UNIVERSITETET I OSLO

Det matematisk-naturvitenskapelige fakultet

Exam in **MBV4230 Eukaryotic transcription factors**
Day of exam: **Wednesday 26.05.2004**
Exam hours: **13 - 16**
This examination paper consists of 3 pages.
Appendices:
Permitted materials:

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

All questions are given in English, but you may choose yourself in what language (Norwegian or English) you prefer to answer.

I

When studying eukaryotic transcription, one encounters a long list of abbreviations. Below is a selection of twelve of these. Write out the full names that these abbreviations refer to.

1. TBP
2. CTD
3. HAT
4. STAT
5. HMT
6. NR
7. N-CoR
8. CPSF
9. IKK
10. POU
11. FACT
12. ARC

II

Transcription activators are grouped into families, usually based on the structure of their DNA-binding domains (DBDs). Below is a list of 10 names of transcription factors as well as 5 families. Place each factor into the correct family:

The transcription factors to classify:

1. TFIIIA
2. Myc
3. RXR
4. E2F1
5. GAL4
6. PPARγ
7. p50/p65
8. c-Jun/c-Fos
9. CREB
10. ER (estrogen receptor)

The families:

A. Helix-loop-helix (bHLH) proteins
B. Zinc finger proteins
C. Rel family
D. Nuclear receptor
E. Leucine zipper (bZIP)

For simplicity you may answer by a list of the form 3C, 8B etc (examples are not correct combinations).

III

One of the GTFs (general transcription factors) has enzymatic activities – which GTF and what type of enzymatic activity?

TAFs are subunits of the TFIID complex. The largest subunit called $TAF_{II}250$ has been found to harbour several distinct enzymatic activities. List these activities.

IV

The "Histone code hypothesis" has become a key to understand how the transcriptional apparatus interacts with chromatin. Describe briefly key elements in this hypothesis, including how code patterns are generated and how they are read (decoded).

V

Several components in or associated with a pre-initiation complex (PIC) become subject to ubiquitylation during the process of transcriptional activation. List some transcriptional targets of this modification and select one example where you explain in more detail its presumed mechanism of action.

VI

ATP is one of the substrates during RNA synthesis by RNA polymerase II, but other ATP-dependent processes linked to transcription initiation also consume ATP. List two examples of the latter and state very briefly what kind of process is taking place here when ATP is consumed.

VII

Several types of signalling (warning signs of DNA damage, oncogenic activation etc) may lead to activation of p53. Limiting your focus to the p53 protein itself, what kind of changes are taking place when p53 is undergoing activation. During this process the interaction of p53 with another key protein is modulated. What is this protein and how is the interaction modulated as a result of signalling?

VIII

Describe briefly the key elements of signalling pathways involving IKK and NF-κB.

IX

RXR acts as a partner for nuclear receptors such as Vitamin D receptor (VDR), thyroid hormone receptor (TR) and PPAR. These dimers bind to related cis-elements in responsive promoters. Explain how discrimination between responsive elements for these factors is obtained? How is it possible to change a promoter responsive to vitamin D into one that is responsive to thyroid hormone using only a simple mutation?