNARWPTQEIVPVDVSETEHH 49 *: *:* : ** ****: . : : : ** ***: : ***: **** * *: .

TAFGLGAGPTLPLMKELAKGWREFDWKKAQDHLNTFEHYMVEIEDLSIHF 98 TAFGLGAGPTLPLMKELAKGWREFDWKKAQDHLNTFEHYMVEIEDLSIHF 98 TAFGLGAGPTLPLMKELAKGWREFDWKKAQDHLNTFEHYMVEIEDLSIHF 98 NAFGLGMGPQLNLMKELANGWRAFDQSALQDHLNSFNNWKVEIEGLSIHF 99

LHHRSTRPNAVPLILCHGWPGHFGEFLNVIPLLTEPSDPSAQAFHVVAPS 148 LHHRSTRPNAVPLILCHGWPGHFGEFLNVIPLLTEPSDPSAQAFHVVAPS 148 LHHRSTRPNAVPLILCHGWPGHFGEFLNVIPLLTEPSDPSAQAFHVVAPS 148 LHHRSTRAGALPLILCHGWPGGYHEFLHVVQLLTEPEGADAQAFHLVVPS 149 *******..*:********** : ***:*: *****....*****:***

MPGYAWSLPPPSSKWNMPDTARVFDKLMTGLGYEKYMAQGGDWGSIAARC 198 MPGYAWSLPPPSSKWNMPDTARVFDKLMTGLGYEKYMAQGGDWGSIAARC 198 MPGYAWSLPPPSSKWNMPDTARVFDKLMTGLGYEKYMAQGGDWGSIAARC 198 MPGYAFSSPPPTAKWGMEDTARVFDKLMTGLGYNKYVAQGGDWGSITARC 199
$\star \star \star * *: * * * *: ~: ~ * * . * * * * * * * * * * * * * * * *: * *: * * * * * * * * *: * * *$

### 1.4 During gene annotation, what do you understand by the following specific nucleotide numbers?

CDS join(101....116,122....132)
1.5 Discuss the difference between the two outputs below following splicing of a gene and translation using the Expacy tool.

[^0]```
3'5' Frame 1
S G L V R Q Q D P H R L P Y V V L G E D L G L L Q R R E V P S S I L C C I L V P P Q V S G S A S
I A F F G R E Q L V G K V G Q S K V V R Q L V P P R R D D E E E G R E V R R V E S V W Q E G G G A N R
A R E P V D R E C R E K S F F A I E G C V R Met L D S S L V N N A R N H L L A A N P R E Q T N R T
I V Q A V R R R A R R Q V L H G G V V G R A A L L D I I G H A A L L N I I G P P L I R R Q D K A R H P
V Q K C A R V E H V E R E R R R G N R A E V E V D S D D A V L L V Q R T Stop A A R R D R P P
V T A L G R I L G V T Stop P R H E L V E F H A S R V L H H A P P F C R L G R R R G E G V T R H G
R H D D Met E G P R P L I L G L R E A L Stop D V Q E L V V A A R P A V A Q D E R E R I G
A R R R V V Q E V D V E T L D L L D A I V L V G V E V V L Q L L L L V L A P P F L R E L L H E
G E A G T S A E S E C A V IN S V I I H I V V G H H H V V F R P P A G S S I I E T A V Q V I Y IL G R K V
D V V G C R R C S K G Met G S H
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## QUESTION 2

Briefly discuss any 4 forces that stabilize nucleic acid.

## QUESTION 3

3.1 Compare all steps of replication (initiation, elongation, termination, primer removal) in prokaryotes with that in eukaryotes.

## QUESTION 4

4.1 Briefly discuss the two important events that must occur before translation initiation can take place in bacteria.
4.2 List the 5 vital functions of the ribosomes.
4.3 How is the initiation codon, identified by the ribosomes during translation in prokaryotes (3) and eukaryotes (2)?
4.4 Discuss of the formation of the 70S initiation complex.
4.5 Describe the steps involved in the elongation cycle of translation.
5.1 Give a detailed discussion on the positive control of the lac operon.
5.2 Present a model to explain negative control of the trp operon in E. coli.
5.3 How is trp attenuation overridden in E. coli when tryptophan is scarce?

QUESTION 6
6.1 The following statement is in incorrect. Rewrite the correct version.
"In E. coli transcription is initiated by the binding of the RNAP core enzyme to the ShineDelgarno sequence of the DNA coding strand which lies downstream of the initiation site."
6.2 "In E. coli rrn promoters are also regulated by a pair of small molecules: The initiating NTP (the iNTP) and an alarmone, guanosine 5'-diphosphate 3'-diphosphate (ppGpp)". Briefly discuss the role played by the small molecules in the regulation of the rrn promoters.
6.3 Use a diagram, or describe in words, the exon splicing reaction involving the lariat structure.


[^0]:    5'3' Frame 1
     H G E H G A F G L G A G P S L A L Met K E L A A Q E W R G Q D Q K Q L Q D H L N S Y K N Y R
    
    
    
    
    
     FA L S N F F P D E L F T P E E R D A R R T G N L R W Y K D A E D G G G H F A A L E K P E V A E H V R E A Met $G V L I S N$ Q A Stop

