UNIVERSITY OF OSLO

Faculty of Mathematics and Natural Sciences

Exam in: **MBV2010 Molecular Biology**

Day of exam: **June 5, 2008**

Exam hours: **9:00-12:00 (3 hours)**

This examination paper consists of **1** page.

Appendices: **None**

Permitted materials: **None**

Make sure that your copy of this examination paper is complete before answering.

Numbers in brackets indicate the maximum number of points for each question. The maximum number of points for the entire exam is 100.

1. In which molecular processes are the following proteins involved?

DnaC	Replication
Cohesins	Replication
Photolyase	DNA repair
UvrC	DNA repair
MutS	DNA repair
Dicer	RNA processing (degradation)
DNA ligase IV	DNA repair
DNA polymerase δ	Replication
TRAP	Transcription
GreA	Transcription

(10)

2. a) List all the proteins involved in translation in prokaryotes and explain briefly (in 1-2 sentences) their functions. (pages 396-406) (15)

aminoacyl tRNA synthetase:	links amino acids to tRNAs
IF1, IF2, and IF3:	initiation of translation
(Proteins in small and large subunits of ribosomes)	
Elongation factors (EF) 1A, 1B, and EF-2:	elongation of translation
Release factor(RF)1, RF2, and RF3:	release of polypeptide
Ribosome recycling factor (RRF):	dissociation of ribosomal subunits

b) Describe how polypeptides can be generally processed after synthesis. (15)
(pages 406-414, Figure 13.24)
Folding: chaperones, chaperonins
Proteolytic cleavage: end processing, polyprotein processing, Figure 13.29
Chemical modification: Table 13.6
Intein splicing: Figure 13.35

3. a) Name at least 2 **physical mutagens** and describe their effect on DNA. (5)
(pages 514-515)
UV radiation: crosslinking of T residues, formation of cyclobutyl dimers
Ionizing radiation: double strand breaks, nucleotide damage
Heat: cleavage of ß-N-glycosidic bonds leading to a baseless site

b) Explain how DNA damage caused by the physical mutagens named in 3.a) is repaired. (5)
Cyclobutyl dimers: photolyase (page 525) or nucleotide excision repair (page 533).
Double strand breaks: non-homologous end joining (pages 530-531) or homologous recombination (pages 546-549).
Nucleotide damage: base excision repair (pages 526-527), nucleotide excision repair (page 533).
Baseless site: base excision repair (pages 526-527).

c) Describe the **short patch nucleotide excision repair system** of *E. coli*. (10)
(pages 527-528)
!. UvrAB complex binds to damaged nucleotide.
2. UvrA leaves the complex and UvrC attaches.
3. DNA is cut by UvrB and UvrC, and segment (usually 12 nucleotides) with damaged nucleotide is removed (by DNA helicase).
4. Synthesis and ligation of new DNA by DNA polymerase and DNA ligase.

4. a) Explain the reasons for the diversity of immunoglobulin genes. (20)
(pages 439-441, Figures 14.17-14.20)
Immunoglobulins consist of heavy and light chains which are both composed of variable and constant amino acid sequences (Figure 14.7). In early B-lymphocyte (or T-cell) development the genes for the immunoglobulin proteins are assembled by recombination from gene segments that code for the variable and constant portions of the immunoglobulins. The variable (V) gene segments are linked to short sequences called diverse (D) segments and joined with (J) segments located upstream of the DNA coding for the constant segments (Figures 14.18 and 14.19). In humans each B-lymphocyte cell has about 125 V, 27 D, and 9 J gene segments to choose from for assembling its own individual immunoglobulin gene. When transcribed the mRNAs containing the V, D, and J sequences are linked by alternative splicing to any of the 11 C segments resulting in additional variability in the final immunoglobulin protein. Thus combining different V, D, and J segments by recombination and linking them to different C segments by alternative splicing in different B-lymphocytes results in

millions of different cell lines expressing millions of different immunoglobulins. Additional variability comes from immunoglobulin class switching (page 440) and hypermutations (pages 521-522, Figure 16.17) in the variable regions of the immunoglobulin genes.

b) What is **diauxie**? Describe its molecular basis in an example. (20)
(pages 429-432)
It's called diauxie when a bacterium provided with two different sugars for growth metabolizes first one of the sugars and uses the second sugar only when the first sugar is used up. Diauxie is visible in a two step growth curve corresponding to the use of the two sugars (Figure 14.7).
Example: the use of glucose and lactose by *E. coli*. Glucose indirectly prevents binding of the catabolite activator protein (CAP) to the DNA upstream of the *lac* operon by causing dephosphorylation of protein IIA^{Glc}. Dephosphorylated IIA^{Glc} inhibits adenylate cyclase, the enzyme that catalyzes the formation of cyclic AMP (cAMP) from ATP, such that the cAMP level in the cell is low. cAMP is required by the catabolite activator protein for binding to DNA. Binding of the catabolite activator protein to the DNA upstream of the *lac* operon is required for transcription of the *lac* operon, even when the *lac* repressor is inactive.
Therefore, in the presence of glucose and lactose, glucose indirectly (via protein IIA^{Glc} and low levels of cAMP) prevents binding of the catabolite activator protein and blocks transcription of the *lac* operon. When glucose is used up, cAMP levels increase in the cells (because adenylate cyclase is no longer inhibited via IIA^{Glc}) and the catabolite activator protein binds to its site on the DNA upstream of the *lac* operon and activates transcription. In addition, lactose induces transcription of the *lac* operon by binding to the *lac* repressor and inactivating it.