UNIVERSITI TEKNOLOGI MARA (UiTM)

# COMPUTATIONAL PREDICTION OF EIGHT E2F TRANSCRIPTION FACTORS (E2F1-E2F8) IN *Mus Musculus*

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**Dissertation submitted in partial fulfillment of the requirements for the PH 210 Bachelor of Pharmacy (Honours)**

Faculty of Pharmacy

November 2009

## Acknowledgements

I would like to thank my supervisor Miss Ruzianisra Binti Mohamed for her enthusiasm, support, encouragement, technical expertise and availability at any time to discuss ideas and results throughout my Degree candidature.

Thank you to all my classmates especially Mohd Noor Asri and housemates for your kindness, friendship and help. To all the people in Faculty of Pharmacy, thank you for making my time at University Teknologi Mara (UiTM) such a pleasure.

A special thank you to my family whose pride, assistance and encouragement extended towards me during my candidature.

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# ABSTRACT

E2F was originally discovered as a cellular component that is required for the early region transforming protein (E1A) of adenovirus to mediate transcriptional activation of the viral E2 promoter. Subsequent studies have shown that E2F controls the transcription of cellular genes that are essential for cell division, such as enzymes involved in the biosynthesis of nucleotides. E2F transcription factors play essential role in cell proliferation control by linking the activities of the cell cycle machinery with the transcriptional regulation of genes whose products are for the S-phase entry and DNA synthesis. E2F of *Mus Musculus* has eight groups, namely from E2F1 to E2F8. They are made from more than 200 amino acids residues, which is the lowest is E2F6 with 272 amino acids residues and the highest is E2F7 with 904 amino acids residues. The cladogram indicates that isoforms can be paired into three phylogenetic subgroups. It is predicted that all E2F groups located in nuclear except E2F6 that located in mitochondrial. Using information from Protein Data Bank (PDB) to compare similarity of amino acid sequences of *Mus Musculus* E2F family members; it is found that E2F4 has 100% similarity with PDB ID of 1CF7, while the rest of the E2F family members have similarity between 39% to 100%. Because of the highest similarity that E2F4 with PDB ID of 1CF7 has compare to the other member, therefore the tertiary structure of 1CF7 is taken to be the template to predict the tertiary structure of E2F family members. These prediction analyses demonstrated significant findings on the molecular similarity relationship between the eight E2F transcription factors. With all these findings, it will be a useful tool to generate more ideas about the functions of E2F transcriptional factors in *Mus Musculus*.

# CHAPTER ONE

# INTRODUCTION

## 1.1 INTRODUCTION TO E2F

E2F transcription factors play essential role in cell proliferation control by linking the activities of the cell cycle machinery with the transcriptional regulation of genes whose products are for the S-phase entry and DNA synthesis. The DNA-binding sites of E2F (TTTC/GG/CCGC/G) are found in the promoters of genes encoding enzymes directly involved in DNA synthesis such as Dyhydrofolate Reductase (DHFR), Thymidinekinase, HsOrc1, and DNA polymerase alpha (Mudryj et al., 1990, Hiebert et al., 1991, Dalton, 1992, Slansky et al., 1993, Dou et al., 1994, Ohtani et al., 1996 and Johnson et al., 1998)

E2F factors appear to be key components in a cell cycle checkpoint that determines whether a cell will arrest in G1 or enter into S-phase. Multiple mitogenic signaling pathways, as well as growth inhibitory signals, ultimately converge upon E2F at this G1 phase checkpoint. In addition to regulating S-phase entry, E2F factors have also been implicated in regulating growth inhibition, differentiation, apoptosis and oncogenic transformation. The E2F family appears to accomplish these diverse activities through